% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLF18, complete sequence [Arabidopsis thaliana]
Seq. No.	133808
Contig ID	92154_1.R1010
5'-most EST	jC-atXLIB327432P2f06a2
Method	BLASTX
NCBI GI	g3402683
BLAST score	323
E value	2.0e-29
Match length	157
% identity	49
NCBI Description	(AC004697) patatin-like protein [Arabidopsis thaliana]
Seq. No.	133809
Contig ID	92156_1.R1010
5'-most EST	jC-atXLIB327432P2f08a1
Method	BLASTN
NCBI GI	g4567259
BLAST score	296
E value	1.0e-165
Match length	545
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F3K23 genomic sequence, complete sequence
Seq. No.	133810
Contig ID	92175_1.R1010
5'-most EST	jC-atXLIB327432P2g10a2
Method	BLASTN
NCBI GI	g3241926
BLAST score	282
E value	1.0e-157
Match length	396
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSG15, complete sequence [Arabidopsis thaliana]
Seq. No.	133811
Contig ID	92177_1.R1010
5'-most EST	jC-atXLIB327432P2g11a2
Seq. No.	133812
Contig ID	92191_1.R1010
5'-most EST	jC-atXLIB327432P3a03a1
Seq. No.	133813
Contig ID	92194_1.R1010
5'-most EST	jC-atXLIB327432P3a05a1
Method	BLASTN
NCBI GI	g1785673
BLAST score	134
E value	4.0e-69
Match length	317
% identity	91
NCBI Description	A.thaliana mitochondrial genome, part A

Seq. No.	133814
Contig ID	92200_1.R1010
5'-most EST	jC-atXLIB327440P1c12a1
Method	BLASTX
NCBI GI	g1903034
BLAST score	569
E value	2.0e-58
Match length	157
% identity	67
NCBI Description	(X94625) amp-binding protein [Brassica napus]

Seq. No.	133815
Contig ID	92208_1.R1010
5'-most EST	jC-atXP4C86D3T7015a1
Method	BLASTN
NCBI GI	g3063438
BLAST score	140
E value	2.0e-72
Match length	599
% identity	99
NCBI Description	Complete sequence of Arabidopsis F22013, complete sequence [Arabidopsis thaliana]

Seq. No.	133816
Contig ID	92219_1.R1010
5'-most EST	jC-atXLIB327432P3b10a1
Method	BLASTN
NCBI GI	g2244829
BLAST score	240
E value	1.0e-132
Match length	416
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	133817
Contig ID	92223_1.R1010
5'-most EST	jC-atXLIB327432P3b12a1
Method	BLASTN
NCBI GI	g2924732
BLAST score	368
E value	0.0e+00
Match length	497
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUA2, complete sequence [Arabidopsis thaliana]

Seq. No.	133818
Contig ID	92228_1.R1010
5'-most EST	jC-atXLIB327432P3c04a1
Method	BLASTX
NCBI GI	g1046225
BLAST score	1122
E value	1.0e-123
Match length	221
% identity	99

NCBI Description	(U21952) ethylene response sensor [Arabidopsis thaliana] >gi_2623308 (AC002409) ethylene response sensor (ERS) [Arabidopsis thaliana] >gi_1584365_prf__2122405A ERS gene [Arabidopsis thaliana]

Seq. No.	133819
Contig ID	92228_2.R1010
5'-most EST	jC-atXP31C145F13T7d2
Method	BLASTX
NCBI GI	g1046225
BLAST score	784
E value	9.0e-84
Match length	171
% identity	89
NCBI Description	(U21952) ethylene response sensor [Arabidopsis thaliana] >gi_2623308 (AC002409) ethylene response sensor (ERS) [Arabidopsis thaliana] >gi_1584365_prf__2122405A ERS gene [Arabidopsis thaliana]

Seq. No.	133820
Contig ID	92228_3.R1010
5'-most EST	jC-atXP31C144G13T7d2
Method	BLASTX
NCBI GI	g1046225
BLAST score	552
E value	1.0e-56
Match length	132
% identity	83
NCBI Description	(U21952) ethylene response sensor [Arabidopsis thaliana] >gi_2623308 (AC002409) ethylene response sensor (ERS) [Arabidopsis thaliana] >gi_1584365_prf__2122405A ERS gene [Arabidopsis thaliana]

Seq. No.	133821
Contig ID	92248_1.R1010
5'-most EST	jC-atXLIB327432P3d04a1
Method	BLASTN
NCBI GI	g3869069
BLAST score	368
E value	0.0e+00
Match length	562
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence [Arabidopsis thaliana]

Seq. No.	133822
Contig ID	92250_1.R1010
5'-most EST	jC-atXLIB327432P3d05a1
Method	BLASTX
NCBI GI	g2911078
BLAST score	178
E value	8.0e-13
Match length	76
% identity	49
NCBI Description	(AL021960) putative protein [Arabidopsis thaliana]

Seq. No.	133823

Contig ID	92258_1.R1010
5'-most EST	jC-atXLIB327432P3d09a1
Method	BLASTX
NCBI GI	g3033400
BLAST score	127
E value	6.0e-26
Match length	88
% identity	68
NCBI Description	(AC004238) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No.	133824
Contig ID	92288_1.R1010
5'-most EST	jC-atXP92CH4B11T7096d1
Method	BLASTN
NCBI GI	g1785673
BLAST score	570
E value	0.0e+00
Match length	609
% identity	99
NCBI Description	A.thaliana mitochondrial genome, part A

Seq. No.	133825
Contig ID	92288_2.R1010
5'-most EST	jC-atXLIB327432P3f02b1
Method	BLASTN
NCBI GI	g1785673
BLAST score	635
E value	0.0e+00
Match length	742
% identity	92
NCBI Description	A.thaliana mitochondrial genome, part A

Seq. No.	133826
Contig ID	92299_1.R1010
5'-most EST	jC-atXLIB327432P3f09a1
Method	BLASTX
NCBI GI	g4467128
BLAST score	812
E value	7.0e-87
Match length	205
% identity	82
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]

Seq. No.	133827
Contig ID	92305_1.R1010
5'-most EST	jC-atXLIB327432P3g01a1
Method	BLASTX
NCBI GI	g2980785
BLAST score	691
E value	9.0e-73
Match length	147
% identity	93
NCBI Description	(AL022198) SERINE CARBOXYPEPTIDASE II - like protein [Arabidopsis thaliana]

Seq. No.	133828

Contig ID	92318_1.R1010
5'-most EST	jC-atXLIB327432P3g09a1
Method	BLASTX
NCBI GI	g1653245
BLAST score	266
E value	4.0e-23
Match length	105
% identity	50
NCBI Description	(D90912) hypothetical protein [Synechocystis sp.]

Seq. No.	133829
Contig ID	92322_1.R1010
5'-most EST	jC-atXLIB327432P3g11a1

Seq. No.	133830
Contig ID	92338_1.R1010
5'-most EST	jC-atXLIB327440P3d08a1
Method	BLASTN
NCBI GI	g4688614
BLAST score	329
E value	0.0e+00
Match length	414
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for D-type cyclin

Seq. No.	133831
Contig ID	92346_1.R1010
5'-most EST	jC-atXLIB327432P3h12a1

Seq. No.	133832
Contig ID	92374_1.R1010
5'-most EST	jC-atXLIB327432P4b05a1
Method	BLASTX
NCBI GI	g2829885
BLAST score	252
E value	3.0e-47
Match length	102
% identity	94
NCBI Description	(AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	133833
Contig ID	92380_1.R1010
5'-most EST	jC-atXLIB327432P4b08a1
Method	BLASTN
NCBI GI	g2351069
BLAST score	602
E value	0.0e+00
Match length	779
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSH12, complete sequence [Arabidopsis thaliana]

Seq. No.	133834
Contig ID	92382_1.R1010
5'-most EST	jC-atXLIB327432P4b09a1
Method	BLASTX
NCBI GI	g140372

BLAST score	154
E value	9.0e-10
Match length	79
% identity	43
NCBI Description	HYPOTHETICAL 86.0 KD PROTEIN IN GLK1-SRO9 INTERGENIC REGION >gi_83159_pir__S19367 hypothetical protein YCL039w - yeast (Saccharomyces cerevisiae)

Seq. No.	133835
Contig ID	92386_1.R1010
5'-most EST	jC-atXLIB327432P4b11a1
Method	BLASTX
NCBI GI	g4454032
BLAST score	436
E value	5.0e-43
Match length	104
% identity	86
NCBI Description	(AL035394) putative protein [Arabidopsis thaliana]

Seq. No.	133836
Contig ID	92390_1.R1010
5'-most EST	jC-atXLIB327432P4c01a1
Method	BLASTX
NCBI GI	g3859715
BLAST score	252
E value	2.0e-21
Match length	119
% identity	43
NCBI Description	(AL033501) transketolase I [Candida albicans]

Seq. No.	133837
Contig ID	92392_1.R1010
5'-most EST	jC-atXLIB327432P4c02a1
Method	BLASTN
NCBI GI	g2262155
BLAST score	260
E value	1.0e-144
Match length	395
% identity	100
NCBI Description	DNA sequence of Arabidopsis thaliana BAC F5J6 from chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No.	133838
Contig ID	92394_1.R1010
5'-most EST	jC-atXLIB327432P4c03a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	50
E value	6.0e-19
Match length	66
% identity	94
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	133839
Contig ID	92419_1.R1010
5'-most EST	jC-atXLIB327432P4d04a1

Method	BLASTN
NCBI GI	g2462264
BLAST score	45
E value	5.0e-16
Match length	53
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	133840
Contig ID	92425_1.R1010
5'-most EST	jC-atXLIB327432P4d08a1
Method	BLASTN
NCBI GI	g4220638
BLAST score	61
E value	3.0e-25
Match length	227
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIF21, complete sequence [Arabidopsis thaliana]

Seq. No.	133841
Contig ID	92425_2.R1010
5'-most EST	jC-atXP96CH2C6T7b1
Method	BLASTN
NCBI GI	g4220638
BLAST score	77
E value	5.0e-35
Match length	263
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIF21, complete sequence [Arabidopsis thaliana]

Seq. No.	133842
Contig ID	92429_1.R1010
5'-most EST	jC-atXLIB327432P4d10a1
Method	BLASTX
NCBI GI	g2829880
BLAST score	48
E value	2.0e-40
Match length	93
% identity	91
NCBI Description	(AC002396) glucose-6-phosphate 1-dehydrogenase [Arabidopsis thaliana]

Seq. No.	133843
Contig ID	92435_1.R1010
5'-most EST	jC-atXLIB327432P4e01a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	54
E value	2.0e-21
Match length	66
% identity	95
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	133844

Contig ID	92440_1.R1010
5'-most EST	jC-atXLIB327432P4e04a1
Method	BLASTX
NCBI GI	g4314355
BLAST score	183
E value	3.0e-13
Match length	125
% identity	33
NCBI Description	(AC006340) unknown protein [Arabidopsis thaliana]

Seq. No.	133845
Contig ID	92444_1.R1010
5'-most EST	jC-atXLIB327432P4e06a1
Method	BLASTN
NCBI GI	g3047100
BLAST score	374
E value	0.0e+00
Match length	418
% identity	97
NCBI Description	Arabidopsis thaliana BAC F6N23

Seq. No.	133846
Contig ID	92460_1.R1010
5'-most EST	jC-atXLIB327432P4f04a1
Method	BLASTX
NCBI GI	g3702323
BLAST score	265
E value	6.0e-23
Match length	111
% identity	54
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	133847
Contig ID	92465_1.R1010
5'-most EST	jC-atXP70C221E5T7060a1
Method	BLASTN
NCBI GI	g3128143
BLAST score	297
E value	1.0e-166
Match length	405
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTI20, complete sequence [Arabidopsis thaliana]

Seq. No.	133848
Contig ID	92477_1.R1010
5'-most EST	jC-atXLIB327432P4g01a1

Seq. No.	133849
Contig ID	92479_1.R1010
5'-most EST	jC-atXLIB327432P4g02a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	45
E value	6.0e-16
Match length	73
% identity	92

NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds
Seq. No.	133850
Contig ID	92508_1.R1010
5'-most EST	jC-atXLIB327432P4h08a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	50
E value	5.0e-19
Match length	58
% identity	97
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds
Seq. No.	133851
Contig ID	92510_1.R1010
5'-most EST	jC-atXLIB327432P4h09a1
Method	BLASTN
NCBI GI	g2351063
BLAST score	242
E value	1.0e-133
Match length	350
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCL19, complete sequence [Arabidopsis thaliana]
Seq. No.	133852
Contig ID	92535_1.R1010
5'-most EST	jC-atXLIB327433P1a10a1
Method	BLASTN
NCBI GI	g2264302
BLAST score	328
E value	0.0e+00
Match length	438
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC12, complete sequence [Arabidopsis thaliana]
Seq. No.	133853
Contig ID	92552_1.R1010
5'-most EST	g1053282
Method	BLASTX
NCBI GI	g3075398
BLAST score	365
E value	1.0e-34
Match length	111
% identity	76
NCBI Description	(AC004484) unknown protein [Arabidopsis thaliana]
Seq. No.	133854
Contig ID	92552_2.R1010
5'-most EST	jC-atXLIB327433P1b07a1
Method	BLASTN
NCBI GI	g3075383
BLAST score	305
E value	1.0e-171

Match length	408
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T1D16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133855
Contig ID	92556_1.R1010
5'-most EST	jC-atXLIB327433P1b09a1
Method	BLASTN
NCBI GI	g10782
BLAST score	44
E value	2.0e-15
Match length	63
% identity	92
NCBI Description	Tetrahymena pyriformis gene for 26S large subunit ribosomal RNA

Seq. No.	133856
Contig ID	92563_1.R1010
5'-most EST	g2062913
Method	BLASTN
NCBI GI	g4539331
BLAST score	370
E value	0.0e+00
Match length	485
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22I13 (ESSA project)

Seq. No.	133857
Contig ID	92571_1.R1010
5'-most EST	jC-atXLIB327439P3f04a2

Seq. No.	133858
Contig ID	92579_1.R1010
5'-most EST	jC-atXLIB327433P1c09a1
Method	BLASTN
NCBI GI	g4756963
BLAST score	544
E value	0.0e+00
Match length	572
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23 (ESSA project)

Seq. No.	133859
Contig ID	92606_1.R1010
5'-most EST	jC-atXLIB327433P1d12a1

Seq. No.	133860
Contig ID	92675_1.R1010
5'-most EST	jC-atXLIB327433P1g12a1
Method	BLASTN
NCBI GI	g2760316
BLAST score	268
E value	1.0e-149
Match length	352

% identity	95
NCBI Description	The sequence of BAC F1N21 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]
Seq. No.	133861
Contig ID	92703_1.R1010
5'-most EST	jC-atXLIB327433P2a09a1
Method	BLASTX
NCBI GI	g4588001
BLAST score	101
E value	4.0e-28
Match length	82
% identity	77
NCBI Description	(AF085279) hypothetical Ser-Thr protein kinase [Arabidopsis thaliana]
Seq. No.	133862
Contig ID	92712_1.R1010
5'-most EST	jC-atXLIB327433P2b06a1
Method	BLASTN
NCBI GI	g4510323
BLAST score	195
E value	1.0e-105
Match length	528
% identity	96
NCBI Description	Arabidopsis thaliana BAC T7B11 from chromosome IV near 10 cM, complete sequence
Seq. No.	133863
Contig ID	92714_1.R1010
5'-most EST	jC-atXP117C143B7T7a1
Method	BLASTN
NCBI GI	g2264321
BLAST score	414
E value	0.0e+00
Match length	555
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXM12, complete sequence [Arabidopsis thaliana]
Seq. No.	133864
Contig ID	92714_2.R1010
5'-most EST	jC-atX24027Q1E1G11a1
Method	BLASTN
NCBI GI	g2264321
BLAST score	250
E value	1.0e-138
Match length	324
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXM12, complete sequence [Arabidopsis thaliana]
Seq. No.	133865
Contig ID	92715_1.R1010
5'-most EST	jC-atXLIB327433P2b08a1
Method	BLASTN
NCBI GI	g2342717

BLAST score	380
E value	0.0e+00
Match length	464
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T14G11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133866
Contig ID	92719_1.R1010
5'-most EST	jC-atXLIB327433P2b12a1

Seq. No.	133867
Contig ID	92727_1.R1010
5'-most EST	jC-atXLIB327433P2c08a1
Method	BLASTN
NCBI GI	g2191126
BLAST score	271
E value	1.0e-151
Match length	463
% identity	98
NCBI Description	Arabidopsis thaliana BAC IG002N01

Seq. No.	133868
Contig ID	92741_1.R1010
5'-most EST	jC-atXLIB327433P2d11a1

Seq. No.	133869
Contig ID	92746_1.R1010
5'-most EST	jC-atXLIB327433P2e05a1
Method	BLASTN
NCBI GI	g2351065
BLAST score	400
E value	0.0e+00
Match length	412
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHF15, complete sequence [Arabidopsis thaliana]

Seq. No.	133870
Contig ID	92759_1.R1010
5'-most EST	jC-atXLIB327433P2f06a1

Seq. No.	133871
Contig ID	92784_1.R1010
5'-most EST	jC-atXP87CG10A4T7b1
Method	BLASTN
NCBI GI	g1280610
BLAST score	39
E value	3.0e-12
Match length	39
% identity	100
NCBI Description	Arabidopsis thaliana steroid reductase DET2 mRNA, complete cds

Seq. No.	133872
Contig ID	92900_1.R1010
5'-most EST	jC-atXLIB327439P1a09a1

Method	BLASTN
NCBI GI	g4006885
BLAST score	336
E value	0.0e+00
Match length	434
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	133873
Contig ID	92944_1.R1010
5'-most EST	jC-atXLIB327439P1e04a2
Method	BLASTX
NCBI GI	g4314400
BLAST score	155
E value	4.0e-10
Match length	97
% identity	19
NCBI Description	(AC006232) putative selenium-binding protein [Arabidopsis thaliana]

Seq. No.	133874
Contig ID	92948_1.R1010
5'-most EST	jC-atXLIB327439P1e08a1
Method	BLASTN
NCBI GI	g4454447
BLAST score	176
E value	4.0e-94
Match length	293
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133875
Contig ID	92967_1.R1010
5'-most EST	jC-atXLIB327439P1f09a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	46
E value	2.0e-16
Match length	65
% identity	94
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	133876
Contig ID	92974_1.R1010
5'-most EST	g2739659
Method	BLASTX
NCBI GI	g4200165
BLAST score	270
E value	1.0e-23
Match length	70
% identity	74
NCBI Description	(Y16262) neutral invertase [Daucus carota]

Seq. No.	133877

Contig ID	92975_1.R1010
5'-most EST	jC-atXLIB327439P1g08a1
Method	BLASTN
NCBI GI	g2980787
BLAST score	80
E value	7.0e-37
Match length	414
% identity	64
NCBI Description	Arabidopsis thaliana DNA chromosome 4, P1 clone M7J2 (ESSAII project)

Seq. No.	133878
Contig ID	93051_1.R1010
5'-most EST	jC-atXLIB327440P1a06a1

Seq. No.	133879
Contig ID	93057_1.R1010
5'-most EST	jC-atXLIB327440P1a09a1
Method	BLASTX
NCBI GI	g2688842
BLAST score	281
E value	1.0e-24
Match length	92
% identity	59
NCBI Description	(AF004830) serine palmitoyltransferase LCB2 subunit [Cricetulus griseus]

Seq. No.	133880
Contig ID	93059_1.R1010
5'-most EST	jC-atXLIB327440P1a10a1
Method	BLASTX
NCBI GI	g1755162
BLAST score	96
E value	3.0e-03
Match length	96
% identity	48
NCBI Description	(U75192) germin-like protein [Arabidopsis thaliana]

Seq. No.	133881
Contig ID	93068_1.R1010
5'-most EST	jC-atXLIB327440P1b04a1
Method	BLASTX
NCBI GI	g2887288
BLAST score	208
E value	2.0e-16
Match length	58
% identity	67
NCBI Description	(AJ001810) mRNA cleavage factor I 25 kDa subunit [Homo sapiens]

Seq. No.	133882
Contig ID	93077_1.R1010
5'-most EST	jC-atXLIB327440P1c11a1
Method	BLASTN
NCBI GI	g4757395
BLAST score	338
E value	0.0e+00

Match length	406
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L13, complete sequence

Seq. No.	133883
Contig ID	93103_2.R1010
5'-most EST	jC-atXLIB327440P1d06a1
Method	BLASTX
NCBI GI	g3319344
BLAST score	561
E value	1.0e-57
Match length	130
% identity	85
NCBI Description	(AF077407) contains similarity to UDP-glucoronosyl and UDP-glucosyl transferases (Pfam: UDPGT.hmm, score: 85.94) [Arabidopsis thaliana]

Seq. No.	133884
Contig ID	93106_1.R1010
5'-most EST	jC-atXLIB327440P1d08a1
Method	BLASTN
NCBI GI	g3641843
BLAST score	122
E value	6.0e-62
Match length	122
% identity	100
NCBI Description	Arabidopsis thaliana SKOR gene

Seq. No.	133885
Contig ID	93121_1.R1010
5'-most EST	jC-atXLIB327440P1e11a1
Method	BLASTX
NCBI GI	g4539303
BLAST score	281
E value	6.0e-25
Match length	69
% identity	78
NCBI Description	(AL049480) putative protein [Arabidopsis thaliana]

Seq. No.	133886
Contig ID	93133_1.R1010
5'-most EST	jC-atXLIB327440P1f09a1
Method	BLASTN
NCBI GI	g2564048
BLAST score	406
E value	0.0e+00
Match length	431
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKD15, complete sequence [Arabidopsis thaliana]

Seq. No.	133887
Contig ID	93177_1.R1010
5'-most EST	jC-atXLIB327440P2b10a1

Seq. No.	133888

Contig ID	93182_1.R1010
5'-most EST	jC-atXP118C143H5T7066a1
Method	BLASTN
NCBI GI	g3600045
BLAST score	309
E value	1.0e-173
Match length	537
% identity	95
NCBI Description	Arabidopsis thaliana BAC F2P3

Seq. No.	133889
Contig ID	93182_2.R1010
5'-most EST	jC-atXLIB327440P2c04a1
Method	BLASTN
NCBI GI	g3600045
BLAST score	300
E value	1.0e-168
Match length	447
% identity	93
NCBI Description	Arabidopsis thaliana BAC F2P3

Seq. No.	133890
Contig ID	93191_1.R1010
5'-most EST	jC-atXLIB327440P2d09a1

Seq. No.	133891
Contig ID	93208_1.R1010
5'-most EST	jC-atXLIB327440P2f07a1
Method	BLASTX
NCBI GI	g2500139
BLAST score	265
E value	5.0e-23
Match length	87
% identity	55
NCBI Description	PEPTIDE CHAIN RELEASE FACTOR 1 (RF-1) >gi_1653916_dbj_BAA18826_ (D90917) peptide chain release factor [Synechocystis sp.]

Seq. No.	133892
Contig ID	93246_1.R1010
5'-most EST	jC-atXLIB327440P4d08a1
Method	BLASTX
NCBI GI	g4006850
BLAST score	378
E value	2.0e-36
Match length	102
% identity	70
NCBI Description	(Z99707) cytochrome like protein [Arabidopsis thaliana]

Seq. No.	133893
Contig ID	93247_1.R1010
5'-most EST	jC-atXLIB327440P4d09a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	40
E value	6.0e-13
Match length	66

% identity	94
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds
Seq. No.	133894
Contig ID	93250_1.R1010
5'-most EST	jC-atXLIB327440P4d11a1
Seq. No.	133895
Contig ID	93281_1.R1010
5'-most EST	jC-atXLIB327401P1b02a1
Method	BLASTN
NCBI GI	g2656030
BLAST score	335
E value	0.0e+00
Match length	414
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUL8
Seq. No.	133896
Contig ID	93282_1.R1010
5'-most EST	jC-atXLIB327401P1a04a1
Method	BLASTN
NCBI GI	g2264314
BLAST score	53
E value	1.0e-20
Match length	196
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQK4, complete sequence [Arabidopsis thaliana]
Seq. No.	133897
Contig ID	93285_1.R1010
5'-most EST	jC-atXLIB327401P1a12a1
Seq. No.	133898
Contig ID	93298_1.R1010
5'-most EST	jC-atXLIB327401P1d07a1
Method	BLASTX
NCBI GI	g1362093
BLAST score	344
E value	3.0e-32
Match length	98
% identity	67
NCBI Description	hypothetical protein (clone TPP15) - tomato (fragment) >gi_924632 (U20595) unknown [Solanum lycopersicum]
Seq. No.	133899
Contig ID	93300_1.R1010
5'-most EST	jC-atXLIB327401P1d09a1
Method	BLASTX
NCBI GI	g2245136
BLAST score	576
E value	2.0e-67
Match length	200
% identity	65

NCBI Description	(Z97344) trehalose-6-phosphate synthase homolog [Arabidopsis thaliana]
Seq. No.	133900
Contig ID	93321_1.R1010
5'-most EST	jC-atXLIB327401P4a02a2
Method	BLASTX
NCBI GI	g3292817
BLAST score	192
E value	2.0e-14
Match length	52
% identity	65
NCBI Description	(AL031018) hypothetical protein [Arabidopsis thaliana]
Seq. No.	133901
Contig ID	93357_1.R1010
5'-most EST	jC-atXLIB327401P2e06a1
Seq. No.	133902
Contig ID	93357_3.R1010
5'-most EST	jC-atXP95CH2B1T7088d1
Method	BLASTX
NCBI GI	g2920706
BLAST score	111
E value	3.0e-29
Match length	252
% identity	34
NCBI Description	(Y13568) beta-xylosidase [Emericella nidulans]
Seq. No.	133903
Contig ID	93357_4.R1010
5'-most EST	g937551
Method	BLASTN
NCBI GI	g2058275
BLAST score	58
E value	9.0e-24
Match length	128
% identity	90
NCBI Description	A.thaliana atran2 gene
Seq. No.	133904
Contig ID	93358_1.R1010
5'-most EST	jC-atXLIB327401P2e07a1
Method	BLASTX
NCBI GI	g112785
BLAST score	214
E value	7.0e-17
Match length	102
% identity	37
NCBI Description	DNA-3-METHYLADENINE GLYCOSIDASE I (3-METHYLADENINE-DNA GLYCOSYLASE I, CONSTITUTIVE) (TAG I) >gi_67508_pir__DGECM1 3-methyladenine DNA glycosylase (EC 3.2.2.-) I - Escherichia coli >gi_43030_emb_CAA27472_ (X03845) TAGI (aa 1-187) [Escherichia coli] >gi_147920 (J02606) 3-methyladenine-DNA glycosylase I (tag) [Escherichia coli] >gi_466687 (U00039) 3-methyladenine DNA glycosylase I, constitutive [Escherichia coli] >gi_1789971 (AE000432)

	3-methyl-adenine DNA glycosylase I, constitutive [Escherichia coli]
Seq. No.	133905
Contig ID	93363_1.R1010
5'-most EST	jC-atXLIB327401P2f10a1
Method	BLASTN
NCBI GI	g4218109
BLAST score	224
E value	1.0e-123
Match length	324
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F16A16 (ESSAII project)
Seq. No.	133906
Contig ID	93381_1.R1010
5'-most EST	jC-atXLIB327401P2h11a1
Method	BLASTX
NCBI GI	g4531444
BLAST score	289
E value	8.0e-26
Match length	68
% identity	87
NCBI Description	(AC006224) putative protein kinase [Arabidopsis thaliana]
Seq. No.	133907
Contig ID	93475_1.R1010
5'-most EST	jC-atXLIB327404P4g02a1
Method	BLASTN
NCBI GI	g4510338
BLAST score	128
E value	1.0e-65
Match length	271
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F2H17 genomic sequence, complete sequence
Seq. No.	133908
Contig ID	93476_1.R1010
5'-most EST	jC-atXLIB327404P4g03a1
Method	BLASTN
NCBI GI	g3128139
BLAST score	132
E value	7.0e-68
Match length	455
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIK19, complete sequence [Arabidopsis thaliana]
Seq. No.	133909
Contig ID	93484_1.R1010
5'-most EST	jC-atXLIB327404P4g08a1
Method	BLASTN
NCBI GI	g2244747
BLAST score	333
E value	0.0e+00

Match length	376
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	133910
Contig ID	93552_1.R1010
5'-most EST	jC-atXLIB327405P3a02a1

Seq. No.	133911
Contig ID	93556_1.R1010
5'-most EST	jC-atXLIB327405P3a04a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	53
E value	1.0e-20
Match length	57
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	133912
Contig ID	93558_1.R1010
5'-most EST	jC-atXP12C99P1T7031a1
Method	BLASTN
NCBI GI	g2264312
BLAST score	576
E value	0.0e+00
Match length	635
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK16, complete sequence [Arabidopsis thaliana]

Seq. No.	133913
Contig ID	93572_1.R1010
5'-most EST	jC-atXLIB327405P3a12a1
Method	BLASTX
NCBI GI	g2388582
BLAST score	401
E value	8.0e-39
Match length	81
% identity	94
NCBI Description	(AC000098) Contains similarity to Rattus O-GlcNAc transferase (gb_U76557). [Arabidopsis thaliana]

Seq. No.	133914
Contig ID	93584_1.R1010
5'-most EST	jC-atXLIB327405P3b08a1
Method	BLASTN
NCBI GI	g2623294
BLAST score	329
E value	0.0e+00
Match length	382
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T20B5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133915

Contig ID	93604_1.R1010
5'-most EST	jC-atXLIB327405P3c08a1
Method	BLASTX
NCBI GI	g3687224
BLAST score	100
E value	2.0e-37
Match length	103
% identity	83
NCBI Description	(AC005169) putative N-acetyl-gamma-glutamyl-phosphate reductase [Arabidopsis thaliana]

Seq. No.	133916
Contig ID	93609_1.R1010
5'-most EST	jC-atXLIB327405P3c11a1
Method	BLASTN
NCBI GI	g2828278
BLAST score	475
E value	0.0e+00
Match length	495
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16 (ESSAII project)

Seq. No.	133917
Contig ID	93628_1.R1010
5'-most EST	jC-atXLIB327405P3d10a1
Method	BLASTX
NCBI GI	g4056441
BLAST score	649
E value	5.0e-68
Match length	136
% identity	93
NCBI Description	(AC005990) Similar to OBP32pep protein gb_U37698 from Arabidopsis thaliana. [Arabidopsis thaliana]

Seq. No.	133918
Contig ID	93632_1.R1010
5'-most EST	jC-atXLIB327405P3d12a1

Seq. No.	133919
Contig ID	93636_1.R1010
5'-most EST	jC-atXLIB327405P3e02a1

Seq. No.	133920
Contig ID	93638_1.R1010
5'-most EST	jC-atXLIB327405P3e03a1
Method	BLASTX
NCBI GI	g2498329
BLAST score	54
E value	2.0e-09
Match length	64
% identity	42
NCBI Description	PATTERN FORMATION PROTEIN EMB30 >gi_2129665_pir__S65571 pattern-formation protein GNOM - Arabidopsis thaliana >gi_1209633 (U36433) GNOM gene product [Arabidopsis thaliana] >gi_1335997 (U56140) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession Number J03918

[Arabidopsis thaliana] >gi_1335999 (U56141) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession Number J03918 [Arabidopsis thaliana]

Seq. No.	133921
Contig ID	93650_1.R1010
5'-most EST	jC-atXLIB327405P3e11a1

Seq. No.	133922
Contig ID	93652_1.R1010
5'-most EST	jC-atXLIB327405P3e12a1

Seq. No.	133923
Contig ID	93656_1.R1010
5'-most EST	jC-atXLIB327405P3f02a1

Seq. No.	133924
Contig ID	93705_1.R1010
5'-most EST	jC-atXLIB327405P3h04a1
Method	BLASTN
NCBI GI	g2618599
BLAST score	256
E value	1.0e-142
Match length	436
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBD2, complete sequence [Arabidopsis thaliana]

Seq. No.	133925
Contig ID	93718_1.R1010
5'-most EST	jC-atXP86CG10B8T7b1
Method	BLASTX
NCBI GI	g2583124
BLAST score	721
E value	2.0e-76
Match length	137
% identity	100
NCBI Description	(AC002387) 5-enolpyruvylshikimate-3-phosphate synthase (EPSP) [Arabidopsis thaliana]

Seq. No.	133926
Contig ID	93737_1.R1010
5'-most EST	jC-atXLIB327405P4b08a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	2.0e-21
Match length	58
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	133927
Contig ID	93740_1.R1010
5'-most EST	jC-atXLIB327405P4b10a1
Method	BLASTX
NCBI GI	g3600035
BLAST score	205

E value	5.0e-16
Match length	135
% identity	79
NCBI Description	(AF080119) contains similarity to GTP-binding proteins [Arabidopsis thaliana]

Seq. No.	133928
Contig ID	93748_1.R1010
5'-most EST	jC-atXLIB327405P4c04a1
Method	BLASTX
NCBI GI	g3201618
BLAST score	180
E value	5.0e-13
Match length	51
% identity	76
NCBI Description	(AC004669) Sop2p-like protein [Arabidopsis thaliana]

Seq. No.	133929
Contig ID	93758_1.R1010
5'-most EST	jC-atXLIB327428P1g05a2
Method	BLASTX
NCBI GI	g3033391
BLAST score	345
E value	2.0e-32
Match length	102
% identity	63
NCBI Description	(AC004238) putative amino acid transporter [Arabidopsis thaliana]

Seq. No.	133930
Contig ID	93758_2.R1010
5'-most EST	jC-atXLIB327405P4c10a1
Method	BLASTX
NCBI GI	g3033391
BLAST score	45
E value	7.0e-12
Match length	61
% identity	58
NCBI Description	(AC004238) putative amino acid transporter [Arabidopsis thaliana]

Seq. No.	133931
Contig ID	93774_1.R1010
5'-most EST	jC-alX24089Q1E1F03a1
Method	BLASTX
NCBI GI	g3914468
BLAST score	153
E value	6.0e-10
Match length	88
% identity	35
NCBI Description	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7) >gi_478411_pir__JQ2257 nuclear antigen 21D7 - carrot >gi_217911_dbj_BAA02696_ (D13434) 21D7 antigen [Daucus carota]

Seq. No.	133932
Contig ID	93794_1.R1010

5'-most EST	jC-atXLIB327405P4e08a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	52
E value	4.0e-20
Match length	56
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	133933
Contig ID	93815_1.R1010
5'-most EST	jC-atXLIB327405P4f08a1
Method	BLASTX
NCBI GI	g2498731
BLAST score	170
E value	1.0e-13
Match length	53
% identity	83
NCBI Description	PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1 >gi_1362013_pir__S57611 zeta-crystallin homolog - Arabidopsis thaliana >gi_886428_emb_CAA89838_ (Z49768) zeta-crystallin homologue [Arabidopsis thaliana]

Seq. No.	133934
Contig ID	93817_1.R1010
5'-most EST	jC-atXLIB327405P4f09a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	49
E value	2.0e-18
Match length	53
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	133935
Contig ID	93835_1.R1010
5'-most EST	jC-atXLIB327405P4g08a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	53
E value	1.0e-20
Match length	57
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	133936
Contig ID	93868_1.R1010
5'-most EST	jC-atXLIB327406P2a08a1
Method	BLASTN
NCBI GI	g1532162
BLAST score	380
E value	0.0e+00
Match length	449
% identity	99
NCBI Description	Arabidopsis thaliana AT.I.24-1, AT.I.24-2, AT.I.24-3, AT.I.24-4, AT.I.24-5, AT.I.24-6, AT.I.24-9 and AT.I.24-14 genes, partial cds, AT.I.24-7, ascorbate peroxidase

(ATHAPX1), EF-1alpha-A1, -A2 and -A3 (EF-1alpha) and AT.I

Seq. No.	133937
Contig ID	93874_1.R1010
5'-most EST	jC-atXLIB327406P3a11a2
Method	BLASTX
NCBI GI	g1706958
BLAST score	517
E value	2.0e-52
Match length	101
% identity	95
NCBI Description	(U58284) cellulose synthase [Gossypium hirsutum]

Seq. No.	133938
Contig ID	93888_1.R1010
5'-most EST	jC-atXP2C75C8T7024a1
Method	BLASTX
NCBI GI	g1946360
BLAST score	572
E value	7.0e-59
Match length	103
% identity	100
NCBI Description	(U93215) elicitor response element binding protein WRKY3 isolog [Arabidopsis thaliana]

Seq. No.	133939
Contig ID	93911_1.R1010
5'-most EST	jC-atXLIB327406P2c11a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	50
E value	6.0e-19
Match length	54
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	133940
Contig ID	93932_1.R1010
5'-most EST	jC-atXLIB327406P2d11a1
Method	BLASTX
NCBI GI	g119354
BLAST score	680
E value	2.0e-71
Match length	188
% identity	70
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_82082_pir__JQ1185 phosphopyruvate hydratase (EC 4.2.1.11) - tomato >gi_19281_emb_CAA41115_ (X58108) enolase [Lycopersicon esculentum]

Seq. No.	133941
Contig ID	93961_1.R1010
5'-most EST	jC-atXLIB327406P2f10a1
Method	BLASTX
NCBI GI	g1708971
BLAST score	152

E value	1.0e-09
Match length	71
% identity	41
NCBI Description	(R)-MANDELONITRILE LYASE ISOFORM 1 PRECURSOR (HYDROXYNITRILE LYASE 1) ((R)-OXYNITRILASE 1) >gi_421871_pir__S32156 mandelonitrile lyase (EC 4.1.2.10) - black cherry >gi_288116_emb_CAA51194_ (X72617) mandelonitrile lyase [Prunus serotina] >gi_1730332 (U78814) (R)-(+)-mandelonitrile lyase isoform MDL1 precursor [Prunus serotina] >gi_1090776_prf__2019441A mandelonitrile lyase [Prunus serotina]

Seq. No.	133942
Contig ID	93975_1.R1010
5'-most EST	jC-atXLIB327406P2g09a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	2.0e-21
Match length	58
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	133943
Contig ID	93979_1.R1010
5'-most EST	jC-atXLIB327438P4b04b2
Method	BLASTX
NCBI GI	g2960364
BLAST score	192
E value	2.0e-14
Match length	112
% identity	42
NCBI Description	(AJ224986) cinnamoyl CoA reductase [Populus balsamifera subsp. trichocarpa]

Seq. No.	133944
Contig ID	94132_1.R1010
5'-most EST	jC-atXLIB327429P3g05b2
Method	BLASTX
NCBI GI	g4678233
BLAST score	690
E value	2.0e-72
Match length	169
% identity	80
NCBI Description	(AC007265) unknown protein [Arabidopsis thaliana]

Seq. No.	133945
Contig ID	94137_1.R1010
5'-most EST	jC-atXLIB327430P2a05a1
Method	BLASTN
NCBI GI	g4538895
BLAST score	155
E value	1.0e-81
Match length	441
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17A8 (ESSA project)

Seq. No.	133946
Contig ID	94142_1.R1010
5'-most EST	jC-atXLIB327430P2a11a1
Method	BLASTX
NCBI GI	g529353
BLAST score	133
E value	2.0e-16
Match length	82
% identity	56
NCBI Description	(U12757) diphenol oxidase [Acer pseudoplatanus]

Seq. No.	133947
Contig ID	94163_1.R1010
5'-most EST	jC-atXLIB327430P2c04a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	2.0e-21
Match length	54
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	133948
Contig ID	94165_1.R1010
5'-most EST	jC-atXLIB327430P2c05a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	44
E value	2.0e-15
Match length	56
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	133949
Contig ID	94203_1.R1010
5'-most EST	jC-atXLIB327430P2e06a1
Method	BLASTN
NCBI GI	g2281081
BLAST score	320
E value	1.0e-180
Match length	324
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F18O19 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133950
Contig ID	94213_1.R1010
5'-most EST	jC-atXLIB327430P2e12a1
Method	BLASTN
NCBI GI	g2924731
BLAST score	263
E value	1.0e-146
Match length	271
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSI17, complete sequence [Arabidopsis thaliana]

Seq. No.	133951
Contig ID	94216_1.R1010
5'-most EST	jC-atXLIB327430P1e05a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	56
E value	2.0e-22
Match length	64
% identity	97
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	133952
Contig ID	94216_3.R1010
5'-most EST	jC-atXP66C210O11T7062a1

Seq. No.	133953
Contig ID	94252_1.R1010
5'-most EST	g936088
Method	BLASTX
NCBI GI	g4220462
BLAST score	674
E value	7.0e-71
Match length	175
% identity	79
NCBI Description	(AC006216) Strong similarity to gb_Z50851 HD-zip (athb-8) gene from Arabidopsis thaliana containing Homeobox PF_00046 and bZIP PF_00170 domains. [Arabidopsis thaliana]

Seq. No.	133954
Contig ID	94252_2.R1010
5'-most EST	jC-atXLIB327439P3f03a2
Method	BLASTX
NCBI GI	g4220462
BLAST score	601
E value	3.0e-62
Match length	111
% identity	100
NCBI Description	(AC006216) Strong similarity to gb_Z50851 HD-zip (athb-8) gene from Arabidopsis thaliana containing Homeobox PF_00046 and bZIP PF_00170 domains. [Arabidopsis thaliana]

Seq. No.	133955
Contig ID	94261_1.R1010
5'-most EST	jC-atXLIB327439P3d09a2
Method	BLASTN
NCBI GI	g4589430
BLAST score	405
E value	0.0e+00
Match length	421
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLD14, complete sequence

Seq. No.	133956
Contig ID	94497_1.R1010

5'-most EST	jC-atX22013Q1E1H01a1
Seq. No.	133957
Contig ID	94558_1.R1010
5'-most EST	jC-atXP112C127F2T7a1
Method	BLASTX
NCBI GI	g4587528
BLAST score	155
E value	5.0e-22
Match length	126
% identity	44
NCBI Description	(AC007060) Strong similarity to F19I3.2 gi_3033375 putative berberine bridge enzyme from Arabidopsis thaliana BAC gb_AC004238. EST gb_R90518 comes from this gene
Seq. No.	133958
Contig ID	94558_3.R1010
5'-most EST	jC-atXLIB327401P4a03a1
Method	BLASTX
NCBI GI	g3033375
BLAST score	133
E value	6.0e-18
Match length	116
% identity	41
NCBI Description	(AC004238) putative berberine bridge enzyme [Arabidopsis thaliana]
Seq. No.	133959
Contig ID	94571_1.R1010
5'-most EST	jC-atXLIB327401P4c01a2
Method	BLASTX
NCBI GI	g3184281
BLAST score	477
E value	2.0e-49
Match length	134
% identity	68
NCBI Description	(AC004136) putative cytochrome P450 [Arabidopsis thaliana]
Seq. No.	133960
Contig ID	94579_1.R1010
5'-most EST	jC-atXLIB327401P4c11a2
Method	BLASTX
NCBI GI	g3805845
BLAST score	184
E value	2.0e-13
Match length	79
% identity	43
NCBI Description	(AL031986) putative protein [Arabidopsis thaliana]
Seq. No.	133961
Contig ID	94625_1.R1010
5'-most EST	jC-atXP122C117N6T7044a1
Seq. No.	133962
Contig ID	94628_1.R1010
5'-most EST	jC-atXLIB327406P1a04a1
Method	BLASTN

NCBI GI	g3702728
BLAST score	34
E value	2.0e-09
Match length	109
% identity	82
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M13, complete sequence [Arabidopsis thaliana]

Seq. No.	133963
Contig ID	94930_1.R1010
5'-most EST	jC-atX24084Q1E1F03a1
Method	BLASTN
NCBI GI	g4557061
BLAST score	280
E value	1.0e-156
Match length	487
% identity	84
NCBI Description	Arabidopsis thaliana chromosome II BAC F23M2 genomic sequence, complete sequence

Seq. No.	133964
Contig ID	94932_1.R1010
5'-most EST	jC-atXLIB327437P3b08a1
Method	BLASTN
NCBI GI	g3402671
BLAST score	227
E value	1.0e-124
Match length	473
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T16B24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133965
Contig ID	95089_1.R1010
5'-most EST	jC-atXLIB327437P2g03b2
Method	BLASTN
NCBI GI	g4191771
BLAST score	241
E value	1.0e-133
Match length	429
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F3P11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133966
Contig ID	95106_1.R1010
5'-most EST	jC-atXLIB327430P1a01a1
Method	BLASTX
NCBI GI	g3236235
BLAST score	299
E value	9.0e-27
Match length	108
% identity	62
NCBI Description	(AC004684) unknown protein [Arabidopsis thaliana] >gi_4056501 (AC005896) unknown protein [Arabidopsis thaliana]

Seq. No.	133967
Contig ID	95109_1.R1010
5'-most EST	jC-atXLIB327430P1a04a1
Method	BLASTX
NCBI GI	g4490316
BLAST score	453
E value	4.0e-45
Match length	92
% identity	100
NCBI Description	(AL035678) nucellin-like protein [Arabidopsis thaliana]

Seq. No.	133968
Contig ID	95111_1.R1010
5'-most EST	jC-atXLIB327430P1c04a1
Method	BLASTX
NCBI GI	g4263784
BLAST score	285
E value	2.0e-25
Match length	61
% identity	90
NCBI Description	(AC006068) putative glycogenin-2 protein [Arabidopsis thaliana]

Seq. No.	133969
Contig ID	95145_1.R1010
5'-most EST	jC-atXLIB327430P1c03a1

Seq. No.	133970
Contig ID	95173_1.R1010
5'-most EST	jC-atXLIB327430P1d08a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	2.0e-21
Match length	62
% identity	97
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	133971
Contig ID	95196_1.R1010
5'-most EST	jC-atXLIB327430P1e11a1
Method	BLASTN
NCBI GI	g3228389
BLAST score	346
E value	0.0e+00
Match length	423
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17L21, complete sequence [Arabidopsis thaliana]

Seq. No.	133972
Contig ID	95205_1.R1010
5'-most EST	jC-atXLIB327430P1f07a1

Seq. No.	133973
Contig ID	95218_1.R1010
5'-most EST	jC-atXLIB327430P1g06a1

Method	BLASTN
NCBI GI	g4063730
BLAST score	449
E value	0.0e+00
Match length	453
% identity	66
NCBI Description	Arabidopsis thaliana BAC F21J6 from chromosome V, containing KNAT3 and mapping near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	133974
Contig ID	95224_1.R1010
5'-most EST	jC-atXLIB327427P1f06a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	3.0e-21
Match length	54
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	133975
Contig ID	95238_1.R1010
5'-most EST	jC-atXLIB327430P1h05a1
Method	BLASTX
NCBI GI	g3834323
BLAST score	177
E value	1.0e-12
Match length	56
% identity	57
NCBI Description	(AC005679) F9K20.25 [Arabidopsis thaliana]

Seq. No.	133976
Contig ID	95245_1.R1010
5'-most EST	jC-atXLIB327430P1h09a1

Seq. No.	133977
Contig ID	95277_1.R1010
5'-most EST	jC-atXLIB327401P4a12a2
Method	BLASTX
NCBI GI	g2760332
BLAST score	181
E value	3.0e-13
Match length	115
% identity	34
NCBI Description	(AC002130) F1N21.17 [Arabidopsis thaliana]

Seq. No.	133978
Contig ID	95289_1.R1010
5'-most EST	jC-atXLIB327401P4b07a2
Method	BLASTX
NCBI GI	g3522949
BLAST score	320
E value	2.0e-29
Match length	68
% identity	91
NCBI Description	(AC004411) hypothetical protein [Arabidopsis thaliana]

Seq. No.	133979
Contig ID	95336_1.R1010
5'-most EST	jC-atXLIB327406P3c04a2
Method	BLASTX
NCBI GI	g3928543
BLAST score	378
E value	9.0e-89
Match length	213
% identity	76
NCBI Description	(AB016819) UDP-glucose glucosyltransferase [Arabidopsis thaliana]

Seq. No.	133980
Contig ID	95383_1.R1010
5'-most EST	jC-atXLIB327401P4h04a2
Method	BLASTX
NCBI GI	g3128190
BLAST score	449
E value	1.0e-44
Match length	82
% identity	100
NCBI Description	(AC004521) putative beta-glucosidase [Arabidopsis thaliana]

Seq. No.	133981
Contig ID	95398_1.R1010
5'-most EST	jC-atXLIB327406P3a01a2
Method	BLASTX
NCBI GI	g4204281
BLAST score	231
E value	9.0e-19
Match length	112
% identity	40
NCBI Description	(AC004146) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	133982
Contig ID	95485_2.R1010
5'-most EST	jC-atXP124C121H16T7d1
Method	BLASTN
NCBI GI	g3643588
BLAST score	179
E value	6.0e-96
Match length	473
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F17H15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133983
Contig ID	95509_1.R1010
5'-most EST	jC-atXLIB327406P3f11a2
Method	BLASTN
NCBI GI	g2290120
BLAST score	56
E value	2.0e-22
Match length	64
% identity	97
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env)

gene, partial cds

Seq. No.	133984
Contig ID	95513_1.R1010
5'-most EST	jC-atXLIB327406P3g01a2
Method	BLASTN
NCBI GI	g3522932
BLAST score	321
E value	0.0e+00
Match length	379
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133985
Contig ID	95524_1.R1010
5'-most EST	jC-atXLIB327406P3g07a2
Method	BLASTN
NCBI GI	g2749918
BLAST score	145
E value	1.0e-75
Match length	345
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC F3I6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133986
Contig ID	95592_1.R1010
5'-most EST	jC-atXLIB327406P4b11a2
Method	BLASTX
NCBI GI	g2511574
BLAST score	449
E value	1.0e-44
Match length	89
% identity	99
NCBI Description	(Y13176) multicatalytic endopeptidase [Arabidopsis thaliana] >gi_3421075 (AF043520) 20S proteasome subunit PAB1 [Arabidopsis thaliana]

Seq. No.	133987
Contig ID	95598_1.R1010
5'-most EST	jC-atXLIB327406P4c02a2
Method	BLASTN
NCBI GI	g3859113
BLAST score	404
E value	0.0e+00
Match length	432
% identity	98
NCBI Description	Arabidopsis thaliana MS5-like protein mRNA, partial cds

Seq. No.	133988
Contig ID	95603_1.R1010
5'-most EST	jC-atXLIB327406P4c05a2
Method	BLASTX
NCBI GI	g2252860
BLAST score	539
E value	4.0e-55

Match length	105
% identity	100
NCBI Description	(AF013294) No definition line found [Arabidopsis thaliana]

Seq. No.	133989
Contig ID	95605_2.R1010
5'-most EST	jC-atXLIB327406P4c06a2
Method	BLASTN
NCBI GI	g2252848
BLAST score	313
E value	1.0e-175
Match length	498
% identity	95
NCBI Description	Arabidopsis thaliana BAC TM018A10

Seq. No.	133990
Contig ID	95612_1.R1010
5'-most EST	jC-atXLIB327406P4c11a2
Method	BLASTN
NCBI GI	g3337347
BLAST score	460
E value	0.0e+00
Match length	464
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F13P17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133991
Contig ID	95648_1.R1010
5'-most EST	jC-atXLIB327406P4e10a2
Method	BLASTX
NCBI GI	g2462754
BLAST score	256
E value	6.0e-22
Match length	127
% identity	40
NCBI Description	(AC002292) Unknown protein [Arabidopsis thaliana]

Seq. No.	133992
Contig ID	95650_1.R1010
5'-most EST	jC-atXLIB327406P4e11a2
Method	BLASTN
NCBI GI	g2290120
BLAST score	53
E value	1.0e-20
Match length	60
% identity	98
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	133993
Contig ID	95652_1.R1010
5'-most EST	jC-atXP25C125G4T7078a1
Method	BLASTX
NCBI GI	g4091080
BLAST score	251
E value	3.0e-21

Match length	58
% identity	69
NCBI Description	(AF045571) nucleic acid binding protein [Oryza sativa]

Seq. No.	133994
Contig ID	95656_1.R1010
5'-most EST	jC-atXLIB327406P4f02a2
Method	BLASTX
NCBI GI	g1665817
BLAST score	228
E value	1.0e-18
Match length	97
% identity	48
NCBI Description	(D87466) Similar to S.cerevisiae hypothetical protein L3111 (S59316) [Homo sapiens]

Seq. No.	133995
Contig ID	95660_1.R1010
5'-most EST	jC-atXLIB327406P4f05a2
Method	BLASTN
NCBI GI	g2182287
BLAST score	299
E value	1.0e-167
Match length	363
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T7N9, complete sequence [Arabidopsis thaliana]

Seq. No.	133996
Contig ID	95663_1.R1010
5'-most EST	jC-atXLIB327406P4f08a2
Method	BLASTN
NCBI GI	g3985949
BLAST score	269
E value	1.0e-149
Match length	457
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOB24, complete sequence [Arabidopsis thaliana]

Seq. No.	133997
Contig ID	95665_1.R1010
5'-most EST	jC-atXLIB327406P4f09a2
Method	BLASTX
NCBI GI	g4469014
BLAST score	279
E value	1.0e-24
Match length	84
% identity	68
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	133998
Contig ID	95667_1.R1010
5'-most EST	jC-atXLIB327406P4f10a2
Method	BLASTN
NCBI GI	g3643588
BLAST score	133

E value	2.0e-68
Match length	401
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F17H15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	133999
Contig ID	95675_1.R1010
5'-most EST	jC-atXLIB327406P4g03a2
Method	BLASTX
NCBI GI	g2304971
BLAST score	166
E value	2.0e-11
Match length	84
% identity	48
NCBI Description	(U82828) ATM [Homo sapiens]

Seq. No.	134000
Contig ID	95688_1.R1010
5'-most EST	jC-atXP26C128K22T7047a1
Method	BLASTX
NCBI GI	g3395432
BLAST score	550
E value	3.0e-56
Match length	108
% identity	100
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	134001
Contig ID	95697_1.R1010
5'-most EST	jC-atXLIB327406P4h08a2

Seq. No.	134002
Contig ID	95705_1.R1010
5'-most EST	jC-atXLIB327407P1a01a2
Method	BLASTN
NCBI GI	g2244788
BLAST score	374
E value	0.0e+00
Match length	457
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	134003
Contig ID	95709_1.R1010
5'-most EST	jC-atXLIB327407P1a03a2
Method	BLASTN
NCBI GI	g2351069
BLAST score	170
E value	2.0e-90
Match length	359
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSH12, complete sequence [Arabidopsis thaliana]

Seq. No.	134004

Contig ID	95721_1.R1010
5'-most EST	jC-atXLIB327407P1a09a2
Method	BLASTN
NCBI GI	g4680765
BLAST score	135
E value	1.0e-69
Match length	207
% identity	91
NCBI Description	Arabidopsis thaliana BAC F14I23 from chromosome V near 69 cM, complete sequence

Seq. No.	134005
Contig ID	95728_1.R1010
5'-most EST	jC-atXLIB327407P1b01a2

Seq. No.	134006
Contig ID	95736_1.R1010
5'-most EST	jC-atXLIB327407P1b06a2
Method	BLASTX
NCBI GI	g4406761
BLAST score	513
E value	7.0e-52
Match length	97
% identity	98
NCBI Description	(AC006836) putative ubiquinone biosynthesis protein [Arabidopsis thaliana]

Seq. No.	134007
Contig ID	95742_1.R1010
5'-most EST	jC-atXLIB327407P1b09a2
Method	BLASTX
NCBI GI	g3668075
BLAST score	73
E value	5.0e-50
Match length	102
% identity	99
NCBI Description	(AC004667) hypothetical protein [Arabidopsis thaliana]

Seq. No.	134008
Contig ID	95753_1.R1010
5'-most EST	jC-atXLIB327407P1c03a2
Method	BLASTN
NCBI GI	g3985952
BLAST score	312
E value	1.0e-175
Match length	399
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MRC8, complete sequence [Arabidopsis thaliana]

Seq. No.	134009
Contig ID	95755_1.R1010
5'-most EST	g2048296

Seq. No.	134010
Contig ID	95760_2.R1010
5'-most EST	jC-atXP12C103E16T7063a1

Method	BLASTX
NCBI GI	g4567197
BLAST score	123
E value	5.0e-36
Match length	171
% identity	51
NCBI Description	(AC007168) unknown protein [Arabidopsis thaliana]

Seq. No.	134011
Contig ID	95760_3.R1010
5'-most EST	jC-atXLIB327407P1c07a2
Method	BLASTN
NCBI GI	g531828
BLAST score	52
E value	4.0e-20
Match length	56
% identity	98
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	134012
Contig ID	95768_1.R1010
5'-most EST	jC-atXLIB327407P1c11a2

Seq. No.	134013
Contig ID	95770_1.R1010
5'-most EST	jC-atXLIB327407P1c12a2
Method	BLASTX
NCBI GI	g2462739
BLAST score	545
E value	7.0e-56
Match length	100
% identity	100
NCBI Description	(AC002292) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	134014
Contig ID	95772_1.R1010
5'-most EST	jC-atXP86CG9G10T7b1
Method	BLASTX
NCBI GI	g4689328
BLAST score	377
E value	6.0e-36
Match length	130
% identity	58
NCBI Description	(AF132552) BcDNA.GM01838 [Drosophila melanogaster]

Seq. No.	134015
Contig ID	95783_1.R1010
5'-most EST	jC-atXLIB327407P1d09a2
Method	BLASTX
NCBI GI	g2688822
BLAST score	194
E value	1.0e-14
Match length	58
% identity	59
NCBI Description	(U93272) pyrophosphate-dependent phosphofructo-1-kinase [Prunus armeniaca]

Seq. No.	134016
Contig ID	95785_1.R1010
5'-most EST	jC-atXLIB327407P1d10a2
Method	BLASTX
NCBI GI	g3335372
BLAST score	350
E value	6.0e-33
Match length	117
% identity	57
NCBI Description	(AC003028) putative SRG1 protein [Arabidopsis thaliana]

Seq. No.	134017
Contig ID	95795_1.R1010
5'-most EST	jC-atXLIB327407P1e04a2
Method	BLASTX
NCBI GI	g4220524
BLAST score	239
E value	6.0e-20
Match length	65
% identity	65
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	134018
Contig ID	95803_1.R1010
5'-most EST	jC-atXLIB327407P1e08a2
Method	BLASTN
NCBI GI	g4199934
BLAST score	64
E value	3.0e-27
Match length	199
% identity	84
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T3P18, complete sequence [Arabidopsis thaliana]

Seq. No.	134019
Contig ID	95814_1.R1010
5'-most EST	jC-atXLIB327407P1f03a2
Method	BLASTX
NCBI GI	g4587685
BLAST score	603
E value	1.0e-62
Match length	117
% identity	100
NCBI Description	(AC007197) putative methylmalonate semi-aldehyde dehydrogenase [Arabidopsis thaliana]

Seq. No.	134020
Contig ID	95819_1.R1010
5'-most EST	jC-atXLIB327407P1f05a2

Seq. No.	134021
Contig ID	95842_1.R1010
5'-most EST	jC-atXLIB327407P1g06a2
Method	BLASTN
NCBI GI	g4432829
BLAST score	265
E value	1.0e-147

Match length	395
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T1B3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134022
Contig ID	95853_1.R1010
5'-most EST	g1517306

Seq. No.	134023
Contig ID	95855_1.R1010
5'-most EST	jC-atXLIB327407P1h01a2
Method	BLASTX
NCBI GI	g3115852
BLAST score	313
E value	2.0e-28
Match length	72
% identity	89
NCBI Description	(AL022023) putative protein [Arabidopsis thaliana]

Seq. No.	134024
Contig ID	95855_2.R1010
5'-most EST	g906093
Method	BLASTX
NCBI GI	g3115852
BLAST score	436
E value	8.0e-50
Match length	128
% identity	85
NCBI Description	(AL022023) putative protein [Arabidopsis thaliana]

Seq. No.	134025
Contig ID	95858_1.R1010
5'-most EST	jC-atXLIB327407P1h03a2
Method	BLASTN
NCBI GI	g3150396
BLAST score	321
E value	1.0e-180
Match length	419
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T27E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134026
Contig ID	95862_1.R1010
5'-most EST	jC-atXLIB327407P1h06a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	48
E value	8.0e-18
Match length	52
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	134027
Contig ID	95864_1.R1010
5'-most EST	jC-atXP15C106M4T7028a1

Method	BLASTX
NCBI GI	g2245107
BLAST score	422
E value	3.0e-41
Match length	126
% identity	39
NCBI Description	(Z97343) thioesterase homolog [Arabidopsis thaliana]

Seq. No.	134028
Contig ID	95864_2.R1010
5'-most EST	jC-atXLIB327407P1h08a2

Seq. No.	134029
Contig ID	95899_1.R1010
5'-most EST	jC-atXLIB327414P4b06a2
Method	BLASTX
NCBI GI	g3335345
BLAST score	229
E value	9.0e-19
Match length	155
% identity	38
NCBI Description	(AC004512) Contains similarity to ABC transporter gb_1651790 from Synechocystis sp. gb_D90900. [Arabidopsis thaliana]

Seq. No.	134030
Contig ID	96027_1.R1010
5'-most EST	jC-atXP117C143A5T7a1
Method	BLASTX
NCBI GI	g3953458
BLAST score	116
E value	4.0e-75
Match length	179
% identity	86
NCBI Description	(AC002328) F20N2.3 [Arabidopsis thaliana]

Seq. No.	134031
Contig ID	96069_1.R1010
5'-most EST	g17554
Method	BLASTX
NCBI GI	g1086989
BLAST score	345
E value	3.0e-32
Match length	82
% identity	84
NCBI Description	(S79323) plasma membrane H(+)-ATPase [Vicia faba, Otafuku, abaxial epidermis, guard cell protoplasts, Peptide, 963 aa] [Vicia faba]

Seq. No.	134032
Contig ID	96115_1.R1010
5'-most EST	jC-atXLIB327415P2e03a2

Seq. No.	134033
Contig ID	96136_1.R1010
5'-most EST	jC-atXLIB327415P2f02a2
Method	BLASTX

NCBI GI	g4490332
BLAST score	157
E value	2.0e-10
Match length	48
% identity	62
NCBI Description	(AL035656) putative protein [Arabidopsis thaliana]

Seq. No.	134034
Contig ID	96201_1.R1010
5'-most EST	jC-atXLIB327419P1a05a2

Seq. No.	134035
Contig ID	96217_1.R1010
5'-most EST	jC-atXLIB327419P3a12a2

Seq. No.	134036
Contig ID	96238_1.R1010
5'-most EST	jC-atXLIB327419P3b12a2
Method	BLASTX
NCBI GI	g1706103
BLAST score	289
E value	1.0e-25
Match length	198
% identity	41
NCBI Description	CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT) >gi_1363022_pir__A56351 cleavage and polyadenylation specificity factor 100K chain - bovine >gi_599683_emb_CAA53535_ (X75931) Cleavage and Polyadenylation specificity factor (CPSF) 100kD subunit [Bos taurus]

Seq. No.	134037
Contig ID	96283_1.R1010
5'-most EST	jC-atXLIB327419P3e03a2

Seq. No.	134038
Contig ID	96285_1.R1010
5'-most EST	jC-atXLIB327419P3e04a2
Method	BLASTX
NCBI GI	g4510396
BLAST score	352
E value	3.0e-33
Match length	126
% identity	55
NCBI Description	(AC006587) hypothetical protein [Arabidopsis thaliana]

Seq. No.	134039
Contig ID	96289_1.R1010
5'-most EST	jC-atXLIB327419P3e06a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	56
E value	2.0e-22
Match length	56
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	134040
Contig ID	96289_3.R1010
5'-most EST	g2047731

Seq. No.	134041
Contig ID	96304_1.R1010
5'-most EST	jC-atXP62C201M15T7067a1
Method	BLASTN
NCBI GI	g2244788
BLAST score	401
E value	0.0e+00
Match length	551
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	134042
Contig ID	96318_1.R1010
5'-most EST	jC-atXLIB327419P3f11a2
Method	BLASTX
NCBI GI	g4335714
BLAST score	397
E value	2.0e-38
Match length	81
% identity	100
NCBI Description	(AC006248) putative glucosyltransferase [Arabidopsis thaliana]

Seq. No.	134043
Contig ID	96320_1.R1010
5'-most EST	jC-atXLIB327419P3f12a2
Method	BLASTN
NCBI GI	g3702732
BLAST score	386
E value	0.0e+00
Match length	418
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGF10, complete sequence [Arabidopsis thaliana]

Seq. No.	134044
Contig ID	96362_1.R1010
5'-most EST	jC-atXLIB327422P2a06a2
Method	BLASTN
NCBI GI	g531828
BLAST score	56
E value	1.0e-22
Match length	60
% identity	98
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	134045
Contig ID	96372_1.R1010
5'-most EST	jC-atXLIB327422P2a11a2
Method	BLASTX
NCBI GI	g3402714
BLAST score	339

E value	1.0e-31
Match length	87
% identity	89
NCBI Description	(AC004261) unknown protein [Arabidopsis thaliana]

Seq. No.	134046
Contig ID	96381_1.R1010
5'-most EST	jC-atXLIB327422P2b08a2
Method	BLASTN
NCBI GI	g4589445
BLAST score	219
E value	1.0e-119
Match length	614
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWL2, complete sequence

Seq. No.	134047
Contig ID	96439_1.R1010
5'-most EST	jC-atXLIB327422P2e12a2
Method	BLASTX
NCBI GI	g1730588
BLAST score	150
E value	2.0e-09
Match length	75
% identity	41
NCBI Description	HYPOTHETICAL 108.7 KD PROTEIN C14B1.5 IN CHROMOSOME III

Seq. No.	134048
Contig ID	96470_1.R1010
5'-most EST	jC-atXLIB327422P3g05a2
Method	BLASTX
NCBI GI	g1076579
BLAST score	635
E value	4.0e-66
Match length	170
% identity	66
NCBI Description	alcohol dehydrogenase homolog ADH3a - tomato

Seq. No.	134049
Contig ID	96472_1.R1010
5'-most EST	jC-atXLIB327422P2g06a2
Method	BLASTX
NCBI GI	g4371293
BLAST score	274
E value	7.0e-24
Match length	101
% identity	64
NCBI Description	(AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No.	134050
Contig ID	96472_2.R1010
5'-most EST	jC-atXLIB327427P1h07a2
Method	BLASTX
NCBI GI	g4371293
BLAST score	169
E value	1.0e-11

Match length	66
% identity	74
NCBI Description	(AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No.	134051
Contig ID	96498_1.R1010
5'-most EST	jC-atXLIB327422P2h10a2
Method	BLASTX
NCBI GI	g2344889
BLAST score	476
E value	1.0e-47
Match length	110
% identity	85
NCBI Description	(AC002388) unknown protein [Arabidopsis thaliana]

Seq. No.	134052
Contig ID	96534_1.R1010
5'-most EST	jC-atXLIB327422P3c02a2
Method	BLASTN
NCBI GI	g531828
BLAST score	44
E value	2.0e-15
Match length	52
% identity	96
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	134053
Contig ID	96560_1.R1010
5'-most EST	jC-atXLIB327422P3d04a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	46
E value	1.0e-16
Match length	54
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	134054
Contig ID	96566_1.R1010
5'-most EST	jC-atXLIB327422P3d08a2
Method	BLASTN
NCBI GI	g4589440
BLAST score	206
E value	1.0e-112
Match length	364
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSD21, complete sequence

Seq. No.	134055
Contig ID	96588_1.R1010
5'-most EST	jC-atX25013Q1E1D06a1
Method	BLASTX
NCBI GI	g3024898
BLAST score	416
E value	2.0e-40
Match length	97

% identity	72
NCBI Description	PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) >gi_1504028_dbj_BAA13213_ (D86977) similar to putative ATP-dependent RNA helicase K03H1.2 of C.elegans(S41025) [Homo sapiens] >gi_3123906 (AF038391) pre-mRNA splicing factor [Homo sapiens]

Seq. No.	134056
Contig ID	96599_1.R1010
5'-most EST	jC-atXLIB327422P3f04a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	46
E value	2.0e-16
Match length	54
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	134057
Contig ID	96673_1.R1010
5'-most EST	jC-atXP4C88H7T7070a1
Method	BLASTN
NCBI GI	g4235150
BLAST score	578
E value	0.0e+00
Match length	614
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC T25B24 genomic sequence, complete sequence

Seq. No.	134058
Contig ID	96781_1.R1010
5'-most EST	jC-atXLIB327427P3h01a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	50
E value	6.0e-19
Match length	50
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	134059
Contig ID	96815_1.R1010
5'-most EST	jC-atXLIB327427P3h07a2
Method	BLASTN
NCBI GI	g4691223
BLAST score	310
E value	1.0e-174
Match length	425
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15 (ESSA project)

Seq. No.	134060
Contig ID	96834_1.R1010
5'-most EST	jC-atXLIB327427P4a07a2
Method	BLASTN

NCBI GI	g2264307
BLAST score	240
E value	1.0e-132
Match length	436
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MED24, complete sequence [Arabidopsis thaliana]

Seq. No.	134061
Contig ID	96840_1.R1010
5'-most EST	jC-atXLIB327427P4a10a2
Method	BLASTN
NCBI GI	g531828
BLAST score	52
E value	4.0e-20
Match length	52
% identity	100
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	134062
Contig ID	96880_1.R1010
5'-most EST	jC-atXLIB327427P4c06a2
Method	BLASTX
NCBI GI	g2880049
BLAST score	356
E value	1.0e-33
Match length	98
% identity	73
NCBI Description	(AC002340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	134063
Contig ID	96898_1.R1010
5'-most EST	jC-atXLIB327427P4d05a2
Method	BLASTX
NCBI GI	g4006853
BLAST score	439
E value	2.0e-43
Match length	84
% identity	100
NCBI Description	(Z99707) cytochrome P450-like protein [Arabidopsis thaliana]

Seq. No.	134064
Contig ID	96900_1.R1010
5'-most EST	jC-atXLIB327427P4d06a2

Seq. No.	134065
Contig ID	96913_1.R1010
5'-most EST	jC-atXLIB327427P4f01a2
Method	BLASTN
NCBI GI	g2264321
BLAST score	396
E value	0.0e+00
Match length	440
% identity	47
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXM12, complete sequence [Arabidopsis thaliana]

Seq. No.	134066
Contig ID	96923_1.R1010
5'-most EST	jC-atXLIB327427P4e06a2
Method	BLASTN
NCBI GI	g4757662
BLAST score	390
E value	0.0e+00
Match length	434
% identity	97
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome I, complete sequence

Seq. No.	134067
Contig ID	96928_1.R1010
5'-most EST	jC-atXLIB327427P4e10a2
Method	BLASTN
NCBI GI	g2244870
BLAST score	212
E value	1.0e-115
Match length	550
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	134068
Contig ID	96938_1.R1010
5'-most EST	jC-atXLIB327427P4f03a2

Seq. No.	134069
Contig ID	96940_1.R1010
5'-most EST	jC-atXLIB327427P4f04a2
Method	BLASTN
NCBI GI	g4325340
BLAST score	354
E value	0.0e+00
Match length	415
% identity	100
NCBI Description	Arabidopsis thaliana BAC T1J1

Seq. No.	134070
Contig ID	96948_1.R1010
5'-most EST	jC-atXLIB327427P4f08a2
Method	BLASTN
NCBI GI	g3510345
BLAST score	283
E value	1.0e-158
Match length	394
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNJ8, complete sequence [Arabidopsis thaliana]

Seq. No.	134071
Contig ID	97077_1.R1010
5'-most EST	g2723090
Method	BLASTX
NCBI GI	g4580389

BLAST score	422
E value	2.0e-41
Match length	93
% identity	87
NCBI Description	(AC007171) unknown protein [Arabidopsis thaliana]

Seq. No.	134072
Contig ID	97163_1.R1010
5'-most EST	jC-atXLIB327429P4d09a2
Method	BLASTN
NCBI GI	g3269280
BLAST score	515
E value	0.0e+00
Match length	580
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, P1 clone M4I22 (ESSAII project)

Seq. No.	134073
Contig ID	97213_1.R1010
5'-most EST	jC-atXLIB327429P4h05b2
Method	BLASTX
NCBI GI	g4314401
BLAST score	382
E value	1.0e-36
Match length	73
% identity	99
NCBI Description	(AC006232) putative beta-1,3-glucanase [Arabidopsis thaliana]

Seq. No.	134074
Contig ID	97215_1.R1010
5'-most EST	jC-atXLIB327429P4h06b2
Method	BLASTN
NCBI GI	g4159709
BLAST score	423
E value	0.0e+00
Match length	423
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLN21, complete sequence

Seq. No.	134075
Contig ID	97224_1.R1010
5'-most EST	jC-atXLIB327432P2a02a2
Method	BLASTX
NCBI GI	g3540184
BLAST score	509
E value	1.0e-51
Match length	105
% identity	92
NCBI Description	(AC004122) Similar to endoxylanases [Arabidopsis thaliana]

Seq. No.	134076
Contig ID	97239_1.R1010
5'-most EST	jC-atXLIB327432P2a10a2
Method	BLASTN

NCBI GI g3789706
BLAST score 607
E value 0.0e+00
Match length 611
% identity 100
NCBI Description Arabidopsis thaliana chromosome 1 BAC F15K9 sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 134077
Contig ID 97245_1.R1010
5'-most EST jC-atXLIB327432P2b01a2
Method BLASTX
NCBI GI g2642433
BLAST score 540
E value 3.0e-55
Match length 107
% identity 100
NCBI Description (AC002391) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No. 134078
Contig ID 97259_1.R1010
5'-most EST jC-atXLIB327432P2b09a2
Method BLASTN
NCBI GI g2618677
BLAST score 199
E value 1.0e-108
Match length 396
% identity 94
NCBI Description Arabidopsis thaliana BAC F21B7 chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No. 134079
Contig ID 97274_1.R1010
5'-most EST jC-atXLIB327432P2c06a2
Method BLASTN
NCBI GI g4519195
BLAST score 133
E value 1.0e-68
Match length 258
% identity 90
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MQC12, complete sequence

Seq. No. 134080
Contig ID 97286_1.R1010
5'-most EST jC-atXLIB327432P2c12b2
Method BLASTN
NCBI GI g1785729
BLAST score 337
E value 0.0e+00
Match length 377
% identity 91
NCBI Description A.thaliana mitochondrial genome, part B

Seq. No. 134081
Contig ID 97300_1.R1010

5'-most EST	jC-atXLIB327419P1f06a2
Seq. No.	134082
Contig ID	97300_2.R1010
5'-most EST	jC-atXLIB327432P2d11a2
Seq. No.	134083
Contig ID	97363_1.R1010
5'-most EST	jC-atXLIB327432P2h08a2
Seq. No.	134084
Contig ID	97367_1.R1010
5'-most EST	jC-atXLIB327432P2h11a2
Method	BLASTX
NCBI GI	g3142300
BLAST score	108
E value	5.0e-19
Match length	98
% identity	58
NCBI Description	(AC002411) Contains similarity to pre-mRNA processing protein PRP39 gb_L29224 from S. cerevisiae. ESTs gb_R64908 and gb_T88158, gb_N38703 and gb_AA651043 come from this gene. [Arabidopsis thaliana]
Seq. No.	134085
Contig ID	97418_1.R1010
5'-most EST	jC-atXLIB327437P2c12b2
Method	BLASTN
NCBI GI	g2290120
BLAST score	52
E value	2.0e-20
Match length	72
% identity	93
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds
Seq. No.	134086
Contig ID	97604_1.R1010
5'-most EST	jC-atXLIB327437P3g05a2
Method	BLASTN
NCBI GI	g2760171
BLAST score	123
E value	2.0e-62
Match length	372
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPA24, complete sequence [Arabidopsis thaliana]
Seq. No.	134087
Contig ID	97662_1.R1010
5'-most EST	jC-atXP53C183O19T7091d1
Method	BLASTX
NCBI GI	g3386614
BLAST score	398
E value	1.0e-38
Match length	133
% identity	49

NCBI Description	(AC004665) putative transcription factor SF3 [Arabidopsis thaliana]
Seq. No.	134088
Contig ID	97774_1.R1010
5'-most EST	jC-atXLIB327438P4b09b2
Method	BLASTN
NCBI GI	g3985950
BLAST score	285
E value	1.0e-159
Match length	353
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPI10, complete sequence [Arabidopsis thaliana]
Seq. No.	134089
Contig ID	97859_1.R1010
5'-most EST	jC-atXLIB327438P4g06b2
Method	BLASTN
NCBI GI	g2351069
BLAST score	326
E value	0.0e+00
Match length	510
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSH12, complete sequence [Arabidopsis thaliana]
Seq. No.	134090
Contig ID	98080_1.R1010
5'-most EST	jC-atXLIB327418P3d07a2
Method	BLASTN
NCBI GI	g3738313
BLAST score	332
E value	0.0e+00
Match length	422
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T29E15 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	134091
Contig ID	98103_2.R1010
5'-most EST	g560139
Method	BLASTX
NCBI GI	g4741197
BLAST score	180
E value	3.0e-13
Match length	83
% identity	41
NCBI Description	(AL049746) aldose 1-epimerase-like protein [Arabidopsis thaliana]
Seq. No.	134092
Contig ID	98104_1.R1010
5'-most EST	jC-atXLIB327418P3f11a2
Method	BLASTX
NCBI GI	g3851586
BLAST score	301

E value	3.0e-27
Match length	75
% identity	76
NCBI Description	(AF092564) chromosome-associated protein-C [Homo sapiens]

Seq. No.	134093
Contig ID	98127_1.R1010
5'-most EST	jC-atXLIB327419P1a02a2
Method	BLASTN
NCBI GI	g4006885
BLAST score	408
E value	0.0e+00
Match length	428
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	134094
Contig ID	98132_1.R1010
5'-most EST	jC-atXLIB327419P1a08a2
Method	BLASTN
NCBI GI	g2264304
BLAST score	355
E value	0.0e+00
Match length	449
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBG8, complete sequence [Arabidopsis thaliana]

Seq. No.	134095
Contig ID	98134_1.R1010
5'-most EST	jC-atXLIB327419P1a10a2
Method	BLASTX
NCBI GI	g3522961
BLAST score	246
E value	8.0e-21
Match length	70
% identity	71
NCBI Description	(AC004411) putative pto kinase [Arabidopsis thaliana]

Seq. No.	134096
Contig ID	98140_1.R1010
5'-most EST	jC-atXLIB327419P1b04a2
Method	BLASTX
NCBI GI	g549975
BLAST score	182
E value	2.0e-13
Match length	35
% identity	97
NCBI Description	(U12858) nucleosome assembly protein I-like protein; similar to mouse nap I, PIR Accession Number JS0707 [Arabidopsis thaliana]

Seq. No.	134097
Contig ID	98143_1.R1010
5'-most EST	jC-atXLIB327419P1b07a2
Method	BLASTX

NCBI GI	g3219815
BLAST score	143
E value	1.0e-08
Match length	57
% identity	49
NCBI Description	MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM22 HOMOLOG >gi_2104453_emb_CAB08780_ (Z95397) unknown [Schizosaccharomyces pombe]

Seq. No.	134098
Contig ID	98144_1.R1010
5'-most EST	jC-atXP112C129M21T7a1
Method	BLASTX
NCBI GI	g4510406
BLAST score	236
E value	2.0e-19
Match length	73
% identity	63
NCBI Description	(AC006587) putative protein kinase [Arabidopsis thaliana]

Seq. No.	134099
Contig ID	98145_1.R1010
5'-most EST	jC-atXLIB327419P1b10a2

Seq. No.	134100
Contig ID	98149_1.R1010
5'-most EST	jC-atXLIB327419P1c02a2
Method	BLASTN
NCBI GI	g3402671
BLAST score	37
E value	5.0e-11
Match length	45
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T16B24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134101
Contig ID	98152_2.R1010
5'-most EST	jC-atXLIB327419P1c05a2
Method	BLASTX
NCBI GI	g4206122
BLAST score	367
E value	7.0e-35
Match length	114
% identity	64
NCBI Description	(AF097667) protein phosphatase 2C homolog [Mesembryanthemum crystallinum]

Seq. No.	134102
Contig ID	98173_1.R1010
5'-most EST	g2047511
Method	BLASTN
NCBI GI	g2351073
BLAST score	197
E value	1.0e-106
Match length	578
% identity	97

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYJ24, complete sequence [Arabidopsis thaliana]
Seq. No.	134103
Contig ID	98173_3.R1010
5'-most EST	jC-atXLIB327419P1e04a2
Method	BLASTN
NCBI GI	g2351073
BLAST score	256
E value	1.0e-142
Match length	423
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYJ24, complete sequence [Arabidopsis thaliana]
Seq. No.	134104
Contig ID	98177_1.R1010
5'-most EST	jC-atXLIB327419P1e09a2
Method	BLASTN
NCBI GI	g3293583
BLAST score	393
E value	0.0e+00
Match length	429
% identity	98
NCBI Description	Arabidopsis thaliana BAC T27D20
Seq. No.	134105
Contig ID	98186_1.R1010
5'-most EST	jC-atXLIB327419P1f07a2
Method	BLASTN
NCBI GI	g4220510
BLAST score	102
E value	6.0e-50
Match length	358
% identity	91
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18 (ESSAII project)
Seq. No.	134106
Contig ID	98187_1.R1010
5'-most EST	jC-atXLIB327419P1f08a2
Method	BLASTN
NCBI GI	g4589433
BLAST score	370
E value	0.0e+00
Match length	422
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNI5, complete sequence
Seq. No.	134107
Contig ID	98188_1.R1010
5'-most EST	jC-atXLIB327419P1f09a2
Method	BLASTX
NCBI GI	g584867
BLAST score	428
E value	4.0e-42

Match length	106
% identity	74
NCBI Description	CYTOCHROME P450 77A2 (CYPLXXVIIA2) (P-450EG5) >gi_481959_pir__S40266 gene CYP77A2 protein - eggplant >gi_542071_pir__S41598 cytochrome P450 77A2 - eggplant >gi_438241_emb_CAA50646_ (X71655) CYP77A2 [Solanum melongena]

Seq. No.	134108
Contig ID	98189_1.R1010
5'-most EST	jC-atXLIB327419P1f10a2
Method	BLASTX
NCBI GI	g1361974
BLAST score	213
E value	2.0e-23
Match length	116
% identity	50
NCBI Description	cysteine proteinase - clove pink (fragment) >gi_595986 (U17135) cysteine proteinase [Dianthus caryophyllus]

Seq. No.	134109
Contig ID	98195_1.R1010
5'-most EST	jC-atXLIB327419P1g04a2
Method	BLASTX
NCBI GI	g4056465
BLAST score	283
E value	4.0e-25
Match length	78
% identity	67
NCBI Description	(AC005990) F5O8.40 [Arabidopsis thaliana]

Seq. No.	134110
Contig ID	98197_1.R1010
5'-most EST	jC-atXP25C123H15T7059a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	52
E value	5.0e-20
Match length	52
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	134111
Contig ID	98197_2.R1010
5'-most EST	jC-atXLIB327419P1g06a2

Seq. No.	134112
Contig ID	98200_1.R1010
5'-most EST	jC-atXLIB327419P1g09a2
Method	BLASTN
NCBI GI	g4589430
BLAST score	303
E value	1.0e-170
Match length	502
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLD14, complete sequence

Seq. No.	134113
Contig ID	98203_1.R1010
5'-most EST	jC-atXLIB327419P1g12a2

Seq. No.	134114
Contig ID	98207_1.R1010
5'-most EST	jC-atXLIB327419P1h05a2

Seq. No.	134115
Contig ID	98211_1.R1010
5'-most EST	jC-atXLIB327419P1h09a2

Seq. No.	134116
Contig ID	98335_1.R1010
5'-most EST	jC-atXP83C241A21T7065a1
Method	BLASTX
NCBI GI	g3980396
BLAST score	454
E value	3.0e-45
Match length	82
% identity	98
NCBI Description	(AC004561) putative C-4 sterol methyl oxidase [Arabidopsis thaliana]

Seq. No.	134117
Contig ID	98343_1.R1010
5'-most EST	jC-atXLIB327419P4e08a2
Method	BLASTX
NCBI GI	g4544449
BLAST score	104
E value	2.0e-57
Match length	126
% identity	98
NCBI Description	(AC006592) putative peroxidase [Arabidopsis thaliana]

Seq. No.	134118
Contig ID	98359_1.R1010
5'-most EST	jC-atXLIB327419P4g10a2
Method	BLASTX
NCBI GI	g4512651
BLAST score	232
E value	5.0e-19
Match length	77
% identity	53
NCBI Description	(AC007048) putative tyrosine transaminase [Arabidopsis thaliana]

Seq. No.	134119
Contig ID	98368_1.R1010
5'-most EST	jC-atXP9C93M5T7s1
Method	BLASTN
NCBI GI	g4662628
BLAST score	193
E value	1.0e-104
Match length	365
% identity	95

NCBI Description	Arabidopsis thaliana chromosome II BAC F27O10 genomic sequence, complete sequence
Seq. No.	134120
Contig ID	98375_1.R1010
5'-most EST	jC-atXLIB327420P2a05a2
Method	BLASTN
NCBI GI	g2290120
BLAST score	58
E value	9.0e-24
Match length	62
% identity	98
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds
Seq. No.	134121
Contig ID	98378_1.R1010
5'-most EST	jC-atXLIB327420P2a08a2
Method	BLASTN
NCBI GI	g3868723
BLAST score	269
E value	1.0e-149
Match length	383
% identity	93
NCBI Description	Arabidopsis thaliana chromosome V map 60.5 cM, complete sequence [Arabidopsis thaliana]
Seq. No.	134122
Contig ID	98383_1.R1010
5'-most EST	jC-atXLIB327420P2b03a2
Method	BLASTX
NCBI GI	g2245029
BLAST score	551
E value	1.0e-56
Match length	115
% identity	90
NCBI Description	(Z97341) limonene cyclase homolog [Arabidopsis thaliana]
Seq. No.	134123
Contig ID	98384_1.R1010
5'-most EST	jC-atXLIB327420P2b04a2
Method	BLASTX
NCBI GI	g2129471
BLAST score	260
E value	2.0e-22
Match length	59
% identity	83
NCBI Description	glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) precursor - Scotch pine >gi_1100223 (L32560) glyceraldehyde-3-phosphate dehydrogenase [Pinus sylvestris]
Seq. No.	134124
Contig ID	98389_1.R1010
5'-most EST	jC-atXLIB327420P2b08a2
Method	BLASTX
NCBI GI	g3328231
BLAST score	296

E value	1.0e-26
Match length	117
% identity	51
NCBI Description	(AF051784) 14S cohesin SMC1 subunit; SMC protein [Xenopus laevis]

Seq. No.	134125
Contig ID	98390_1.R1010
5'-most EST	jC-atXLIB327420P2b09a2
Method	BLASTX
NCBI GI	g4544387
BLAST score	566
E value	2.0e-58
Match length	109
% identity	94
NCBI Description	(AC007047) putative purple acid phosphatase precursor [Arabidopsis thaliana]

Seq. No.	134126
Contig ID	98392_1.R1010
5'-most EST	jC-atXLIB327420P2b11a2
Method	BLASTN
NCBI GI	g2245073
BLAST score	227
E value	1.0e-124
Match length	373
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	134127
Contig ID	98400_1.R1010
5'-most EST	jC-atXLIB327420P2c07a2
Method	BLASTN
NCBI GI	g3228389
BLAST score	270
E value	1.0e-150
Match length	431
% identity	98
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17L21, complete sequence [Arabidopsis thaliana]

Seq. No.	134128
Contig ID	98415_1.R1010
5'-most EST	jC-atXLIB327420P2d09a2
Method	BLASTN
NCBI GI	g2264312
BLAST score	295
E value	1.0e-165
Match length	468
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK16, complete sequence [Arabidopsis thaliana]

Seq. No.	134129
Contig ID	98430_1.R1010
5'-most EST	jC-atXLIB327420P2e12a2

Method	BLASTN
NCBI GI	g4519193
BLAST score	397
E value	0.0e+00
Match length	417
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC11, complete sequence

Seq. No.	134130
Contig ID	98445_1.R1010
5'-most EST	jC-atXLIB327420P2g04a2
Method	BLASTN
NCBI GI	g2642152
BLAST score	205
E value	1.0e-111
Match length	418
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T5I7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134131
Contig ID	98464_1.R1010
5'-most EST	jC-atXLIB327420P2h12a2
Method	BLASTX
NCBI GI	g399028
BLAST score	179
E value	6.0e-13
Match length	77
% identity	45
NCBI Description	ALLIIN LYASE PRECURSOR (ALLIINASE) (CYSTEINE SULPHOXIDE LYASE) >gi_419808_pir__S29302 alliin lyase (EC 4.4.1.4) precursor - garlic >gi_16109_emb_CAA78268_ (Z12622) precursor alliinase [Allium sativum]

Seq. No.	134132
Contig ID	98594_1.R1010
5'-most EST	jC-atXP37C156F24T7d2
Method	BLASTX
NCBI GI	g3451078
BLAST score	261
E value	1.0e-42
Match length	140
% identity	72
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	134133
Contig ID	98594_2.R1010
5'-most EST	jC-atXP37C156F24T7s2
Method	BLASTN
NCBI GI	g3451055
BLAST score	335
E value	0.0e+00
Match length	404
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F16G20 (ESSAII project)

Seq. No.	134134
Contig ID	98670_1.R1010
5'-most EST	jC-atXLIB327427P1a07a2
Method	BLASTN
NCBI GI	g4376087
BLAST score	307
E value	1.0e-172
Match length	416
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	134135
Contig ID	98676_1.R1010
5'-most EST	jC-atXLIB327427P1b01a2
Method	BLASTN
NCBI GI	g540252
BLAST score	33
E value	7.0e-09
Match length	33
% identity	100
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No.	134136
Contig ID	98684_1.R1010
5'-most EST	jC-atXLIB327427P1b09a2
Method	BLASTX
NCBI GI	g4006872
BLAST score	525
E value	2.0e-53
Match length	100
% identity	99
NCBI Description	(Z99707) methionyl aminopeptidase-like protein [Arabidopsis thaliana]

Seq. No.	134137
Contig ID	98691_1.R1010
5'-most EST	jC-atXLIB327427P1c05a2
Method	BLASTX
NCBI GI	g4544454
BLAST score	170
E value	7.0e-12
Match length	88
% identity	58
NCBI Description	(AC006592) putative DNAJ protein [Arabidopsis thaliana]

Seq. No.	134138
Contig ID	98695_2.R1010
5'-most EST	jC-atXP28C135H20T7s1
Method	BLASTX
NCBI GI	g3386595
BLAST score	485
E value	1.0e-48
Match length	98
% identity	97
NCBI Description	(AC004665) hypothetical protein [Arabidopsis thaliana]

>gi_3702345 (AC005397) hypothetical protein [Arabidopsis thaliana]

Seq. No.	134139
Contig ID	98696_1.R1010
5'-most EST	jC-atXLIB327427P1c10a2
Method	BLASTN
NCBI GI	g2477521
BLAST score	230
E value	1.0e-126
Match length	492
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC F22K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134140
Contig ID	98702_1.R1010
5'-most EST	jC-atXLIB327427P1d04a2
Method	BLASTN
NCBI GI	g2584827
BLAST score	394
E value	0.0e+00
Match length	414
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F12F1 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134141
Contig ID	98703_1.R1010
5'-most EST	jC-atXLIB327427P1d05a2
Method	BLASTN
NCBI GI	g4220645
BLAST score	221
E value	1.0e-121
Match length	440
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYA6, complete sequence [Arabidopsis thaliana]

Seq. No.	134142
Contig ID	98707_1.R1010
5'-most EST	jC-atXLIB327427P1d09a2

Seq. No.	134143
Contig ID	98708_1.R1010
5'-most EST	jC-atXLIB327427P1d10a2

Seq. No.	134144
Contig ID	98723_1.R1010
5'-most EST	jC-atXLIB327427P1f02a2
Method	BLASTN
NCBI GI	g1871173
BLAST score	421
E value	0.0e+00
Match length	442
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T06D20 genomic

sequence, complete sequence

Seq. No.	134145
Contig ID	98725_1.R1010
5'-most EST	jC-atXLIB327427P1f04a2
Method	BLASTX
NCBI GI	g4512660
BLAST score	195
E value	9.0e-15
Match length	81
% identity	51
NCBI Description	(AC006931) hypothetical protein [Arabidopsis thaliana] >gi_4544467_gb_AAD22374.1_AC006580_6 (AC006580) hypothetical protein [Arabidopsis thaliana]

Seq. No.	134146
Contig ID	98726_1.R1010
5'-most EST	jC-atXLIB327427P1f05a2

Seq. No.	134147
Contig ID	98728_1.R1010
5'-most EST	jC-atXLIB327427P1f07a2

Seq. No.	134148
Contig ID	98737_1.R1010
5'-most EST	jC-atXLIB327427P1g04a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	2.0e-21
Match length	54
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	134149
Contig ID	98742_1.R1010
5'-most EST	jC-atXLIB327427P1g12a2
Method	BLASTX
NCBI GI	g2961388
BLAST score	294
E value	2.0e-26
Match length	82
% identity	84
NCBI Description	(AL022141) putative protein [Arabidopsis thaliana]

Seq. No.	134150
Contig ID	98751_1.R1010
5'-most EST	jC-atXLIB327427P1h10a2
Method	BLASTN
NCBI GI	g540252
BLAST score	34
E value	2.0e-09
Match length	34
% identity	100
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No. 134151

Contig ID	98804_1.R1010
5'-most EST	jC-atXP112C129H2T7a1
Method	BLASTN
NCBI GI	g4159707
BLAST score	590
E value	0.0e+00
Match length	695
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJK13, complete sequence

Seq. No.	134152
Contig ID	98806_1.R1010
5'-most EST	jC-atXLIB327429P3a07a2
Method	BLASTX
NCBI GI	g2980805
BLAST score	108
E value	8.0e-52
Match length	147
% identity	87
NCBI Description	(AL022197) putative protein [Arabidopsis thaliana]

Seq. No.	134153
Contig ID	98851_1.R1010
5'-most EST	jC-atXLIB327429P3d08a2

Seq. No.	134154
Contig ID	98922_1.R1010
5'-most EST	jC-atXLIB327403P3a07a2
Method	BLASTX
NCBI GI	g2462753
BLAST score	573
E value	7.0e-59
Match length	128
% identity	77
NCBI Description	(AC002292) putative polygalacturonase [Arabidopsis thaliana]

Seq. No.	134155
Contig ID	98938_1.R1010
5'-most EST	jC-atXLIB327403P3c02a2
Method	BLASTN
NCBI GI	g3449330
BLAST score	46
E value	1.0e-16
Match length	150
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDJ14, complete sequence [Arabidopsis thaliana]

Seq. No.	134156
Contig ID	98941_1.R1010
5'-most EST	jC-atXLIB327403P3c06a2

Seq. No.	134157
Contig ID	98955_1.R1010
5'-most EST	jC-atXLIB327403P3e01a2

Method	BLASTN
NCBI GI	g2656028
BLAST score	229
E value	1.0e-126
Match length	350
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNF13

Seq. No.	134158
Contig ID	98970_1.R1010
5'-most EST	jC-atXLIB327403P3f06a2
Method	BLASTN
NCBI GI	g3327922
BLAST score	213
E value	1.0e-116
Match length	426
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T31E10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134159
Contig ID	98983_1.R1010
5'-most EST	jC-atXLIB327403P3g11a2
Method	BLASTX
NCBI GI	g3287696
BLAST score	507
E value	3.0e-66
Match length	157
% identity	75
NCBI Description	(AC003979) Strong similarity to phosphoribosylanthranilate transferase gb_D86180 from Pisum sativum. This ORF may be part of a larger gene that lies in the overlapping region. [Arabidopsis thaliana]

Seq. No.	134160
Contig ID	98985_1.R1010
5'-most EST	g2047966

Seq. No.	134161
Contig ID	98995_1.R1010
5'-most EST	jC-atXLIB327404P3a05a1
Method	BLASTN
NCBI GI	g2914688
BLAST score	501
E value	0.0e+00
Match length	558
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F24L7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134162
Contig ID	99026_1.R1010
5'-most EST	jC-atXLIB327404P3d12a1
Method	BLASTX
NCBI GI	g3033392
BLAST score	43

E value	3.0e-25
Match length	75
% identity	77
NCBI Description	(AC004238) putative translation initiation factor EIF-2B-epsilon subunit [Arabidopsis thaliana]

Seq. No.	134163
Contig ID	99035_1.R1010
5'-most EST	jC-atXLIB327404P3f03a1
Method	BLASTX
NCBI GI	g3047124
BLAST score	179
E value	9.0e-13
Match length	57
% identity	65
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	134164
Contig ID	99037_1.R1010
5'-most EST	jC-atXLIB327404P3f06a1
Method	BLASTX
NCBI GI	g4587570
BLAST score	560
E value	2.0e-57
Match length	130
% identity	89
NCBI Description	(AC006550) Strong similarity to gi_2244833 centromere protein homolog from Arabidopsis thaliana chromosome 4 contig gb_Z97337. ESTs gb_T20765 and gb_AA586277 come from this gene

Seq. No.	134165
Contig ID	99043_1.R1010
5'-most EST	jC-atXLIB327404P3g02a1
Method	BLASTX
NCBI GI	g4432844
BLAST score	276
E value	3.0e-24
Match length	107
% identity	46
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	134166
Contig ID	99046_1.R1010
5'-most EST	jC-atXP44C170L2T7062a1
Method	BLASTX
NCBI GI	g4585989
BLAST score	144
E value	1.0e-08
Match length	114
% identity	39
NCBI Description	(AC005287) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	134167
Contig ID	99050_1.R1010
5'-most EST	jC-atXLIB327404P3g09a1

Seq. No.	134168
Contig ID	99052_1.R1010
5'-most EST	jC-atXLIB327404P3h12a1
Method	BLASTX
NCBI GI	g4539399
BLAST score	509
E value	2.0e-51
Match length	128
% identity	79
NCBI Description	(AL035526) ras-like GTP-binding protein [Arabidopsis thaliana]

Seq. No.	134169
Contig ID	99059_1.R1010
5'-most EST	jC-atXLIB327404P3h07a1
Method	BLASTN
NCBI GI	g3176695
BLAST score	304
E value	1.0e-170
Match length	437
% identity	96
NCBI Description	Arabidopsis thaliana chromosome I BAC F14J9 genomic sequence contains phyA marker, complete sequence [Arabidopsis thaliana]

Seq. No.	134170
Contig ID	99061_1.R1010
5'-most EST	jC-atXP2C77E7T7059a1
Method	BLASTX
NCBI GI	g4586044
BLAST score	361
E value	4.0e-34
Match length	92
% identity	75
NCBI Description	(AC007020) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	134171
Contig ID	99068_1.R1010
5'-most EST	jC-atXLIB327405P2a08a1
Method	BLASTX
NCBI GI	g4567260
BLAST score	424
E value	1.0e-41
Match length	82
% identity	100
NCBI Description	(AC006841) putative NADPH dependent mannose 6-phosphate reductase [Arabidopsis thaliana] >gi_4582440_gb_AAD24825.1_AC007142_3 (AC007142) putative NADPH-dependent mannose-6-phosphate reductase [Arabidopsis thaliana]

Seq. No.	134172
Contig ID	99073_2.R1010
5'-most EST	g502080

Seq. No.	134173

Contig ID	99101_1.R1010
5'-most EST	jC-atXLIB327405P2d10a1
Method	BLASTX
NCBI GI	g4325345
BLAST score	250
E value	3.0e-21
Match length	73
% identity	23
NCBI Description	(AF128393) similar to thioredoxin-like proteins (Pfam: PF00085, Score=42.9, E=1.4e-11, N=1); contains similarity to dihydroorotases (Pfam: PF00744, Score=154.9, E=1.4e-42, N=1) [Arabidopsis thaliana]

Seq. No.	134174
Contig ID	99112_1.R1010
5'-most EST	jC-atXLIB327405P2e10a1
Method	BLASTN
NCBI GI	g3063690
BLAST score	400
E value	0.0e+00
Match length	515
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11 (ESSAII project)

Seq. No.	134175
Contig ID	99124_1.R1010
5'-most EST	jC-atXLIB327405P2f10a1

Seq. No.	134176
Contig ID	99128_1.R1010
5'-most EST	jC-atXLIB327405P2g03a1
Method	BLASTN
NCBI GI	g4406776
BLAST score	58
E value	1.0e-23
Match length	204
% identity	82
NCBI Description	Arabidopsis thaliana chromosome II BAC F14H20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134177
Contig ID	99134_1.R1010
5'-most EST	jC-atXLIB327405P2g10a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	50
E value	6.0e-19
Match length	50
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	134178
Contig ID	99153_1.R1010
5'-most EST	jC-atXLIB327428P1a03a2
Method	BLASTN
NCBI GI	g3059018

BLAST score	442
E value	0.0e+00
Match length	454
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F1C12 (ESSAII project)

Seq. No.	134179
Contig ID	99200_1.R1010
5'-most EST	jC-atXLIB327428P1c06a2
Method	BLASTX
NCBI GI	g4262147
BLAST score	255
E value	8.0e-22
Match length	94
% identity	53
NCBI Description	(AC005275) putative homolog of transport inhibitor response 1 [Arabidopsis thaliana]

Seq. No.	134180
Contig ID	99238_1.R1010
5'-most EST	jC-atXLIB327428P1e03a2
Method	BLASTX
NCBI GI	g4097543
BLAST score	349
E value	7.0e-33
Match length	68
% identity	87
NCBI Description	(U64904) ATFP1 [Arabidopsis thaliana]

Seq. No.	134181
Contig ID	99242_1.R1010
5'-most EST	jC-atXLIB327428P1e05a2
Method	BLASTN
NCBI GI	g2564049
BLAST score	103
E value	1.0e-50
Match length	239
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLE2, complete sequence [Arabidopsis thaliana]

Seq. No.	134182
Contig ID	99251_1.R1010
5'-most EST	jC-atXLIB327428P1e10a2
Method	BLASTN
NCBI GI	g4589420
BLAST score	398
E value	0.0e+00
Match length	428
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K3G17, complete sequence

Seq. No.	134183
Contig ID	99253_1.R1010
5'-most EST	jC-atXLIB327428P1e11a2

Method	BLASTX
NCBI GI	g2493321
BLAST score	274
E value	2.0e-67
Match length	226
% identity	56
NCBI Description	L-ASCORBATE OXIDASE PRECURSOR (ASCORBASE) (ASO) >gi_2129952_pir__S66353 L-ascorbate oxidase (EC 1.10.3.3) precursor - common tobacco >gi_599594_dbj_BAA07734_ (D43624) ascorbate oxidase precursor [Nicotiana tabacum]

Seq. No.	134184
Contig ID	99253_2.R1010
5'-most EST	jC-atXP17C110F23T7s3
Method	BLASTN
NCBI GI	g2208902
BLAST score	422
E value	0.0e+00
Match length	458
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for ascorbate oxidase, partial cds

Seq. No.	134185
Contig ID	99257_1.R1010
5'-most EST	jC-atXLIB327428P1f02a2
Method	BLASTN
NCBI GI	g4544381
BLAST score	208
E value	1.0e-113
Match length	423
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F16F14 genomic sequence, complete sequence

Seq. No.	134186
Contig ID	99285_1.R1010
5'-most EST	jC-atXLIB327428P1g06a2
Method	BLASTN
NCBI GI	g531828
BLAST score	43
E value	4.0e-15
Match length	47
% identity	98
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	134187
Contig ID	99289_1.R1010
5'-most EST	jC-atXLIB327428P1g09a2
Method	BLASTN
NCBI GI	g4092471
BLAST score	120
E value	9.0e-61
Match length	339
% identity	85
NCBI Description	Arabidopsis thaliana BAC F9M13 from chromosome IV near 21.5 cM, complete sequence

Seq. No.	134188
Contig ID	99307_1.R1010
5'-most EST	jC-atXLIB327428P1h06a2
Method	BLASTN
NCBI GI	g540252
BLAST score	50
E value	6.0e-19
Match length	50
% identity	100
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No.	134189
Contig ID	99310_1.R1010
5'-most EST	jC-atXLIB327428P1h09a2
Method	BLASTN
NCBI GI	g3449312
BLAST score	371
E value	0.0e+00
Match length	505
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K16L22, complete sequence [Arabidopsis thaliana]

Seq. No.	134190
Contig ID	99316_1.R1010
5'-most EST	jC-atXLIB327428P4a01a2
Method	BLASTN
NCBI GI	g4519195
BLAST score	401
E value	0.0e+00
Match length	425
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MQC12, complete sequence

Seq. No.	134191
Contig ID	99317_2.R1010
5'-most EST	jC-atXLIB327428P4a02a2

Seq. No.	134192
Contig ID	99346_1.R1010
5'-most EST	jC-atXP34C149G13T7a1
Method	BLASTX
NCBI GI	g4678332
BLAST score	290
E value	1.0e-25
Match length	135
% identity	49
NCBI Description	(AL049658) putative peptide transporter [Arabidopsis thaliana]

Seq. No.	134193
Contig ID	99347_1.R1010
5'-most EST	jC-atXLIB327428P4g12a2
Method	BLASTX
NCBI GI	g2462763

BLAST score	303
E value	2.0e-27
Match length	61
% identity	100
NCBI Description	(AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No.	134194
Contig ID	99349_1.R1010
5'-most EST	jC-atXLIB327428P4g07a2
Method	BLASTN
NCBI GI	g17686
BLAST score	174
E value	7.0e-93
Match length	252
% identity	98
NCBI Description	A.thaliana telomere associated sequence DNA

Seq. No.	134195
Contig ID	99356_1.R1010
5'-most EST	jC-atXLIB327428P4d10a2
Method	BLASTX
NCBI GI	g4006896
BLAST score	585
E value	3.0e-60
Match length	124
% identity	91
NCBI Description	(Z99708) SCARECROW-like protein [Arabidopsis thaliana]

Seq. No.	134196
Contig ID	99361_1.R1010
5'-most EST	jC-atXLIB327428P4e04a2
Method	BLASTX
NCBI GI	g3763932
BLAST score	288
E value	1.0e-25
Match length	71
% identity	77
NCBI Description	(AC004450) putative protein kinase [Arabidopsis thaliana]

Seq. No.	134197
Contig ID	99371_1.R1010
5'-most EST	jC-atXLIB327428P4f02a2
Method	BLASTN
NCBI GI	g3789706
BLAST score	397
E value	0.0e+00
Match length	429
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F15K9 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134198
Contig ID	99372_1.R1010
5'-most EST	jC-atXLIB327428P4f03a2
Method	BLASTN
NCBI GI	g2264311

BLAST score	432
E value	0.0e+00
Match length	452
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLN1, complete sequence [Arabidopsis thaliana]

Seq. No.	134199
Contig ID	99375_1.R1010
5'-most EST	jC-atXLIB327428P4f06a2

Seq. No.	134200
Contig ID	99376_1.R1010
5'-most EST	jC-atXLIB327428P4f07a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	52
E value	4.0e-20
Match length	52
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	134201
Contig ID	99378_1.R1010
5'-most EST	jC-atXLIB327428P4f09a2
Method	BLASTX
NCBI GI	g3928543
BLAST score	380
E value	2.0e-36
Match length	104
% identity	68
NCBI Description	(AB016819) UDP-glucose glucosyltransferase [Arabidopsis thaliana]

Seq. No.	134202
Contig ID	99389_1.R1010
5'-most EST	jC-atXLIB327428P4g08a2
Method	BLASTX
NCBI GI	g3355470
BLAST score	274
E value	5.0e-24
Match length	98
% identity	54
NCBI Description	(AC004218) putative lysophospholipase [Arabidopsis thaliana]

Seq. No.	134203
Contig ID	99400_1.R1010
5'-most EST	jC-atXLIB327428P4h09a2
Method	BLASTN
NCBI GI	g3176701
BLAST score	340
E value	0.0e+00
Match length	474
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T20K24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134204
Contig ID	99415_1.R1010
5'-most EST	jC-atXP39C161F15T7s1
Method	BLASTN
NCBI GI	g2262097
BLAST score	584
E value	0.0e+00
Match length	604
% identity	99
NCBI Description	Arabidopsis thaliana chromosome IV BAC T19F6 genomic sequence, complete sequence

Seq. No.	134205
Contig ID	99425_1.R1010
5'-most EST	g735942
Method	BLASTN
NCBI GI	g2392894
BLAST score	138
E value	2.0e-71
Match length	376
% identity	96
NCBI Description	Arabidopsis thaliana brassinosteroid insensitive 1 (BRI1) gene, complete cds

Seq. No.	134206
Contig ID	99434_1.R1010
5'-most EST	jC-atXLIB327438P3d12b1

Seq. No.	134207
Contig ID	99434_2.R1010
5'-most EST	jC-atXP31C144K1T7s1

Seq. No.	134208
Contig ID	99444_1.R1010
5'-most EST	jC-atXLIB327438P3e11b1
Method	BLASTX
NCBI GI	g4097505
BLAST score	588
E value	6.0e-61
Match length	116
% identity	97
NCBI Description	(U63020) D1 protein [Magnolia pyramidata]

Seq. No.	134209
Contig ID	99444_2.R1010
5'-most EST	g2747932
Method	BLASTX
NCBI GI	g4097505
BLAST score	46
E value	3.0e-18
Match length	58
% identity	100
NCBI Description	(U63020) D1 protein [Magnolia pyramidata]

Seq. No.	134210
Contig ID	99581_1.R1010

5'-most EST	jC-atXLIB327439P1h02a2
Method	BLASTX
NCBI GI	g4115383
BLAST score	43
E value	4.0e-25
Match length	159
% identity	47
NCBI Description	(AC005967) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	134211
Contig ID	99731_1.R1010
5'-most EST	jC-atXLIB327403P3h04b2
Method	BLASTN
NCBI GI	g4510360
BLAST score	192
E value	1.0e-103
Match length	437
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F11F19 genomic sequence, complete sequence

Seq. No.	134212
Contig ID	99743_1.R1010
5'-most EST	jC-atXP70C220P10T7054a1
Method	BLASTN
NCBI GI	g4589445
BLAST score	222
E value	1.0e-121
Match length	379
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWL2, complete sequence

Seq. No.	134213
Contig ID	99749_1.R1010
5'-most EST	jC-atXLIB327405P1a10a2
Method	BLASTN
NCBI GI	g4757395
BLAST score	415
E value	0.0e+00
Match length	415
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L13, complete sequence

Seq. No.	134214
Contig ID	99759_1.R1010
5'-most EST	jC-atXLIB327405P1b07a2
Method	BLASTX
NCBI GI	g728868
BLAST score	95
E value	2.0e-21
Match length	111
% identity	48
NCBI Description	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX) >gi_99824_pir__S16748 proline-rich protein - rape

(fragment) >gi_22597_emb_CAA42924_ (X60376) proline-rich protein [Brassica napus]

Seq. No.	134215
Contig ID	99761_1.R1010
5'-most EST	jC-atXLIB327405P1b08a2
Method	BLASTN
NCBI GI	g2351073
BLAST score	356
E value	0.0e+00
Match length	400
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	134216
Contig ID	99766_1.R1010
5'-most EST	jC-atXLIB327405P1c01a2
Method	BLASTX
NCBI GI	g2388580
BLAST score	425
E value	9.0e-42
Match length	96
% identity	74
NCBI Description	(AC000098) Similar to Sequence 10 from patent 5477002 (gb_1253956). [Arabidopsis thaliana]

Seq. No.	134217
Contig ID	99768_1.R1010
5'-most EST	jC-atXLIB327405P1c02a2
Method	BLASTX
NCBI GI	g2827659
BLAST score	467
E value	1.0e-46
Match length	95
% identity	97
NCBI Description	(AL021637) putative protein [Arabidopsis thaliana]

Seq. No.	134218
Contig ID	99771_1.R1010
5'-most EST	jC-atXLIB327405P1c04a2
Method	BLASTN
NCBI GI	g4455229
BLAST score	209
E value	1.0e-114
Match length	418
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F13M23 (ESSAII project)

Seq. No.	134219
Contig ID	99778_1.R1010
5'-most EST	jC-atXLIB327405P1c09a2
Method	BLASTX
NCBI GI	g4455293
BLAST score	67
E value	3.0e-11

Match length	70
% identity	67
NCBI Description	(AL035528) putative protein [Arabidopsis thaliana]

Seq. No.	134220
Contig ID	99786_1.R1010
5'-most EST	jC-atXLIB327405P1d03a2
Method	BLASTN
NCBI GI	g2262155
BLAST score	354
E value	0.0e+00
Match length	527
% identity	96
NCBI Description	DNA sequence of Arabidopsis thaliana BAC F5J6 from chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No.	134221
Contig ID	99786_2.R1010
5'-most EST	jC-atXP92C247O15T7019d1
Method	BLASTN
NCBI GI	g2262155
BLAST score	273
E value	1.0e-152
Match length	595
% identity	99
NCBI Description	DNA sequence of Arabidopsis thaliana BAC F5J6 from chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No.	134222
Contig ID	99788_1.R1010
5'-most EST	jC-atXLIB327405P1d05a2
Method	BLASTN
NCBI GI	g2462264
BLAST score	57
E value	4.0e-23
Match length	57
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	134223
Contig ID	99810_1.R1010
5'-most EST	jC-atXLIB327405P1e08a2
Method	BLASTN
NCBI GI	g2564049
BLAST score	229
E value	1.0e-126
Match length	431
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLE2, complete sequence [Arabidopsis thaliana]

Seq. No.	134224
Contig ID	99819_1.R1010
5'-most EST	jC-atXLIB327405P1f01a2
Method	BLASTN
NCBI GI	g3128137
BLAST score	54

E value	2.0e-21
Match length	130
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9I9, complete sequence [Arabidopsis thaliana]

Seq. No.	134225
Contig ID	99830_1.R1010
5'-most EST	jC-atXLIB327405P1f09a2

Seq. No.	134226
Contig ID	99834_1.R1010
5'-most EST	jC-atXLIB327405P1f11a2
Method	BLASTN
NCBI GI	g2335089
BLAST score	331
E value	0.0e+00
Match length	413
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T11A7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134227
Contig ID	99838_1.R1010
5'-most EST	jC-atXP19C113B6T7072a1
Method	BLASTN
NCBI GI	g3785992
BLAST score	362
E value	0.0e+00
Match length	548
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T6A23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134228
Contig ID	99851_1.R1010
5'-most EST	jC-atXLIB327405P1h04a2
Method	BLASTN
NCBI GI	g4454587
BLAST score	430
E value	0.0e+00
Match length	512
% identity	100
NCBI Description	Arabidopsis thaliana BAC F21A20 from chromosome V near 61 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	134229
Contig ID	99870_1.R1010
5'-most EST	jC-atXLIB327405P2b01b2
Method	BLASTN
NCBI GI	g3869068
BLAST score	370
E value	0.0e+00
Match length	370
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC16, complete sequence [Arabidopsis thaliana]

Seq. No.	134230
Contig ID	100024_1.R1010
5'-most EST	jC-atXLIB327439P2d04a2
Method	BLASTN
NCBI GI	g2264312
BLAST score	264
E value	1.0e-146
Match length	404
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK16, complete sequence [Arabidopsis thaliana]

Seq. No.	134231
Contig ID	100032_1.R1010
5'-most EST	jC-atXLIB327439P2e04a2

Seq. No.	134232
Contig ID	100035_1.R1010
5'-most EST	jC-atXLIB327439P2e10a2
Method	BLASTX
NCBI GI	g4006918
BLAST score	407
E value	1.0e-39
Match length	81
% identity	100
NCBI Description	(Z99708) peroxidase like protein [Arabidopsis thaliana]

Seq. No.	134233
Contig ID	100042_1.R1010
5'-most EST	jC-atXLIB327439P2f08a2
Method	BLASTN
NCBI GI	g2656029
BLAST score	311
E value	1.0e-174
Match length	398
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQB2

Seq. No.	134234
Contig ID	100064_1.R1010
5'-most EST	jC-atXLIB327439P2h10a2
Method	BLASTX
NCBI GI	g3033384
BLAST score	288
E value	1.0e-25
Match length	62
% identity	84
NCBI Description	(AC004238) putative CTP synthase [Arabidopsis thaliana]

Seq. No.	134235
Contig ID	100067_1.R1010
5'-most EST	g773535
Method	BLASTN
NCBI GI	g4376087
BLAST score	114

E value	4.0e-57
Match length	122
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	134236
Contig ID	100091_1.R1010
5'-most EST	jC-atXLIB327439P3b07a2
Method	BLASTX
NCBI GI	g4406756
BLAST score	608
E value	4.0e-63
Match length	145
% identity	77
NCBI Description	(AC006836) putative integral membrane protein A3 [Arabidopsis thaliana]

Seq. No.	134237
Contig ID	100111_1.R1010
5'-most EST	jC-atXLIB327439P3c11a2
Method	BLASTN
NCBI GI	g4220643
BLAST score	230
E value	1.0e-126
Match length	338
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD22, complete sequence [Arabidopsis thaliana]

Seq. No.	134238
Contig ID	100114_1.R1010
5'-most EST	jC-atXLIB327439P3d04a2
Method	BLASTN
NCBI GI	g4519194
BLAST score	264
E value	1.0e-146
Match length	411
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHM17, complete sequence

Seq. No.	134239
Contig ID	100121_1.R1010
5'-most EST	jC-atXLIB327439P3d10a2

Seq. No.	134240
Contig ID	100125_1.R1010
5'-most EST	jC-atXLIB327439P3e01a2
Method	BLASTX
NCBI GI	g2688828
BLAST score	405
E value	2.0e-39
Match length	118
% identity	64
NCBI Description	(U97530) ethylene-forming-enzyme-like dioxygenase [Prunus armeniaca]

Seq. No.	134241
Contig ID	100130_1.R1010
5'-most EST	jC-atXLIB327439P3e05a2

Seq. No.	134242
Contig ID	100157_1.R1010
5'-most EST	jC-atXLIB327439P3g03a2

Seq. No.	134243
Contig ID	100161_1.R1010
5'-most EST	jC-atXLIB327439P3g05a2
Method	BLASTX
NCBI GI	g4115377
BLAST score	337
E value	2.0e-31
Match length	96
% identity	65
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	134244
Contig ID	100162_1.R1010
5'-most EST	jC-atXLIB327439P3g06a2
Method	BLASTX
NCBI GI	g3688598
BLAST score	510
E value	1.0e-51
Match length	127
% identity	72
NCBI Description	(AB009029) Cycloartenol Synthase [Panax ginseng]

Seq. No.	134245
Contig ID	100166_1.R1010
5'-most EST	jC-atXLIB327439P3g09a2

Seq. No.	134246
Contig ID	100306_1.R1010
5'-most EST	jC-atXP73CF3D8T7b1
Method	BLASTX
NCBI GI	g2507097
BLAST score	189
E value	1.0e-13
Match length	180
% identity	36
NCBI Description	PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP)

Seq. No.	134247
Contig ID	100311_1.R1010
5'-most EST	jC-atXP73CF3A11T7b1
Method	BLASTX
NCBI GI	g4587589
BLAST score	56
E value	3.0e-14
Match length	66
% identity	61
NCBI Description	(AC007232) hypothetical protein [Arabidopsis thaliana]

Seq. No.	134248
Contig ID	100348_1.R1010
5'-most EST	jC-atXP73C224E2T7b1
Method	BLASTX
NCBI GI	g4587525
BLAST score	596
E value	2.0e-61
Match length	240
% identity	49
NCBI Description	(AC007060) Contains the PF_00650 CRAL/TRIO phosphatidyl-inositol-transfer protein domain. ESTs gb_T76582, gb_N06574 and gb_Z25700 come from this gene. [Arabidopsis thaliana]

Seq. No.	134249
Contig ID	100349_1.R1010
5'-most EST	jC-atXP73C224D8T7b1
Method	BLASTX
NCBI GI	g1651907
BLAST score	220
E value	9.0e-41
Match length	174
% identity	52
NCBI Description	(D90901) spore germination protein c2 [Synechocystis sp.]

Seq. No.	134250
Contig ID	100354_1.R1010
5'-most EST	jC-atXP73C224B4T7d2
Method	BLASTX
NCBI GI	g547706
BLAST score	219
E value	2.0e-17
Match length	126
% identity	40
NCBI Description	INSULIN-DEGRADING ENZYME (INSULYSIN) (INSULINASE) (INSULIN PROTEASE) >gi_347022_pir__S29509 insulinase (EC 3.4.99.45) - rat >gi_56492_emb_CAA47689_ (X67269) insulin-degrading enzyme [Rattus norvegicus]

Seq. No.	134251
Contig ID	100362_1.R1010
5'-most EST	jC-atXP73C223K9T7d2
Method	BLASTX
NCBI GI	g3080427
BLAST score	1045
E value	1.0e-114
Match length	294
% identity	67
NCBI Description	(AL022604) putative protein [Arabidopsis thaliana]

Seq. No.	134252
Contig ID	100364_1.R1010
5'-most EST	jC-atXP73C223K12T7b1
Method	BLASTN
NCBI GI	g3249094
BLAST score	822
E value	0.0e+00

Match length	860
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T12M4 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134253
Contig ID	100378_1.R1010
5'-most EST	jC-atXP73C223F20T7b1
Method	BLASTX
NCBI GI	g2618699
BLAST score	1149
E value	1.0e-126
Match length	266
% identity	83
NCBI Description	(AC002510) unknown protein [Arabidopsis thaliana]

Seq. No.	134254
Contig ID	100388_1.R1010
5'-most EST	jC-atXP91CH1G5T7b1
Method	BLASTN
NCBI GI	g3869069
BLAST score	58
E value	1.0e-23
Match length	331
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence [Arabidopsis thaliana]

Seq. No.	134255
Contig ID	100400_1.R1010
5'-most EST	jC-atXP91CH1D7T7b1
Method	BLASTX
NCBI GI	g4220523
BLAST score	297
E value	1.0e-26
Match length	148
% identity	39
NCBI Description	(AL035356) putative alliin lyase [Arabidopsis thaliana]

Seq. No.	134256
Contig ID	100423_1.R1010
5'-most EST	jC-atXP91CG6H6T7b1
Method	BLASTX
NCBI GI	g4176531
BLAST score	150
E value	3.0e-09
Match length	84
% identity	42
NCBI Description	(AL035263) weak similarity to chick phosphatidylcholine-sterol acetyltransferase [Schizosaccharomyces pombe]

Seq. No.	134257
Contig ID	100425_1.R1010
5'-most EST	jC-atXP91CG6G8T7b1
Method	BLASTX
NCBI GI	g1698548
BLAST score	404

E value	5.0e-39
Match length	131
% identity	63
NCBI Description	(U58971) calmodulin-binding protein [Nicotiana tabacum]

Seq. No.	134258
Contig ID	100426_1.R1010
5'-most EST	jC-atXP91C247K7T7b1
Method	BLASTN
NCBI GI	g3241916
BLAST score	219
E value	1.0e-120
Match length	374
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15N18, complete sequence [Arabidopsis thaliana]

Seq. No.	134259
Contig ID	100428_1.R1010
5'-most EST	jC-atXP91C247K19T7b1
Method	BLASTN
NCBI GI	g3047100
BLAST score	346
E value	0.0e+00
Match length	346
% identity	100
NCBI Description	Arabidopsis thaliana BAC F6N23

Seq. No.	134260
Contig ID	100434_1.R1010
5'-most EST	jC-atXP91C247J10T7b1
Method	BLASTX
NCBI GI	g3582340
BLAST score	246
E value	2.0e-20
Match length	91
% identity	57
NCBI Description	(AC005496) unknown protein [Arabidopsis thaliana]

Seq. No.	134261
Contig ID	100435_1.R1010
5'-most EST	jC-atXP91C247I6T7b1
Method	BLASTX
NCBI GI	g4587546
BLAST score	591
E value	5.0e-61
Match length	155
% identity	81
NCBI Description	(AC006577) Belongs to the PF_00011 Hsp20/alpha crystallin family. EST gb_W4312 comes from this gene. [Arabidopsis thaliana]

Seq. No.	134262
Contig ID	100441_1.R1010
5'-most EST	jC-atXP91C247G24T7b1
Method	BLASTX
NCBI GI	g4490297

BLAST score	296
E value	2.0e-26
Match length	170
% identity	39
NCBI Description	(AL035678) putative protein [Arabidopsis thaliana]

Seq. No.	134263
Contig ID	100445_1.R1010
5'-most EST	jC-atXP91C247G14T7b1

Seq. No.	134264
Contig ID	100447_1.R1010
5'-most EST	jC-atXP91C247E4T7b1

Seq. No.	134265
Contig ID	100513_1.R1010
5'-most EST	jC-atXP73CF2F2T7d2
Method	BLASTN
NCBI GI	g3461810
BLAST score	577
E value	0.0e+00
Match length	743
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T17M13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134266
Contig ID	100569_1.R1010
5'-most EST	jC-atXP118C155K3T7024a1
Method	BLASTN
NCBI GI	g3046855
BLAST score	82
E value	7.0e-38
Match length	321
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSL1, complete sequence [Arabidopsis thaliana]

Seq. No.	134267
Contig ID	100574_1.R1010
5'-most EST	g2759178
Method	BLASTN
NCBI GI	g4544435
BLAST score	487
E value	0.0e+00
Match length	605
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F14M13 genomic sequence, complete sequence

Seq. No.	134268
Contig ID	100574_4.R1010
5'-most EST	g2597355
Method	BLASTN
NCBI GI	g4544435
BLAST score	320
E value	1.0e-180

Match length	335
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F14M13 genomic sequence, complete sequence

Seq. No.	134269
Contig ID	100609_1.R1010
5'-most EST	jC-atXP118C146F12T7029d2
Method	BLASTX
NCBI GI	g3128201
BLAST score	761
E value	1.0e-132
Match length	246
% identity	92
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	134270
Contig ID	100618_1.R1010
5'-most EST	jC-atXP118C145M5T7005a1
Method	BLASTX
NCBI GI	g4337187
BLAST score	874
E value	3.0e-94
Match length	167
% identity	96
NCBI Description	(AC006403) putative prolylcarboxypeptidase, 5' partial [Arabidopsis thaliana]

Seq. No.	134271
Contig ID	100618_2.R1010
5'-most EST	g3450328
Method	BLASTN
NCBI GI	g4337186
BLAST score	265
E value	1.0e-147
Match length	305
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T28I24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134272
Contig ID	100633_1.R1010
5'-most EST	jC-atXP118C144M20T7046a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	58
E value	1.0e-23
Match length	58
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	134273
Contig ID	100633_2.R1010
5'-most EST	g2393488

Seq. No.	134274
Contig ID	100659_1.R1010

5'-most EST	jC-atXP119C209B10T7031a1
Method	BLASTX
NCBI GI	g1542941
BLAST score	794
E value	9.0e-85
Match length	198
% identity	77
NCBI Description	(X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus]

Seq. No.	134275
Contig ID	100661_1.R1010
5'-most EST	jC-atXP118C144B3T7075d2
Method	BLASTN
NCBI GI	g2213606
BLAST score	208
E value	1.0e-113
Match length	694
% identity	98
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F21J9, complete sequence [Arabidopsis thaliana]

Seq. No.	134276
Contig ID	100670_1.R1010
5'-most EST	jC-atXP118C143N23T7027d2
Method	BLASTN
NCBI GI	g4589437
BLAST score	545
E value	0.0e+00
Match length	716
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPN9, complete sequence

Seq. No.	134277
Contig ID	100671_1.R1010
5'-most EST	jC-atXP118C143N23T7027a1
Method	BLASTN
NCBI GI	g4589437
BLAST score	604
E value	0.0e+00
Match length	680
% identity	74
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPN9, complete sequence

Seq. No.	134278
Contig ID	100682_1.R1010
5'-most EST	jC-atXP118C143H5T7066d2
Method	BLASTN
NCBI GI	g3600045
BLAST score	270
E value	1.0e-150
Match length	552
% identity	93
NCBI Description	Arabidopsis thaliana BAC F2P3

Seq. No.	134279

0004074.95-4804-9950

Contig ID	100686_1.R1010
5'-most EST	jC-atXP118C143G21T7058d2
Method	BLASTX
NCBI GI	g322752
BLAST score	354
E value	4.0e-33
Match length	130
% identity	53
NCBI Description	auxin-independent growth promoter - Nicotiana tabacum >gi_559921_emb_CAA56570_ (X80301) axi 1 [Nicotiana tabacum]

Seq. No.	134280
Contig ID	100709_1.R1010
5'-most EST	jC-atXP118C142N22T7035d2
Method	BLASTX
NCBI GI	g3236241
BLAST score	310
E value	4.0e-28
Match length	86
% identity	63
NCBI Description	(AC004684) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	134281
Contig ID	100713_1.R1010
5'-most EST	jC-atXP118C142N16T7050a1
Method	BLASTX
NCBI GI	g3513739
BLAST score	534
E value	2.0e-54
Match length	113
% identity	88
NCBI Description	(AF080118) Similar to uridine diphosphate glucose epimerase; F8M12.10 [Arabidopsis thaliana]

Seq. No.	134282
Contig ID	100722_1.R1010
5'-most EST	jC-atXP113C133J6T7090a2
Method	BLASTX
NCBI GI	g2924784
BLAST score	713
E value	2.0e-97
Match length	185
% identity	61
NCBI Description	(AC002334) similar to jasmonate inducible protein [Arabidopsis thaliana]

Seq. No.	134283
Contig ID	100740_1.R1010
5'-most EST	jC-atXP113C228M12T7031a1

Seq. No.	134284
Contig ID	100740_4.R1010
5'-most EST	g9480766

Seq. No.	134285
Contig ID	100742_2.R1010

5'-most EST	jC-atXP113C230D23T7095a1
Method	BLASTX
NCBI GI	g3641252
BLAST score	178
E value	8.0e-13
Match length	90
% identity	48
NCBI Description	(AF053127) leucine-rich receptor-like protein kinase [Malus domestica]

Seq. No.	134286
Contig ID	100744_1.R1010
5'-most EST	jC-atXP113C133N20T7067a1
Method	BLASTN
NCBI GI	g4589437
BLAST score	217
E value	1.0e-118
Match length	393
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPN9, complete sequence

Seq. No.	134287
Contig ID	100744_4.R1010
5'-most EST	jC-atXP113C223D5T7070a1
Method	BLASTN
NCBI GI	g4589437
BLAST score	227
E value	1.0e-124
Match length	338
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPN9, complete sequence

Seq. No.	134288
Contig ID	100749_1.R1010
5'-most EST	jC-atXP113C125G5T7029a1
Method	BLASTN
NCBI GI	g4757388
BLAST score	636
E value	0.0e+00
Match length	716
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F15L12, complete sequence

Seq. No.	134289
Contig ID	100752_2.R1010
5'-most EST	jC-atXP39C161H12T7s1
Method	BLASTN
NCBI GI	g3337347
BLAST score	422
E value	0.0e+00
Match length	450
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F13P17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134290
Contig ID	100756_1.R1010
5'-most EST	jC-atXP113C217O6T7037a2
Method	BLASTN
NCBI GI	g3212846
BLAST score	210
E value	1.0e-114
Match length	630
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134291
Contig ID	100775_1.R1010
5'-most EST	jC-atXP113C133N23T7075a2
Method	BLASTN
NCBI GI	g4519195
BLAST score	251
E value	1.0e-138
Match length	826
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MQC12, complete sequence

Seq. No.	134292
Contig ID	100808_1.R1010
5'-most EST	jC-atXP79CF4H9T7d2
Method	BLASTN
NCBI GI	g4725940
BLAST score	301
E value	1.0e-168
Match length	377
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T1P17 (ESSA project)

Seq. No.	134293
Contig ID	100808_2.R1010
5'-most EST	jC-atXP79CF4H9T7b1
Method	BLASTX
NCBI GI	g112717
BLAST score	381
E value	3.0e-36
Match length	162
% identity	46
NCBI Description	21 KD PROTEIN PRECURSOR (1.2 PROTEIN) >gi_82050_pir__S10911 hypothetical protein precursor - carrot >gi_18312_emb_CAA36642_ (X52395) precursor polypeptide (AA -22 to 171) [Daucus carota]

Seq. No.	134294
Contig ID	100810_1.R1010
5'-most EST	jC-atXP79CF4H7T7b1
Method	BLASTX
NCBI GI	g4689473
BLAST score	515

E value 5.0e-52
Match length 124
% identity 79
NCBI Description (AC007213) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No. 134295
Contig ID 100810_2.R1010
5'-most EST jC-atXP79CF4G9T7d2
Method BLASTX
NCBI GI g4689473
BLAST score 817
E value 2.0e-87
Match length 201
% identity 78
NCBI Description (AC007213) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No. 134296
Contig ID 100830_1.R1010
5'-most EST jC-atXP79C239E2T7b1
Method BLASTX
NCBI GI g4567225
BLAST score 424
E value 2.0e-41
Match length 80
% identity 99
NCBI Description (AC007119) unknown protein [Arabidopsis thaliana]

Seq. No. 134297
Contig ID 100842_1.R1010
5'-most EST jC-atXP79C237B2T7b1
Method BLASTX
NCBI GI g629692
BLAST score 674
E value 1.0e-70
Match length 223
% identity 62
NCBI Description hypothetical protein - common tobacco >gi_506471_emb_CAA56189_ (X79794) unnamed protein product [Nicotiana tabacum]

Seq. No. 134298
Contig ID 100842_2.R1010
5'-most EST g932909
Method BLASTX
NCBI GI g629692
BLAST score 333
E value 5.0e-31
Match length 100
% identity 66
NCBI Description hypothetical protein - common tobacco >gi_506471_emb_CAA56189_ (X79794) unnamed protein product [Nicotiana tabacum]

Seq. No. 134299
Contig ID 100844_1.R1010

5'-most EST	jC-atXP79C231J2T7b1
Method	BLASTN
NCBI GI	g4539415
BLAST score	449
E value	0.0e+00
Match length	551
% identity	55
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	134300
Contig ID	100845_1.R1010
5'-most EST	jC-atXP79C231I16T7b1
Method	BLASTX
NCBI GI	g135483
BLAST score	649
E value	1.0e-82
Match length	167
% identity	92
NCBI Description	TUBULIN BETA CHAIN >gi_84364_pir__B30309 tubulin beta chain - Euplotes crassus (SGC9) >gi_290685 (J04534) beta-tubulin [Euplotes crassus]

Seq. No.	134301
Contig ID	100856_1.R1010
5'-most EST	jC-atXP79C231F8T7b1
Method	BLASTN
NCBI GI	g2351063
BLAST score	533
E value	0.0e+00
Match length	716
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCL19, complete sequence [Arabidopsis thaliana]

Seq. No.	134302
Contig ID	100861_1.R1010
5'-most EST	jC-atXP79C231E7T7b1
Method	BLASTN
NCBI GI	g4589451
BLAST score	305
E value	1.0e-171
Match length	550
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: T32G24, complete sequence

Seq. No.	134303
Contig ID	100884_1.R1010
5'-most EST	jC-atXP20C115H1T7063a1
Method	BLASTX
NCBI GI	g4008006
BLAST score	379
E value	4.0e-69
Match length	240
% identity	53
NCBI Description	(AF084034) receptor-like protein kinase [Arabidopsis

thaliana]

Seq. No.	134304
Contig ID	100892_1.R1010
5'-most EST	jC-atXP85CG8A6T7b1
Method	BLASTX
NCBI GI	g2809246
BLAST score	646
E value	1.0e-67
Match length	188
% identity	74
NCBI Description	(AC002560) F24O1.15 [Arabidopsis thaliana]

Seq. No.	134305
Contig ID	100898_1.R1010
5'-most EST	jC-atXP85CG7H9T7b1
Method	BLASTX
NCBI GI	g3894191
BLAST score	326
E value	6.0e-30
Match length	146
% identity	48
NCBI Description	(AC005662) unknown protein [Arabidopsis thaliana]

Seq. No.	134306
Contig ID	100904_1.R1010
5'-most EST	jC-atXP85CG7H10T7b1
Method	BLASTX
NCBI GI	g4678262
BLAST score	703
E value	3.0e-74
Match length	169
% identity	86
NCBI Description	(AL049657) argininosuccinate synthase-like protein [Arabidopsis thaliana]

Seq. No.	134307
Contig ID	100912_1.R1010
5'-most EST	jC-atXP85CG7F11T7b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	71
E value	2.0e-31
Match length	71
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	134308
Contig ID	100931_1.R1010
5'-most EST	jC-atXP85C241H16T7b1
Method	BLASTX
NCBI GI	g2129956
BLAST score	170
E value	5.0e-31
Match length	140
% identity	54

NCBI Description	photoassimilate-responsive protein PAR-1c precursor - common tobacco >gi_871489_emb_CAA58732_ (X83852) mRNA inducible by sucrose and salicylic acid and potato virus Y expressed in sugar-accumulating plants [Nicotiana tabacum]
Seq. No.	134309
Contig ID	100931_2.R1010
5'-most EST	g2759097
Seq. No.	134310
Contig ID	100931_3.R1010
5'-most EST	g2758893
Method	BLASTX
NCBI GI	g2129957
BLAST score	318
E value	2.0e-29
Match length	124
% identity	51
NCBI Description	photoassimilate-responsive protein precursor (clone PAR-1a) - common tobacco
Seq. No.	134311
Contig ID	100939_1.R1010
5'-most EST	jC-atXP85C241F8T7b1
Method	BLASTX
NCBI GI	g3236253
BLAST score	548
E value	5.0e-56
Match length	182
% identity	57
NCBI Description	(AC004684) receptor-like protein kinase [Arabidopsis thaliana]
Seq. No.	134312
Contig ID	100942_1.R1010
5'-most EST	jC-atXP85C241F21T7b1
Method	BLASTX
NCBI GI	g2529663
BLAST score	484
E value	1.0e-113
Match length	247
% identity	85
NCBI Description	(AC002535) putative lysophospholipase [Arabidopsis thaliana] >gi_3738277 (AC005309) putative lysophospholipase [Arabidopsis thaliana]
Seq. No.	134313
Contig ID	100945_1.R1010
5'-most EST	jC-atXP85C241E4T7b1
Method	BLASTN
NCBI GI	g2760164
BLAST score	173
E value	4.0e-92
Match length	181
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18P6, complete sequence [Arabidopsis thaliana]

Seq. No.	134314
Contig ID	100945_2.R1010
5'-most EST	g1520690
Method	BLASTN
NCBI GI	g2760164
BLAST score	65
E value	7.0e-28
Match length	139
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18P6, complete sequence [Arabidopsis thaliana]

Seq. No.	134315
Contig ID	100946_1.R1010
5'-most EST	jC-atXP85C241E2T7b1
Method	BLASTN
NCBI GI	g3800746
BLAST score	42
E value	5.0e-14
Match length	50
% identity	96
NCBI Description	Cuphea pulcherrima 3-ketoacyl-ACP synthase (Kas4) mRNA, complete cds

Seq. No.	134316
Contig ID	100949_1.R1010
5'-most EST	jC-atXP85C241D9T7b1
Method	BLASTN
NCBI GI	g3075383
BLAST score	577
E value	0.0e+00
Match length	667
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T1D16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134317
Contig ID	100975_1.R1010
5'-most EST	jC-atXP82C240P20T7b1
Method	BLASTX
NCBI GI	g3283893
BLAST score	236
E value	2.0e-19
Match length	77
% identity	56
NCBI Description	(AF070626) unknown [Homo sapiens]

Seq. No.	134318
Contig ID	101020_1.R1010
5'-most EST	jC-atXP82CG2B2T7d3
Method	BLASTN
NCBI GI	g4455168
BLAST score	438
E value	0.0e+00
Match length	700
% identity	98

NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)
Seq. No.	134319
Contig ID	101026_1.R1010
5'-most EST	jC-atXP83CG3D10T7085d1
Method	BLASTN
NCBI GI	g3063438
BLAST score	458
E value	0.0e+00
Match length	597
% identity	98
NCBI Description	Complete sequence of Arabidopsis F22O13, complete sequence [Arabidopsis thaliana]
Seq. No.	134320
Contig ID	101106_1.R1010
5'-most EST	jC-atXP82CG1E11T7b1
Method	BLASTX
NCBI GI	g3287693
BLAST score	419
E value	7.0e-41
Match length	153
% identity	58
NCBI Description	(AC003979) Similar to LIM17 gene product gb_1653769 from the genome of Synechocystis sp. gb_D90916. [Arabidopsis thaliana]
Seq. No.	134321
Contig ID	101130_1.R1010
5'-most EST	jC-atXP82C241A2T7b1
Method	BLASTN
NCBI GI	g2656024
BLAST score	188
E value	1.0e-101
Match length	689
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15E6
Seq. No.	134322
Contig ID	101156_1.R1010
5'-most EST	g2048347
Method	BLASTN
NCBI GI	g3449330
BLAST score	95
E value	2.0e-45
Match length	1018
% identity	76
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDJ14, complete sequence [Arabidopsis thaliana]
Seq. No.	134323
Contig ID	101225_1.R1010
5'-most EST	jC-atXP95CH2A5T7048d1
Method	BLASTX
NCBI GI	g2102691

BLAST score	362
E value	3.0e-34
Match length	102
% identity	68
NCBI Description	(U64817) fructokinase [Lycopersicon esculentum]

Seq. No.	134324
Contig ID	101225_2.R1010
5'-most EST	jC-atXP89C245B20T7s1
Method	BLASTX
NCBI GI	g2102691
BLAST score	122
E value	3.0e-27
Match length	116
% identity	61
NCBI Description	(U64817) fructokinase [Lycopersicon esculentum]

Seq. No.	134325
Contig ID	101242_1.R1010
5'-most EST	jC-atXP98CH8E5T7064d1
Method	BLASTN
NCBI GI	g2244950
BLAST score	317
E value	1.0e-178
Match length	456
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	134326
Contig ID	101243_1.R1010
5'-most EST	jC-atXP86CG9H5T7d2

Seq. No.	134327
Contig ID	101246_1.R1010
5'-most EST	jC-atXP58C192P1T7s3

Seq. No.	134328
Contig ID	101246_2.R1010
5'-most EST	jC-atXP95CG12G6T7029d1
Method	BLASTN
NCBI GI	g4467358
BLAST score	41
E value	1.0e-13
Match length	49
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for Phosphatidylinositol 4-Kinase

Seq. No.	134329
Contig ID	101266_1.R1010
5'-most EST	jC-atXP95CG12F3T7028b1
Method	BLASTN
NCBI GI	g4325340
BLAST score	350
E value	0.0e+00
Match length	433
% identity	94

NCBI Description	Arabidopsis thaliana BAC T1J1
Seq. No.	134330
Contig ID	101274_1.R1010
5'-most EST	jC-atXP95CG12E8T7091d1
Seq. No.	134331
Contig ID	101276_1.R1010
5'-most EST	jC-atXP95CG12E5T7083d1
Seq. No.	134332
Contig ID	101283_1.R1010
5'-most EST	jC-atXP95CG12E1T7051d1
Method	BLASTX
NCBI GI	g4582436
BLAST score	485
E value	1.0e-48
Match length	198
% identity	56
NCBI Description	(AC007196) unknown protein [Arabidopsis thaliana]
Seq. No.	134333
Contig ID	101283_3.R1010
5'-most EST	g2393386
Method	BLASTX
NCBI GI	g4582436
BLAST score	145
E value	5.0e-09
Match length	59
% identity	47
NCBI Description	(AC007196) unknown protein [Arabidopsis thaliana]
Seq. No.	134334
Contig ID	101298_1.R1010
5'-most EST	jC-atXP95CG12D11T7035d1
Method	BLASTN
NCBI GI	g3985950
BLAST score	514
E value	0.0e+00
Match length	673
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPI10, complete sequence [Arabidopsis thaliana]
Seq. No.	134335
Contig ID	101298_2.R1010
5'-most EST	jC-atXP84CG5F12T7b1
Method	BLASTN
NCBI GI	g3985950
BLAST score	444
E value	0.0e+00
Match length	578
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPI10, complete sequence [Arabidopsis thaliana]
Seq. No.	134336

Contig ID	101306_1.R1010
5'-most EST	g2580736
Method	BLASTN
NCBI GI	g1871173
BLAST score	392
E value	0.0e+00
Match length	424
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T06D20 genomic sequence, complete sequence

Seq. No.	134337
Contig ID	101306_2.R1010
5'-most EST	g2580922
Method	BLASTN
NCBI GI	g1871173
BLAST score	378
E value	0.0e+00
Match length	400
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T06D20 genomic sequence, complete sequence

Seq. No.	134338
Contig ID	101335_1.R1010
5'-most EST	jC-atXP95CG11H2T7079d1
Method	BLASTX
NCBI GI	g1653702
BLAST score	230
E value	2.0e-64
Match length	271
% identity	52
NCBI Description	(D90915) dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex [Synechocystis sp.]

Seq. No.	134339
Contig ID	101341_1.R1010
5'-most EST	jC-atXP95CG11H10T7087d1

Seq. No.	134340
Contig ID	101343_1.R1010
5'-most EST	jC-atXP95CG11G8T7039d1
Method	BLASTX
NCBI GI	g3885330
BLAST score	333
E value	6.0e-31
Match length	117
% identity	55
NCBI Description	(AC005623) putative cytochrome p450 protein [Arabidopsis thaliana]

Seq. No.	134341
Contig ID	101360_1.R1010
5'-most EST	jC-atXP95CG11F8T7054d1

Seq. No.	134342
Contig ID	101364_1.R1010

5'-most EST	jC-atXP95CG11F5T7038d1
Method	BLASTX
NCBI GI	g2911058
BLAST score	192
E value	2.0e-14
Match length	89
% identity	40
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	134343
Contig ID	101378_1.R1010
5'-most EST	jC-atXP95CG11E8T7077d1
Method	BLASTN
NCBI GI	g4415905
BLAST score	384
E value	0.0e+00
Match length	436
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F13K3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134344
Contig ID	101419_1.R1010
5'-most EST	jC-atXP94CH4F4T7027d1
Method	BLASTX
NCBI GI	g2341041
BLAST score	77
E value	2.0e-32
Match length	145
% identity	62
NCBI Description	(AC000104) Arabidopsis thaliana putative ethylene receptor (ERS2) gene (gb_AF047976). EST gb_W43451 comes from this gene. [Arabidopsis thaliana] >gi_3687656 (AF047976) putative ethylene receptor; ERS2 [Arabidopsis thaliana]

Seq. No.	134345
Contig ID	101422_1.R1010
5'-most EST	jC-atXP94CH4F11T7059d1
Method	BLASTN
NCBI GI	g4467358
BLAST score	35
E value	6.0e-10
Match length	39
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for Phosphatidylinositol 4-Kinase

Seq. No.	134346
Contig ID	101429_1.R1010
5'-most EST	jC-atXP94CG12A1T7090d1

Seq. No.	134347
Contig ID	101444_1.R1010
5'-most EST	jC-atXP94CG11C7T7015d1
Method	BLASTN
NCBI GI	g1070003
BLAST score	40
E value	6.0e-13

Match length	40
% identity	100
NCBI Description	B.napus mRNA for biotin carboxyl carrier protein (pBP3) >gi_3715065_emb_A59874.1_A59874 Sequence 3 from Patent WO9707222

Seq. No.	134348
Contig ID	101446_1.R1010
5'-most EST	jC-atXP94CG11C5T7094d1
Method	BLASTX
NCBI GI	g4415931
BLAST score	323
E value	1.0e-29
Match length	147
% identity	50
NCBI Description	(AC006418) unknown protein [Arabidopsis thaliana] >gi_4559393_gb_AAD23053.1_AC006526_18 (AC006526) unknown protein [Arabidopsis thaliana]

Seq. No.	134349
Contig ID	101459_2.R1010
5'-most EST	jC-atXP94CG11B12T7054d1
Method	BLASTX
NCBI GI	g4454039
BLAST score	276
E value	4.0e-24
Match length	73
% identity	79
NCBI Description	(AL035394) putative Na+/H+-exchanging protein [Arabidopsis thaliana]

Seq. No.	134350
Contig ID	101459_3.R1010
5'-most EST	g506597
Method	BLASTN
NCBI GI	g4454022
BLAST score	371
E value	0.0e+00
Match length	465
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16 (ESSAII project)

Seq. No.	134351
Contig ID	101462_1.R1010
5'-most EST	jC-atXP94CG11A8T7045d1
Method	BLASTX
NCBI GI	g4759286
BLAST score	65
E value	2.0e-14
Match length	85
% identity	47
NCBI Description	uncoupling protein 4 >gi_4324701_gb_AAD16995_ (AF110532) uncoupling protein UCP-4 [Homo sapiens]

Seq. No.	134352
Contig ID	101465_1.R1010

5'-most EST	jC-atXP94CG11A2T7005d1
Method	BLASTX
NCBI GI	g1652678
BLAST score	49
E value	6.0e-12
Match length	103
% identity	48
NCBI Description	(D90907) amidase [Synechocystis sp.]

Seq. No.	134353
Contig ID	101466_1.R1010
5'-most EST	jC-atXP94CG11A12T7077d1
Method	BLASTX
NCBI GI	g3047104
BLAST score	256
E value	7.0e-22
Match length	118
% identity	51
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	134354
Contig ID	101474_1.R1010
5'-most EST	jC-atXP89CG6E6T7094d1
Method	BLASTN
NCBI GI	g2696018
BLAST score	274
E value	1.0e-152
Match length	443
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC9, complete sequence [Arabidopsis thaliana]

Seq. No.	134355
Contig ID	101495_2.R1010
5'-most EST	jC-atXP89CG6B5T7013d1

Seq. No.	134356
Contig ID	101510_1.R1010
5'-most EST	jC-atXP89C245C6T7063d1

Seq. No.	134357
Contig ID	101518_1.R1010
5'-most EST	jC-atXP89C245B2T7036d1
Method	BLASTX
NCBI GI	g3877655
BLAST score	218
E value	3.0e-17
Match length	73
% identity	56
NCBI Description	(Z72511) possible zinc finger protein; cDNA EST EMBL:M89115 comes from this gene; cDNA EST EMBL:D71533 comes from this gene; cDNA EST EMBL:D72314 comes from this gene; cDNA EST EMBL:D75164 comes from this gene; cDNA EST EMBL:C1

Seq. No.	134358
Contig ID	101520_1.R1010
5'-most EST	jC-atXP89C245B19T7060d1

Method	BLASTX
NCBI GI	g1565227
BLAST score	433
E value	2.0e-42
Match length	156
% identity	63
NCBI Description	(X95573) salt-tolerance zinc finger protein [Arabidopsis thaliana]

Seq. No.	134359
Contig ID	101524_1.R1010
5'-most EST	jC-atXP89C245A15T7020d1
Method	BLASTX
NCBI GI	g2244896
BLAST score	1077
E value	1.0e-118
Match length	227
% identity	94
NCBI Description	(Z97338) similar to HSR201 protein N.tabacum [Arabidopsis thaliana]

Seq. No.	134360
Contig ID	101526_1.R1010
5'-most EST	jC-atXP89C244P2T7035d1
Method	BLASTX
NCBI GI	g4467096
BLAST score	578
E value	8.0e-79
Match length	157
% identity	71
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]

Seq. No.	134361
Contig ID	101531_1.R1010
5'-most EST	jC-atXP89C244P16T7059d1

Seq. No.	134362
Contig ID	101538_1.R1010
5'-most EST	jC-atXP89C244M23T7082d1
Method	BLASTN
NCBI GI	g3046851
BLAST score	318
E value	1.0e-179
Match length	488
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	134363
Contig ID	101540_1.R1010
5'-most EST	g2747922
Method	BLASTN
NCBI GI	g4325365
BLAST score	389
E value	0.0e+00
Match length	449
% identity	98

NCBI Description	Arabidopsis thaliana BAC T3H13
Seq. No.	134364
Contig ID	101540_2.R1010
5'-most EST	g1269450
Method	BLASTN
NCBI GI	g3367500
BLAST score	444
E value	0.0e+00
Match length	460
% identity	99
NCBI Description	REVERSE-COMPLEMENT OF: F23J3.GCG.SEQ CHECK: 2754 FROM: 1 TO: 93489, complete sequence [Arabidopsis thaliana]
Seq. No.	134365
Contig ID	101542_1.R1010
5'-most EST	jC-atXP89C244L13T7050d1
Method	BLASTX
NCBI GI	g2506938
BLAST score	566
E value	3.0e-58
Match length	154
% identity	75
NCBI Description	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 4, CHLOROPLAST
Seq. No.	134366
Contig ID	101564_1.R1010
5'-most EST	jC-atXP87CG8H1T7b1
Method	BLASTX
NCBI GI	g3355464
BLAST score	185
E value	1.0e-13
Match length	147
% identity	40
NCBI Description	(AC004218) putative ATP-binding-cassette protein, 3' partial [Arabidopsis thaliana]
Seq. No.	134367
Contig ID	101586_1.R1010
5'-most EST	jC-atXP87CG8E10T7b1
Method	BLASTX
NCBI GI	g3402672
BLAST score	335
E value	4.0e-31
Match length	100
% identity	64
NCBI Description	(AC004697) putative white protein [Arabidopsis thaliana]
Seq. No.	134368
Contig ID	101596_1.R1010
5'-most EST	jC-atXP87CG10H7T7b1
Seq. No.	134369
Contig ID	101598_1.R1010
5'-most EST	g5070133
Method	BLASTX
NCBI GI	g267120

BLAST score	174
E value	9.0e-23
Match length	85
% identity	67
NCBI Description	THIOREDOXIN F-TYPE PRECURSOR (TRX-F) >gi_100070_pir__S20929 thioredoxin f precursor - garden pea >gi_20907_emb_CAA45098_ (X63537) thioredoxin F [Pisum sativum] >gi_1388086 (U35830) thioredoxin f [Pisum sativum]

Seq. No.	134370
Contig ID	101600_1.R1010
5'-most EST	jC-atXP87CG10H11T7b1
Method	BLASTN
NCBI GI	g3212102
BLAST score	458
E value	0.0e+00
Match length	465
% identity	100
NCBI Description	Arabidopsis Thaliana BAC F6A4, Chromosome IV, near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	134371
Contig ID	101605_1.R1010
5'-most EST	g2393148
Method	BLASTN
NCBI GI	g2264312
BLAST score	537
E value	0.0e+00
Match length	594
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK16, complete sequence [Arabidopsis thaliana]

Seq. No.	134372
Contig ID	101606_1.R1010
5'-most EST	jC-atXP87CG10G11T7b1
Method	BLASTX
NCBI GI	g4262167
BLAST score	625
E value	3.0e-65
Match length	124
% identity	96
NCBI Description	(AC005275) putative LRR receptor-linked protein kinase [Arabidopsis thaliana]

Seq. No.	134373
Contig ID	101611_1.R1010
5'-most EST	jC-atX24061Q1E1C10a1
Method	BLASTN
NCBI GI	g2264318
BLAST score	379
E value	0.0e+00
Match length	591
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUP24, complete sequence [Arabidopsis thaliana]

Seq. No.	134374
Contig ID	101629_1.R1010
5'-most EST	jC-atXP87C244H11T7b1
Method	BLASTN
NCBI GI	g3080430
BLAST score	521
E value	0.0e+00
Match length	521
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T19P19 (ESSAII project)

Seq. No.	134375
Contig ID	101642_1.R1010
5'-most EST	jC-atXP87C244C12T7b1
Method	BLASTX
NCBI GI	g2498069
BLAST score	215
E value	2.0e-21
Match length	118
% identity	51
NCBI Description	NUCLEOSIDE DIPHOSPHATE KINASE (NDK) (NDP KINASE) >gi_1353658 (U41267) Ndk [Pseudomonas aeruginosa]

Seq. No.	134376
Contig ID	101658_1.R1010
5'-most EST	jC-atXP84CG5G4T7b1
Method	BLASTX
NCBI GI	g3023956
BLAST score	58
E value	3.0e-08
Match length	157
% identity	7
NCBI Description	VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1 >gi_607003 (L28125) beta transducin-like protein [Podospora anserina]

Seq. No.	134377
Contig ID	101658_2.R1010
5'-most EST	g2048795
Method	BLASTX
NCBI GI	g1346729
BLAST score	132
E value	2.0e-11
Match length	195
% identity	11
NCBI Description	PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA >gi_886024 (U23820) protein kinase PkwA [Thermomonospora curvata]

Seq. No.	134378
Contig ID	101681_1.R1010
5'-most EST	jC-atXP84CG5D5T7b1
Method	BLASTN
NCBI GI	g4519791
BLAST score	49
E value	2.0e-18
Match length	73
% identity	92

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NCBI Description	Arabidopsis thaliana mRNA for Asp1, complete cds
Seq. No.	134379
Contig ID	101693_1.R1010
5'-most EST	jC-atXP84CG5B4T7b1
Method	BLASTN
NCBI GI	g416352
BLAST score	36
E value	1.0e-10
Match length	44
% identity	95
NCBI Description	Drosophila melanogaster C/EBP gene, complete cds
Seq. No.	134380
Contig ID	101700_2.R1010
5'-most EST	g2749613
Method	BLASTX
NCBI GI	g1103322
BLAST score	205
E value	6.0e-16
Match length	63
% identity	71
NCBI Description	(X78820) casein kinase I [Arabidopsis thaliana]
Seq. No.	134381
Contig ID	101726_1.R1010
5'-most EST	jC-atXP83CG3H2T7040a1
Method	BLASTX
NCBI GI	g1706130
BLAST score	174
E value	3.0e-12
Match length	61
% identity	62
NCBI Description	CDPK-RELATED PROTEIN KINASE (PK421) >gi_2129917_pir__S60052 calcium-dependent protein kinase homolog - carrot >gi_1103386_emb_CAA58750_ (X83869) CDPK-related protein kinase [Daucus carota]
Seq. No.	134382
Contig ID	101734_1.R1010
5'-most EST	jC-atXP83CG3G3T7071a1
Method	BLASTX
NCBI GI	g4185133
BLAST score	525
E value	2.0e-53
Match length	147
% identity	73
NCBI Description	(AC005724) putative zinc finger protein [Arabidopsis thaliana]
Seq. No.	134383
Contig ID	101775_1.R1010
5'-most EST	jC-atXP2C78F1T7079a1
Method	BLASTX
NCBI GI	g3873707
BLAST score	216
E value	7.0e-17

Match length	147
% identity	38
NCBI Description	(Z73102) Similarity to B.subtilis DNAJ protein (SW:DNAJ_BACSU); cDNA EST yk437a1.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	134384
Contig ID	101778_1.R1010
5'-most EST	g1268724

Seq. No.	134385
Contig ID	101783_1.R1010
5'-most EST	jC-atXP83CG3D1T7029a1
Method	BLASTN
NCBI GI	g2833627
BLAST score	386
E value	0.0e+00
Match length	386
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F17O7 complete sequence [Arabidopsis thaliana]

Seq. No.	134386
Contig ID	101796_1.R1010
5'-most EST	jC-atXP83CG3C4T7084d1

Seq. No.	134387
Contig ID	101799_1.R1010
5'-most EST	jC-atXP83CG3C2T7076a1
Method	BLASTX
NCBI GI	g2739376
BLAST score	551
E value	2.0e-56
Match length	112
% identity	96
NCBI Description	(AC002505) putative permease [Arabidopsis thaliana]

Seq. No.	134388
Contig ID	101814_1.R1010
5'-most EST	jC-atXP83CG3B10T7060a1
Method	BLASTN
NCBI GI	g4519193
BLAST score	462
E value	0.0e+00
Match length	466
% identity	53
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC11, complete sequence

Seq. No.	134389
Contig ID	101819_1.R1010
5'-most EST	jC-atXP83CG3A6T7059d1
Method	BLASTX
NCBI GI	g3746059
BLAST score	804
E value	3.0e-86
Match length	161

% identity	95
NCBI Description	(AC005311) putative cysteinyl-tRNA synthetase [Arabidopsis thaliana] >gi_4432812_gb_AAD20662_ (AC006593) putative cysteinyl-tRNA synthetase [Arabidopsis thaliana]
Seq. No.	134390
Contig ID	101830_1.R1010
5'-most EST	jC-atXP83CG2H5T7096d1
Seq. No.	134391
Contig ID	101838_1.R1010
5'-most EST	jC-atXP83CG2G7T7048a1
Method	BLASTN
NCBI GI	g4159708
BLAST score	405
E value	0.0e+00
Match length	439
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MKP6, complete sequence
Seq. No.	134392
Contig ID	101840_1.R1010
5'-most EST	jC-atXP83CG2G11T7072a1
Method	BLASTN
NCBI GI	g4071007
BLAST score	36
E value	1.0e-10
Match length	40
% identity	97
NCBI Description	Strongylocentrotus purpuratus stage specific activator protein mRNA, complete cds
Seq. No.	134393
Contig ID	101897_1.R1010
5'-most EST	jC-atXP78CF6D5T7b1
Seq. No.	134394
Contig ID	101956_1.R1010
5'-most EST	jC-atXP78C229O4T7b1
Method	BLASTX
NCBI GI	g4490743
BLAST score	55
E value	2.0e-41
Match length	159
% identity	77
NCBI Description	(AL035708) putative protein [Arabidopsis thaliana]
Seq. No.	134395
Contig ID	101962_1.R1010
5'-most EST	jC-atXP78C229L4T7b1
Seq. No.	134396
Contig ID	101997_1.R1010
5'-most EST	jC-atXP70C221D24T7052a1
Method	BLASTX
NCBI GI	g4512683

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BLAST score	552
E value	1.0e-56
Match length	103
% identity	98
NCBI Description	(AC006931) putative lipase [Arabidopsis thaliana] >gi_4559323_gb_AAD22985.1_AC007087_4 (AC007087) putative lipase [Arabidopsis thaliana]

Seq. No.	134397
Contig ID	102030_1.R1010
5'-most EST	jC-atXP70C220K21T7021a1
Method	BLASTX
NCBI GI	g4585907
BLAST score	414
E value	9.0e-79
Match length	153
% identity	99
NCBI Description	(AC006298) unknown protein [Arabidopsis thaliana]

Seq. No.	134398
Contig ID	102033_1.R1010
5'-most EST	jC-atXP70C220K15T7019a1
Method	BLASTN
NCBI GI	g4263813
BLAST score	168
E value	2.0e-89
Match length	215
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T13P21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134399
Contig ID	102039_1.R1010
5'-most EST	jC-atXP70C220H22T7058a1
Method	BLASTX
NCBI GI	g4335749
BLAST score	353
E value	2.0e-33
Match length	80
% identity	93
NCBI Description	(AC006284) unknown protein [Arabidopsis thaliana]

Seq. No.	134400
Contig ID	102049_1.R1010
5'-most EST	jC-atXP70C220D2T7049a1
Method	BLASTN
NCBI GI	g2564050
BLAST score	344
E value	0.0e+00
Match length	384
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUA22, complete sequence [Arabidopsis thaliana]

Seq. No.	134401
Contig ID	102056_1.R1010
5'-most EST	jC-atXP69C220G13T7092d1

Method	BLASTN
NCBI GI	g3451055
BLAST score	264
E value	1.0e-146
Match length	730
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F16G20 (ESSAII project)

Seq. No.	134402
Contig ID	102068_1.R1010
5'-most EST	jC-atXP69C219M8T7047a1
Method	BLASTN
NCBI GI	g4455168
BLAST score	558
E value	0.0e+00
Match length	931
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)

Seq. No.	134403
Contig ID	102068_2.R1010
5'-most EST	jC-atXP69C219O8T7087a1
Method	BLASTN
NCBI GI	g3763944
BLAST score	362
E value	0.0e+00
Match length	594
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28A23 (ESSAII project)

Seq. No.	134404
Contig ID	102084_1.R1010
5'-most EST	jC-atXP69C219I4T7062a1
Method	BLASTN
NCBI GI	g4159706
BLAST score	291
E value	1.0e-162
Match length	755
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGL6, complete sequence

Seq. No.	134405
Contig ID	102108_1.R1010
5'-most EST	jC-atXP69C218L18T7066a1
Method	BLASTN
NCBI GI	g2582640
BLAST score	38
E value	1.0e-11
Match length	38
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	134406
Contig ID	102117_1.R1010
5'-most EST	jC-atXP69C217N5T7028a1
Method	BLASTN
NCBI GI	g3869072
BLAST score	425
E value	0.0e+00
Match length	767
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJB24, complete sequence [Arabidopsis thaliana]

Seq. No.	134407
Contig ID	102129_1.R1010
5'-most EST	jC-atXP25C125G6T7086a1
Method	BLASTN
NCBI GI	g2351066
BLAST score	440
E value	0.0e+00
Match length	523
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOP9, complete sequence [Arabidopsis thaliana]

Seq. No.	134408
Contig ID	102134_1.R1010
5'-most EST	jC-atXP69C217E19T7057a1
Method	BLASTN
NCBI GI	g3800746
BLAST score	39
E value	4.0e-12
Match length	39
% identity	100
NCBI Description	Cuphea pulcherrima 3-ketoacyl-ACP synthase (Kas4) mRNA, complete cds

Seq. No.	134409
Contig ID	102144_1.R1010
5'-most EST	jC-atXP67C214I6T7060a1
Method	BLASTX
NCBI GI	g3360289
BLAST score	339
E value	2.0e-31
Match length	85
% identity	78
NCBI Description	(AF023164) leucine-rich repeat transmembrane protein kinase 1 [Zea mays]

Seq. No.	134410
Contig ID	102188_1.R1010
5'-most EST	jC-atXP67C213F20T7021a1
Method	BLASTX
NCBI GI	g4454009
BLAST score	497
E value	9.0e-71
Match length	157
% identity	89

NCBI Description	(AL035396) putative protein [Arabidopsis thaliana]
Seq. No.	134411
Contig ID	102196_1.R1010
5'-most EST	jC-atXP67C213A16T7065a1
Method	BLASTN
NCBI GI	g1707006
BLAST score	381
E value	0.0e+00
Match length	453
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T1B8 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	134412
Contig ID	102212_1.R1010
5'-most EST	jC-atXP67C212C9T7042a1
Method	BLASTN
NCBI GI	g2244788
BLAST score	124
E value	5.0e-63
Match length	544
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No
Seq. No.	134413
Contig ID	102231_1.R1010
5'-most EST	jC-atXP66C211C6T7016a1
Method	BLASTN
NCBI GI	g531828
BLAST score	53
E value	1.0e-20
Match length	67
% identity	96
NCBI Description	Cloning vector pSport1, complete cds
Seq. No.	134414
Contig ID	102247_1.R1010
5'-most EST	jC-atXP66C210M14T7014a1
Method	BLASTN
NCBI GI	g4415905
BLAST score	229
E value	1.0e-125
Match length	675
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F13K3 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	134415
Contig ID	102249_1.R1010
5'-most EST	jC-atXP66C210L23T7006a1
Method	BLASTN
NCBI GI	g3702731
BLAST score	407
E value	0.0e+00
Match length	467

% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFC19, complete sequence [Arabidopsis thaliana]
Seq. No.	134416
Contig ID	102251_1.R1010
5'-most EST	jC-atXP66C210L14T7077a1
Seq. No.	134417
Contig ID	102251_2.R1010
5'-most EST	g458782
Seq. No.	134418
Contig ID	102254_2.R1010
5'-most EST	jC-atXP66C210K13T7045a1
Method	BLASTX
NCBI GI	g3176726
BLAST score	289
E value	8.0e-26
Match length	94
% identity	62
NCBI Description	(AC002392) putative serine proteinase [Arabidopsis thaliana]
Seq. No.	134419
Contig ID	102265_1.R1010
5'-most EST	jC-atXP66C210G6T7012a1
Method	BLASTN
NCBI GI	g3402695
BLAST score	65
E value	6.0e-28
Match length	125
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC T3K9 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	134420
Contig ID	102274_1.R1010
5'-most EST	jC-atXP19C109K2T7053a1
Method	BLASTN
NCBI GI	g3869064
BLAST score	81
E value	3.0e-37
Match length	141
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1O13, complete sequence [Arabidopsis thaliana]
Seq. No.	134421
Contig ID	102274_2.R1010
5'-most EST	g1158495
Method	BLASTX
NCBI GI	g3047104
BLAST score	312
E value	2.0e-28
Match length	89
% identity	66

NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]
Seq. No.	134422
Contig ID	102281_1.R1010
5'-most EST	jC-atXP66C210C16T7003a1
Seq. No.	134423
Contig ID	102304_1.R1010
5'-most EST	jC-atXP66C208N19T7089a1
Method	BLASTN
NCBI GI	g4756963
BLAST score	255
E value	1.0e-141
Match length	443
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23 (ESSA project)
Seq. No.	134424
Contig ID	102319_2.R1010
5'-most EST	jC-atXP62C204A22T7071a1
Method	BLASTN
NCBI GI	g2760316
BLAST score	260
E value	1.0e-144
Match length	435
% identity	96
NCBI Description	The sequence of BAC F1N21 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]
Seq. No.	134425
Contig ID	102341_1.R1010
5'-most EST	jC-atXP62C203B4T7061a1
Method	BLASTX
NCBI GI	g3169175
BLAST score	179
E value	5.0e-13
Match length	40
% identity	82
NCBI Description	(AC004401) putative serine carboxypeptidase I [Arabidopsis thaliana]
Seq. No.	134426
Contig ID	102354_1.R1010
5'-most EST	jC-atXP62C202M10T7066a1
Method	BLASTX
NCBI GI	g2244888
BLAST score	349
E value	1.0e-32
Match length	155
% identity	45
NCBI Description	(Z97338) similarity to cytochrome P450 [Arabidopsis thaliana]
Seq. No.	134427
Contig ID	102356_1.R1010
5'-most EST	g1054301

Method	BLASTX
NCBI GI	g1064883
BLAST score	234
E value	2.0e-19
Match length	136
% identity	40
NCBI Description	(X92976) ZAP1 [Arabidopsis thaliana]

Seq. No.	134428
Contig ID	102361_1.R1010
5'-most EST	jC-atXP81C240M6T7s1
Method	BLASTX
NCBI GI	g2494140
BLAST score	333
E value	1.0e-30
Match length	127
% identity	51
NCBI Description	(AC003002) R29515_1 [Homo sapiens] >gi_3068727 (AF058918) unknown [Homo sapiens]

Seq. No.	134429
Contig ID	102364_1.R1010
5'-most EST	jC-atXP62C202H21T7057a1
Method	BLASTX
NCBI GI	g2829925
BLAST score	1048
E value	1.0e-114
Match length	221
% identity	94
NCBI Description	(AC002291) Similar to dnaj-like protein, gp_Y11969_2230757 [Arabidopsis thaliana]

Seq. No.	134430
Contig ID	102381_1.R1010
5'-most EST	jC-atXP62C201N13T7091a1
Method	BLASTX
NCBI GI	g3402699
BLAST score	499
E value	2.0e-50
Match length	89
% identity	100
NCBI Description	(AC004261) unknown protein [Arabidopsis thaliana]

Seq. No.	134431
Contig ID	102391_1.R1010
5'-most EST	jC-atXP60C200E12T7077d1
Method	BLASTX
NCBI GI	g400483
BLAST score	515
E value	4.0e-52
Match length	203
% identity	51
NCBI Description	BACTERIOPHAGE N4 ADSORPTION PROTEIN B >gi_538730_pir__A49351 bacteriophage N4 adsorption inner membrane protein nfrB - Escherichia coli >gi_290459 (L16945) GTG start codon [Escherichia coli] >gi_1651237_dbj_BAA35203_ (D90699) Bacteriophage n4

adsorption inner membrane protein NfrB. [Escherichia coli] >gi_1778484 (U82598) bacteriophage N4 adsorption protein B precursor [Escherichia coli] >gi_1786781 (AE000161) bacteriophage N4 receptor, outer membrane protein [Escherichia coli]

Seq. No.	134432
Contig ID	102393_1.R1010
5'-most EST	jC-atXP60C198B24T7059d1
Method	BLASTX
NCBI GI	g4027895
BLAST score	300
E value	2.0e-31
Match length	104
% identity	60
NCBI Description	(AF049352) alpha-expansin precursor [Nicotiana tabacum]

Seq. No.	134433
Contig ID	102394_1.R1010
5'-most EST	jC-atXP60C200D4T7069a1
Method	BLASTX
NCBI GI	g1040877
BLAST score	220
E value	9.0e-18
Match length	62
% identity	63
NCBI Description	(U30460) expansin S2 precursor [Cucumis sativus]

Seq. No.	134434
Contig ID	102405_1.R1010
5'-most EST	g2733284
Method	BLASTN
NCBI GI	g2244901
BLAST score	272
E value	1.0e-151
Match length	657
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	134435
Contig ID	102405_2.R1010
5'-most EST	jC-atXP60C200A22T7045d1
Method	BLASTN
NCBI GI	g2244901
BLAST score	279
E value	1.0e-155
Match length	407
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	134436
Contig ID	102412_1.R1010
5'-most EST	g1054196
Method	BLASTX
NCBI GI	g2979562

BLAST score	289
E value	7.0e-26
Match length	98
% identity	59
NCBI Description	(AC003680) unknown protein [Arabidopsis thaliana] >gi_3386623 (AC004665) unknown protein [Arabidopsis thaliana]

Seq. No.	134437
Contig ID	102412_2.R1010
5'-most EST	jC-atXP60C199K22T7084d1
Method	BLASTX
NCBI GI	g2979562
BLAST score	154
E value	7.0e-10
Match length	52
% identity	60
NCBI Description	(AC003680) unknown protein [Arabidopsis thaliana] >gi_3386623 (AC004665) unknown protein [Arabidopsis thaliana]

Seq. No.	134438
Contig ID	102428_1.R1010
5'-most EST	g1053435
Method	BLASTN
NCBI GI	g2262097
BLAST score	478
E value	0.0e+00
Match length	675
% identity	99
NCBI Description	Arabidopsis thaliana chromosome IV BAC T19F6 genomic sequence, complete sequence

Seq. No.	134439
Contig ID	102432_1.R1010
5'-most EST	jC-atXP60C199F15T7080d1

Seq. No.	134440
Contig ID	102441_1.R1010
5'-most EST	jC-atXP60C198O20T7064d1
Method	BLASTX
NCBI GI	g3152568
BLAST score	300
E value	4.0e-49
Match length	118
% identity	96
NCBI Description	(AC002986) Similar to hypothetical protein product gb_Z97337 from A. thaliana. EST gb_H76597 comes from this gene. [Arabidopsis thaliana]

Seq. No.	134441
Contig ID	102479_1.R1010
5'-most EST	jC-atXP60C198H14T7086d1
Method	BLASTX
NCBI GI	g4335773
BLAST score	212
E value	9.0e-17

Match length	77
% identity	62
NCBI Description	(AC006284) unknown protein [Arabidopsis thaliana]

Seq. No.	134442
Contig ID	102488_1.R1010
5'-most EST	jC-atXP60C198F3T7014a1

Seq. No.	134443
Contig ID	102512_1.R1010
5'-most EST	g1053548
Method	BLASTN
NCBI GI	g4249393
BLAST score	317
E value	1.0e-178
Match length	414
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T9J23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134444
Contig ID	102519_1.R1010
5'-most EST	jC-atXP60C197I20T7050a1
Method	BLASTX
NCBI GI	g2462741
BLAST score	306
E value	1.0e-27
Match length	61
% identity	98
NCBI Description	(AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No.	134445
Contig ID	102529_1.R1010
5'-most EST	jC-atXP60C197G24T7049d1
Method	BLASTN
NCBI GI	g531828
BLAST score	51
E value	2.0e-19
Match length	70
% identity	94
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	134446
Contig ID	102529_2.R1010
5'-most EST	jC-atXP38C158H22T7d1
Method	BLASTX
NCBI GI	g4432823
BLAST score	330
E value	1.0e-30
Match length	104
% identity	59
NCBI Description	(AC006593) hypothetical protein [Arabidopsis thaliana]

Seq. No.	134447
Contig ID	102536_1.R1010
5'-most EST	jC-atXP60C196P6T7043d1

Seq. No.	134448
Contig ID	102549_1.R1010
5'-most EST	jC-atXP25C125F22T7054a1
Method	BLASTN
NCBI GI	g4757411
BLAST score	187
E value	1.0e-100
Match length	416
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXC7, complete sequence

Seq. No.	134449
Contig ID	102549_2.R1010
5'-most EST	g315216
Method	BLASTN
NCBI GI	g4757411
BLAST score	346
E value	0.0e+00
Match length	415
% identity	81
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXC7, complete sequence

Seq. No.	134450
Contig ID	102551_1.R1010
5'-most EST	jC-atXP57C192C1T7080a1
Method	BLASTN
NCBI GI	g2656025
BLAST score	333
E value	0.0e+00
Match length	422
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCD7

Seq. No.	134451
Contig ID	102552_1.R1010
5'-most EST	g958212

Seq. No.	134452
Contig ID	102565_1.R1010
5'-most EST	jC-atXP57C192A5T7052a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	33
E value	8.0e-09
Match length	53
% identity	91
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	134453
Contig ID	102569_1.R1010
5'-most EST	jC-atXP43C163P22T7056d1
Method	BLASTX
NCBI GI	g4218991

D0004704.050

BLAST score	563
E value	9.0e-58
Match length	118
% identity	95
NCBI Description	(AF098632) subtilisin-like protease [Arabidopsis thaliana]

Seq. No.	134454
Contig ID	102572_1.R1010
5'-most EST	jC-atXP57C192A3T7050a1

Seq. No.	134455
Contig ID	102584_1.R1010
5'-most EST	jC-atXP57C190H19T7009a1
Method	BLASTN
NCBI GI	g2689438
BLAST score	276
E value	1.0e-154
Match length	350
% identity	98
NCBI Description	Arabidopsis thaliana BAC F24O1 chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	134456
Contig ID	102605_1.R1010
5'-most EST	jC-atXP57C190M7T7031a1
Method	BLASTN
NCBI GI	g3449321
BLAST score	279
E value	1.0e-155
Match length	414
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTG10, complete sequence [Arabidopsis thaliana]

Seq. No.	134457
Contig ID	102617_1.R1010
5'-most EST	jC-atXP57C190J16T7019a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	51
E value	2.0e-19
Match length	66
% identity	96
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	134458
Contig ID	102619_1.R1010
5'-most EST	jC-atXP57C190I9T7013a1
Method	BLASTN
NCBI GI	g4587641
BLAST score	416
E value	0.0e+00
Match length	420
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No.	134459
Contig ID	102663_1.R1010
5'-most EST	jC-atXP54C186H2T7095a1
Method	BLASTN
NCBI GI	g3869075
BLAST score	98
E value	1.0e-47
Match length	374
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence [Arabidopsis thaliana]

Seq. No.	134460
Contig ID	102675_1.R1010
5'-most EST	g2445913
Method	BLASTX
NCBI GI	g4584257
BLAST score	258
E value	4.0e-22
Match length	110
% identity	54
NCBI Description	(Y18472) SINA2p [Vitis vinifera]

Seq. No.	134461
Contig ID	102675_2.R1010
5'-most EST	jC-atXP54C186F24T7047d1
Method	BLASTX
NCBI GI	g4584255
BLAST score	521
E value	5.0e-53
Match length	135
% identity	76
NCBI Description	(Y18471) SINA1p [Vitis vinifera]

Seq. No.	134462
Contig ID	102689_1.R1010
5'-most EST	jC-atXP54C186E19T7038a1
Method	BLASTN
NCBI GI	g4539448
BLAST score	235
E value	1.0e-129
Match length	395
% identity	91
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T5C23 (ESSA project)

Seq. No.	134463
Contig ID	102691_2.R1010
5'-most EST	g2445900
Method	BLASTN
NCBI GI	g4455348
BLAST score	503
E value	0.0e+00
Match length	525
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T13J8

(ESSAII project)

Seq. No.	134464
Contig ID	102701_1.R1010
5'-most EST	jC-atXP54C185N3T7068d1
Method	BLASTN
NCBI GI	g4580454
BLAST score	107
E value	5.0e-53
Match length	408
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T2G17 genomic sequence, complete sequence

Seq. No.	134465
Contig ID	102718_1.R1010
5'-most EST	jC-atXP54C186B15T7019a1
Method	BLASTN
NCBI GI	g3860243
BLAST score	209
E value	1.0e-114
Match length	333
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC F15K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134466
Contig ID	102735_1.R1010
5'-most EST	jC-atXP54C185P17T7029d1
Method	BLASTN
NCBI GI	g2961335
BLAST score	207
E value	1.0e-112
Match length	445
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F1N20 (ESSAII project)

Seq. No.	134467
Contig ID	102736_1.R1010
5'-most EST	g957922
Method	BLASTX
NCBI GI	g4753652
BLAST score	171
E value	8.0e-16
Match length	123
% identity	49
NCBI Description	(AL049751) short-chain alcohol dehydrogenase like protein [Arabidopsis thaliana]

Seq. No.	134468
Contig ID	102750_1.R1010
5'-most EST	g2445897
Method	BLASTX
NCBI GI	g2494749
BLAST score	147
E value	5.0e-09

Match length	96
% identity	33
NCBI Description	GLUTAMINE SYNTHETASE (GLUTAMATE--AMMONIA LIGASE) (GS) >gi_1134886_emb_CAA54030_ (X76490) glutamine synthetase [Staphylococcus aureus]

Seq. No.	134469
Contig ID	102763_1.R1010
5'-most EST	jC-atXP54C184P8T7081a1
Method	BLASTN
NCBI GI	g3047100
BLAST score	174
E value	5.0e-93
Match length	290
% identity	92
NCBI Description	Arabidopsis thaliana BAC F6N23

Seq. No.	134470
Contig ID	102787_1.R1010
5'-most EST	jC-atXP53C185F10T7079a1
Method	BLASTX
NCBI GI	g3482924
BLAST score	55
E value	6.0e-54
Match length	114
% identity	98
NCBI Description	(AC003970) Highly similar to cinnamyl alcohol dehydrogenase, gi_1143445 [Arabidopsis thaliana]

Seq. No.	134471
Contig ID	102789_1.R1010
5'-most EST	jC-atXP53C185E10T7063a1

Seq. No.	134472
Contig ID	102790_1.R1010
5'-most EST	jC-atXP53C185D3T7031d1
Method	BLASTN
NCBI GI	g3941523
BLAST score	50
E value	6.0e-19
Match length	50
% identity	100
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	134473
Contig ID	102806_1.R1010
5'-most EST	jC-atXP53C185B13T7092d1
Method	BLASTX
NCBI GI	g1871178
BLAST score	778
E value	3.0e-86
Match length	167
% identity	91
NCBI Description	(U90439) unknown protein [Arabidopsis thaliana]

Seq. No. 134474

Contig ID	102828_1.R1010
5'-most EST	jC-atXP53C184J10T7038d1
Method	BLASTX
NCBI GI	g2281083
BLAST score	254
E value	8.0e-72
Match length	206
% identity	73
NCBI Description	(AC002333) polygalacturonase isolog [Arabidopsis thaliana]

Seq. No.	134475
Contig ID	102828_2.R1010
5'-most EST	jC-atXP90C246F17T7d2
Method	BLASTX
NCBI GI	g2281083
BLAST score	435
E value	5.0e-43
Match length	156
% identity	63
NCBI Description	(AC002333) polygalacturonase isolog [Arabidopsis thaliana]

Seq. No.	134476
Contig ID	102836_1.R1010
5'-most EST	jC-atXP53C184H18T7069a1
Method	BLASTN
NCBI GI	g2351063
BLAST score	270
E value	1.0e-150
Match length	501
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCL19, complete sequence [Arabidopsis thaliana]

Seq. No.	134477
Contig ID	102892_1.R1010
5'-most EST	jC-atXP50C180L21T7094d1
Method	BLASTX
NCBI GI	g419760
BLAST score	268
E value	3.0e-23
Match length	118
% identity	24
NCBI Description	P-glycoprotein atpgp1 - Arabidopsis thaliana >gi_3849833_emb_CAA43646_ (X61370) P-glycoprotein [Arabidopsis thaliana]

Seq. No.	134478
Contig ID	102896_1.R1010
5'-most EST	jC-atXP50C180K16T7054d1
Method	BLASTX
NCBI GI	g1730149
BLAST score	399
E value	2.0e-45
Match length	163
% identity	66
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi_1181548 (L27668) glyceraldehyde-3-phosphate

dehydrogenase [Chlamydomonas reinhardtii]

Seq. No.	134479
Contig ID	102898_1.R1010
5'-most EST	jC-atXP50C180J23T7022d1
Method	BLASTX
NCBI GI	g2443876
BLAST score	238
E value	8.0e-20
Match length	95
% identity	60
NCBI Description	(AC002294) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	134480
Contig ID	102900_1.R1010
5'-most EST	jC-atXP50C180J13T7093d1

Seq. No.	134481
Contig ID	102954_1.R1010
5'-most EST	jC-atXP50C179E11T7051d1
Method	BLASTX
NCBI GI	g4455217
BLAST score	508
E value	3.0e-60
Match length	161
% identity	77
NCBI Description	(AL035440) Avr9 elicitor response like protein [Arabidopsis thaliana]

Seq. No.	134482
Contig ID	102956_1.R1010
5'-most EST	jC-atXP50C179D10T7019d1
Method	BLASTX
NCBI GI	g3450842
BLAST score	376
E value	1.0e-40
Match length	159
% identity	53
NCBI Description	(AF080436) mitogen activated protein kinase kinase [Oryza sativa]

Seq. No.	134483
Contig ID	102973_1.R1010
5'-most EST	jC-atXP45C172B22T7015a1

Seq. No.	134484
Contig ID	102999_1.R1010
5'-most EST	g2733772

Seq. No.	134485
Contig ID	103002_1.R1010
5'-most EST	jC-atXP45C171L9T7005a1
Method	BLASTN
NCBI GI	g4589434
BLAST score	402
E value	0.0e+00
Match length	418

% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNJ7, complete sequence
Seq. No.	134486
Contig ID	103016_1.R1010
5'-most EST	jC-atXP45C171I4T7075a1
Method	BLASTX
NCBI GI	g1616787
BLAST score	345
E value	2.0e-32
Match length	68
% identity	96
NCBI Description	(U71122) pyruvate decarboxylase [Arabidopsis thaliana]
Seq. No.	134487
Contig ID	103039_1.R1010
5'-most EST	jC-atXP45C170N11T7002a1
Method	BLASTX
NCBI GI	g3367522
BLAST score	376
E value	9.0e-36
Match length	124
% identity	53
NCBI Description	(AC004392) EST gb_T04691 comes from this gene. [Arabidopsis thaliana]
Seq. No.	134488
Contig ID	103055_1.R1010
5'-most EST	jC-atXP11C98O20T7082d1
Method	BLASTX
NCBI GI	g4678360
BLAST score	944
E value	1.0e-102
Match length	209
% identity	90
NCBI Description	(AL049659) Cytochrome P450-like protein [Arabidopsis thaliana]
Seq. No.	134489
Contig ID	103061_1.R1010
5'-most EST	jC-atXP11C98K3T7065d1
Method	BLASTN
NCBI GI	g3702728
BLAST score	504
E value	0.0e+00
Match length	684
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M13, complete sequence [Arabidopsis thaliana]
Seq. No.	134490
Contig ID	103063_1.R1010
5'-most EST	jC-atXP24C122I20T7068d1
Method	BLASTX
NCBI GI	g2244891
BLAST score	86

E value	1.0e-102
Match length	227
% identity	92
NCBI Description	(Z97338) strong similarity to cytochrome P450 [Arabidopsis thaliana]

Seq. No.	134491
Contig ID	103065_1.R1010
5'-most EST	jC-atXP11C98J7T7062d1
Method	BLASTX
NCBI GI	g2370459
BLAST score	465
E value	4.0e-46
Match length	112
% identity	80
NCBI Description	(Y11987) FPF1 protein [Sinapis alba]

Seq. No.	134492
Contig ID	103085_2.R1010
5'-most EST	jC-atXP11C97P16T7034d1
Method	BLASTX
NCBI GI	g2765817
BLAST score	540
E value	2.0e-71
Match length	172
% identity	84
NCBI Description	(Z95352) AtMlo-h1 [Arabidopsis thaliana] >gi_3892049_gb_AAC78258.1_AAC78258 (AC002330) AtMlo-h1 [Arabidopsis thaliana]

Seq. No.	134493
Contig ID	103097_1.R1010
5'-most EST	jC-atXP11C97H2T7012d1
Method	BLASTN
NCBI GI	g3128141
BLAST score	355
E value	0.0e+00
Match length	863
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQD22, complete sequence [Arabidopsis thaliana]

Seq. No.	134494
Contig ID	103102_1.R1010
5'-most EST	jC-atXP11C97E4T7003d1
Method	BLASTX
NCBI GI	g4586114
BLAST score	105
E value	3.0e-21
Match length	107
% identity	50
NCBI Description	(AL049638) putative protein [Arabidopsis thaliana]

Seq. No.	134495
Contig ID	103229_1.R1010
5'-most EST	jC-atXP101CE2C10T7015d1

Seq. No.	134496
Contig ID	103229_2.R1010
5'-most EST	jC-atXP75C225K17T7s1
Method	BLASTX
NCBI GI	g4467100
BLAST score	363
E value	3.0e-34
Match length	150
% identity	49
NCBI Description	(AL035538) MADS-box protein AGL17-like protein [Arabidopsis thaliana]

Seq. No.	134497
Contig ID	103253_1.R1010
5'-most EST	jC-atXP101CE2A12T7061d1

Seq. No.	134498
Contig ID	103271_1.R1010
5'-most EST	jC-atXP101CE1G8T7075d1
Method	BLASTX
NCBI GI	g4490309
BLAST score	422
E value	4.0e-41
Match length	197
% identity	34
NCBI Description	(AL035678) peroxidase ATP17a-like protein [Arabidopsis thaliana]

Seq. No.	134499
Contig ID	103297_1.R1010
5'-most EST	jC-atXP101CE1E7T7034d1
Method	BLASTX
NCBI GI	g4262239
BLAST score	569
E value	1.0e-58
Match length	156
% identity	57
NCBI Description	(AC006200) putative membrane transporter [Arabidopsis thaliana]

Seq. No.	134500
Contig ID	103298_1.R1010
5'-most EST	jC-alX25043Q1E1H07a1
Method	BLASTN
NCBI GI	g4262221
BLAST score	255
E value	1.0e-141
Match length	552
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134501
Contig ID	103341_1.R1010
5'-most EST	jC-alX22037Q1E1A04a1

Seq. No.	134502

Contig ID	103371_1.R1010
5'-most EST	jC-atX22085Q1E1A09a1
Method	BLASTN
NCBI GI	g3046848
BLAST score	64
E value	2.0e-27
Match length	236
% identity	82
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18C1, complete sequence [Arabidopsis thaliana]

Seq. No.	134503
Contig ID	103380_1.R1010
5'-most EST	g2393198

Seq. No.	134504
Contig ID	103382_1.R1010
5'-most EST	jC-atXP12C99L17T7019a1
Method	BLASTX
NCBI GI	g1495366
BLAST score	211
E value	2.0e-16
Match length	120
% identity	35
NCBI Description	(Z69370) nitrite transporter [Cucumis sativus]

Seq. No.	134505
Contig ID	103382_3.R1010
5'-most EST	jC-atXmonuni10Ab03a1

Seq. No.	134506
Contig ID	103390_1.R1010
5'-most EST	jC-atXmonuni10Bb02a1
Method	BLASTX
NCBI GI	g4204278
BLAST score	568
E value	1.0e-58
Match length	109
% identity	100
NCBI Description	(AC004146) putative Cytochrome P450 protein [Arabidopsis thaliana]

Seq. No.	134507
Contig ID	103421_1.R1010
5'-most EST	g315779
Method	BLASTX
NCBI GI	g2980774
BLAST score	351
E value	2.0e-33
Match length	68
% identity	99
NCBI Description	(AL022198) leucyl aminopeptidase - like protein [Arabidopsis thaliana]

Seq. No.	134508
Contig ID	103444_1.R1010
5'-most EST	jC-atXmonuni10Af02a1

Seq. No.	134509
Contig ID	103459_1.R1010
5'-most EST	jC-atXmonuni10Bb06a1
Method	BLASTN
NCBI GI	g2760168
BLAST score	376
E value	0.0e+00
Match length	432
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MEE6, complete sequence [Arabidopsis thaliana]

Seq. No.	134510
Contig ID	103511_1.R1010
5'-most EST	jC-alX22043Q1E1H08a1
Method	BLASTX
NCBI GI	g2894559
BLAST score	218
E value	1.0e-17
Match length	70
% identity	67
NCBI Description	(AL021890) putative protein [Arabidopsis thaliana]

Seq. No.	134511
Contig ID	103523_1.R1010
5'-most EST	jC-atXmonuni10Dc03a1
Method	BLASTX
NCBI GI	g4510342
BLAST score	389
E value	8.0e-38
Match length	85
% identity	87
NCBI Description	(AC006921) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	134512
Contig ID	103526_1.R1010
5'-most EST	g2764195
Method	BLASTN
NCBI GI	g4376087
BLAST score	483
E value	0.0e+00
Match length	525
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	134513
Contig ID	103557_1.R1010
5'-most EST	jC-alX22044Q1E1H02a1

Seq. No.	134514
Contig ID	103599_1.R1010
5'-most EST	jC-alX22045Q1E1F09a1
Method	BLASTN
NCBI GI	g4538990

BLAST score	383
E value	0.0e+00
Match length	387
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T5L19 (ESSA project)

Seq. No.	134515
Contig ID	103615_1.R1010
5'-most EST	g2048276
Method	BLASTN
NCBI GI	g4262221
BLAST score	37
E value	4.0e-11
Match length	137
% identity	82
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134516
Contig ID	103629_1.R1010
5'-most EST	jC-atXP37C157M20T7d2
Method	BLASTX
NCBI GI	g3894178
BLAST score	88
E value	1.0e-27
Match length	112
% identity	54
NCBI Description	(AC005312) putative nucleic acid binding protein [Arabidopsis thaliana]

Seq. No.	134517
Contig ID	103636_1.R1010
5'-most EST	jC-alX22046Q1E1D01a1
Method	BLASTX
NCBI GI	g3021279
BLAST score	313
E value	7.0e-29
Match length	67
% identity	93
NCBI Description	(AL022347) serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	134518
Contig ID	103667_1.R1010
5'-most EST	jC-alX22047Q1E1A11a1
Method	BLASTX
NCBI GI	g2982437
BLAST score	243
E value	1.0e-20
Match length	70
% identity	70
NCBI Description	(AL022224) terpene cyclase like protein [Arabidopsis thaliana]

Seq. No.	134519
Contig ID	103681_1.R1010
5'-most EST	jC-atXmonuni10Df04a1

Method	BLASTX
NCBI GI	g4006818
BLAST score	300
E value	3.0e-27
Match length	59
% identity	100
NCBI Description	(AC005970) putative translation initiation factor eIF-2B, alpha subunit [Arabidopsis thaliana]

Seq. No.	134520
Contig ID	103695_1.R1010
5'-most EST	g747703
Method	BLASTX
NCBI GI	g1841355
BLAST score	233
E value	2.0e-19
Match length	53
% identity	74
NCBI Description	(D85381) cytochrome c oxidase subunit Vb precursor [Oryza sativa]

Seq. No.	134521
Contig ID	103741_1.R1010
5'-most EST	g1269157
Method	BLASTN
NCBI GI	g4757402
BLAST score	262
E value	1.0e-145
Match length	315
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MIG5, complete sequence

Seq. No.	134522
Contig ID	103751_1.R1010
5'-most EST	jC-alX22049Q1E1F03a1
Method	BLASTX
NCBI GI	g2618689
BLAST score	310
E value	2.0e-28
Match length	94
% identity	67
NCBI Description	(AC002510) unknown protein [Arabidopsis thaliana]

Seq. No.	134523
Contig ID	103770_1.R1010
5'-most EST	jC-alX22050Q1E1B04a1
Method	BLASTX
NCBI GI	g4220485
BLAST score	148
E value	2.0e-09
Match length	42
% identity	60
NCBI Description	(AC006069) putative beta-1,3-glucanase [Arabidopsis thaliana]

Seq. No. 134524

Contig ID	103783_1.R1010
5'-most EST	jC-atXmonuni10Dg08a1
Method	BLASTX
NCBI GI	g1523800
BLAST score	211
E value	8.0e-17
Match length	69
% identity	55
NCBI Description	(Y07694) MAP kinase kinase alpha protein kinase [Arabidopsis thaliana]

Seq. No.	134525
Contig ID	103784_1.R1010
5'-most EST	jC-alX22050Q1E1E04a1
Method	BLASTX
NCBI GI	g2961357
BLAST score	654
E value	2.0e-68
Match length	158
% identity	85
NCBI Description	(AL022140) putative protein [Arabidopsis thaliana]

Seq. No.	134526
Contig ID	103790_1.R1010
5'-most EST	jC-alX22050Q1E1F09a1
Method	BLASTN
NCBI GI	g3298532
BLAST score	380
E value	0.0e+00
Match length	408
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T26B15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134527
Contig ID	103798_1.R1010
5'-most EST	g2446099
Method	BLASTX
NCBI GI	g2827544
BLAST score	314
E value	8.0e-29
Match length	61
% identity	100
NCBI Description	(AL021635) HSP associated protein like [Arabidopsis thaliana]

Seq. No.	134528
Contig ID	103818_1.R1010
5'-most EST	g2723264
Method	BLASTN
NCBI GI	g3822224
BLAST score	286
E value	1.0e-160
Match length	399
% identity	92
NCBI Description	Arabidopsis thaliana RING-H2 finger protein RHG1a mRNA, partial cds

Seq. No.	134529
Contig ID	103841_1.R1010
5'-most EST	jC-alX22082Q1E1A04a1
Method	BLASTN
NCBI GI	g4589434
BLAST score	369
E value	0.0e+00
Match length	417
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNJ7, complete sequence

Seq. No.	134530
Contig ID	103842_1.R1010
5'-most EST	jC-atX22014Q1E1C04a1
Method	BLASTN
NCBI GI	g1839239
BLAST score	384
E value	0.0e+00
Match length	479
% identity	95
NCBI Description	Arabidopsis thaliana aVps41p (AVPS41) gene, partial cds

Seq. No.	134531
Contig ID	103849_1.R1010
5'-most EST	jC-alX22082Q1E2A08a1
Method	BLASTX
NCBI GI	g4455341
BLAST score	348
E value	1.0e-32
Match length	80
% identity	86
NCBI Description	(AL035522) O-methyltransferase-like protein [Arabidopsis thaliana]

Seq. No.	134532
Contig ID	103937_1.R1010
5'-most EST	g1216080
Method	BLASTN
NCBI GI	g2894591
BLAST score	296
E value	1.0e-166
Match length	384
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T6K21 (ESSAII project)

Seq. No.	134533
Contig ID	103976_1.R1010
5'-most EST	jC-alX24002Q1E1G08a1
Method	BLASTN
NCBI GI	g4056476
BLAST score	39
E value	2.0e-12
Match length	132
% identity	86

NCBI Description	Arabidopsis thaliana chromosome II BAC F3G5 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	134534
Contig ID	103990_1.R1010
5'-most EST	jC-atXP94CH4F11T7b1
Seq. No.	134535
Contig ID	104004_1.R1010
5'-most EST	jC-alX24004Q1E1A06a1
Method	BLASTN
NCBI GI	g3047100
BLAST score	267
E value	1.0e-148
Match length	500
% identity	99
NCBI Description	Arabidopsis thaliana BAC F6N23
Seq. No.	134536
Contig ID	104016_1.R1010
5'-most EST	jC-alX24004Q1E1D07a1
Seq. No.	134537
Contig ID	104041_1.R1010
5'-most EST	jC-atXP34C153D10T7a1
Method	BLASTX
NCBI GI	g4335719
BLAST score	97
E value	6.0e-13
Match length	72
% identity	50
NCBI Description	(AC006248) putative RING-H2 finger protein RHG1a [Arabidopsis thaliana]
Seq. No.	134538
Contig ID	104148_1.R1010
5'-most EST	jC-atXP10C95G22T7s2
Method	BLASTX
NCBI GI	g475719
BLAST score	484
E value	1.0e-48
Match length	116
% identity	46
NCBI Description	(U08467) RNA-binding protein 2 [Arabidopsis thaliana]
Seq. No.	134539
Contig ID	104250_1.R1010
5'-most EST	jC-atX24009Q1E1G11a1
Method	BLASTX
NCBI GI	g3335372
BLAST score	560
E value	1.0e-57
Match length	109
% identity	100
NCBI Description	(AC003028) putative SRG1 protein [Arabidopsis thaliana]
Seq. No.	134540

Contig ID	104297_1.R1010
5'-most EST	jC-alX24077Q1E1A02a1
Method	BLASTX
NCBI GI	g2191152
BLAST score	660
E value	3.0e-69
Match length	143
% identity	89
NCBI Description	(AF007269) A_IG002N01.31 gene product [Arabidopsis thaliana]

Seq. No.	134541
Contig ID	104406_1.R1010
5'-most EST	jC-atXL1025Q1B1G06b1
Method	BLASTN
NCBI GI	g1255986
BLAST score	177
E value	8.0e-95
Match length	209
% identity	96
NCBI Description	Arabidopsis thaliana GF14chi isoform (GRF1) gene, complete cds

Seq. No.	134542
Contig ID	104542_1.R1010
5'-most EST	g853726
Method	BLASTN
NCBI GI	g4587641
BLAST score	215
E value	1.0e-117
Match length	425
% identity	91
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No.	134543
Contig ID	104544_1.R1010
5'-most EST	jC-atXP123C119P20T7043a1
Method	BLASTX
NCBI GI	g2213590
BLAST score	457
E value	3.0e-45
Match length	133
% identity	67
NCBI Description	(AC000348) T7N9.10 [Arabidopsis thaliana]

Seq. No.	134544
Contig ID	104664_1.R1010
5'-most EST	jC-alX24089Q1E1F11a1

Seq. No.	134545
Contig ID	104684_1.R1010
5'-most EST	jC-atXP25C125A5T7091a1

Seq. No.	134546
Contig ID	104698_1.R1010
5'-most EST	g2596639

Method	BLASTX
NCBI GI	g2194117
BLAST score	267
E value	3.0e-23
Match length	103
% identity	54
NCBI Description	(AC002062) Strong similarity to Arabidopsis receptor protein kinase PR5K (gb_ATU48698). [Arabidopsis thaliana]

Seq. No.	134547
Contig ID	104706_1.R1010
5'-most EST	jC-atX24061Q1E1C06a1
Method	BLASTX
NCBI GI	g2880051
BLAST score	234
E value	2.0e-19
Match length	70
% identity	67
NCBI Description	(AC002340) putative protein kinase [Arabidopsis thaliana]

Seq. No.	134548
Contig ID	104719_1.R1010
5'-most EST	g1054203
Method	BLASTN
NCBI GI	g4220638
BLAST score	54
E value	4.0e-21
Match length	225
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIF21, complete sequence [Arabidopsis thaliana]

Seq. No.	134549
Contig ID	104719_2.R1010
5'-most EST	jC-atXP33C151B13T7s2

Seq. No.	134550
Contig ID	104757_1.R1010
5'-most EST	jC-alX24093Q1E1A05b1

Seq. No.	134551
Contig ID	104766_1.R1010
5'-most EST	jC-alX24093Q1E1C08a1
Method	BLASTN
NCBI GI	g2264305
BLAST score	347
E value	0.0e+00
Match length	395
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK23, complete sequence [Arabidopsis thaliana]

Seq. No.	134552
Contig ID	104801_1.R1010
5'-most EST	jC-atX24063Q1E1E02a1

Seq. No.	134553

Contig ID	104893_1.R1010
5'-most EST	g1103341

Seq. No.	134554
Contig ID	105213_1.R1010
5'-most EST	jC-alX24132Q1E1B03a1
Method	BLASTX
NCBI GI	g4007800
BLAST score	159
E value	2.0e-10
Match length	54
% identity	48
NCBI Description	(AL034463) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	134555
Contig ID	105391_1.R1010
5'-most EST	jC-alX25032Q1E1H03a1

Seq. No.	134556
Contig ID	105405_1.R1010
5'-most EST	jC-alX25033Q1E1E04a1
Method	BLASTX
NCBI GI	g2673910
BLAST score	177
E value	1.0e-12
Match length	85
% identity	53
NCBI Description	(AC002561) hypothetical protein [Arabidopsis thaliana]

Seq. No.	134557
Contig ID	105443_1.R1010
5'-most EST	jC-alX25036Q1E1F03a1
Method	BLASTN
NCBI GI	g3746057
BLAST score	302
E value	1.0e-169
Match length	456
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T16B12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134558
Contig ID	105476_1.R1010
5'-most EST	jC-alX25042Q1E1A12a1
Method	BLASTX
NCBI GI	g4314365
BLAST score	428
E value	2.0e-42
Match length	86
% identity	100
NCBI Description	(AC006340) putative copia-like retrotransposon Hopscotch [Arabidopsis thaliana]

Seq. No.	134559
Contig ID	105490_1.R1010
5'-most EST	jC-atXmonuni25Ca07b1
Method	BLASTN

09504405 - 041000

NCBI GI g4454587
BLAST score 346
E value 0.0e+00
Match length 497
% identity 99
NCBI Description Arabidopsis thaliana BAC F21A20 from chromosome V near 61 cM, complete sequence [Arabidopsis thaliana]

Seq. No. 134560
Contig ID 105493_1.R1010
5'-most EST jC-alX25042Q1E1E01a1
Method BLASTN
NCBI GI g2244950
BLAST score 335
E value 0.0e+00
Match length 389
% identity 96
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No. 134561
Contig ID 105498_1.R1010
5'-most EST jC-atXmonuni25Ac01a1
Method BLASTN
NCBI GI g4455348
BLAST score 326
E value 0.0e+00
Match length 429
% identity 100
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T13J8 (ESSAII project)

Seq. No. 134562
Contig ID 105506_1.R1010
5'-most EST jC-atXP4C86H11T7027a1
Method BLASTX
NCBI GI g2160185
BLAST score 427
E value 8.0e-42
Match length 142
% identity 52
NCBI Description (AC000132) Similar to S. pombe ISP4 (gb_D83992). [Arabidopsis thaliana]

Seq. No. 134563
Contig ID 105507_1.R1010
5'-most EST jC-atXmonuni25Ac11a1

Seq. No. 134564
Contig ID 105517_1.R1010
5'-most EST jC-alX25042Q1E1H09a1
Method BLASTX
NCBI GI g4220475
BLAST score 114
E value 2.0e-05
Match length 113
% identity 7

NCBI Description	(AC006069) hypothetical protein [Arabidopsis thaliana]
Seq. No.	134565
Contig ID	105518_1.R1010
5'-most EST	jC-alX25042Q1E1H11a1
Method	BLASTX
NCBI GI	g4063755
BLAST score	153
E value	6.0e-10
Match length	70
% identity	49
NCBI Description	(AC005851) putative chloroplast nucleoid DNA binding protein [Arabidopsis thaliana]
Seq. No.	134566
Contig ID	105520_1.R1010
5'-most EST	jC-alX25043Q1E1A03a1
Seq. No.	134567
Contig ID	105531_1.R1010
5'-most EST	g2413254
Method	BLASTN
NCBI GI	g4581084
BLAST score	186
E value	1.0e-100
Match length	291
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC T30F21 genomic sequence, complete sequence
Seq. No.	134568
Contig ID	105533_1.R1010
5'-most EST	jC-atXP112C126O22T7a1
Method	BLASTX
NCBI GI	g4056506
BLAST score	322
E value	2.0e-29
Match length	142
% identity	46
NCBI Description	(AC005896) nodulin-like protein [Arabidopsis thaliana]
Seq. No.	134569
Contig ID	105540_1.R1010
5'-most EST	jC-atXP44C171C15T7094a1
Method	BLASTX
NCBI GI	g3928150
BLAST score	568
E value	2.0e-58
Match length	162
% identity	75
NCBI Description	(AJ131049) hypothetical protein [Cicer arietinum]
Seq. No.	134570
Contig ID	105548_1.R1010
5'-most EST	jC-atXmonuni25Cb02b1
Method	BLASTN
NCBI GI	g2618599

BLAST score 107
E value 2.0e-53
Match length 175
% identity 90
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBD2, complete sequence [Arabidopsis thaliana]

Seq. No. 134571
Contig ID 105555_1.R1010
5'-most EST jC-alX25051Q1E1E04a1

Seq. No. 134572
Contig ID 105564_1.R1010
5'-most EST jC-alX25043Q1E1H06a1
Method BLASTN
NCBI GI g2244829
BLAST score 101
E value 1.0e-49
Match length 230
% identity 43
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No. 134573
Contig ID 105596_1.R1010
5'-most EST jC-atXmonuni25Cb06b1
Method BLASTX
NCBI GI g1663724
BLAST score 248
E value 4.0e-21
Match length 78
% identity 58
NCBI Description (U50846) 4-coumarate:coenzyme A ligase [Nicotiana tabacum]

Seq. No. 134574
Contig ID 105600_1.R1010
5'-most EST jC-atXmonuni25Ac08a1

Seq. No. 134575
Contig ID 105611_1.R1010
5'-most EST jC-alX25045Q1E1H04a1
Method BLASTN
NCBI GI g4490734
BLAST score 238
E value 1.0e-131
Match length 307
% identity 96
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No. 134576
Contig ID 105619_1.R1010
5'-most EST jC-alX25045Q1E1B04a1
Method BLASTX
NCBI GI g4056488
BLAST score 157
E value 2.0e-10

Match length	81
% identity	60
NCBI Description	(AC005896) unknown protein [Arabidopsis thaliana]
Seq. No.	134577
Contig ID	105634_1.R1010
5'-most EST	jC-atXmonuni25Db01a1
Seq. No.	134578
Contig ID	105638_1.R1010
5'-most EST	jC-alX25045Q1E1E07a1
Method	BLASTN
NCBI GI	g3046853
BLAST score	335
E value	0.0e+00
Match length	360
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRA19, complete sequence [Arabidopsis thaliana]
Seq. No.	134579
Contig ID	105645_1.R1010
5'-most EST	jC-alX25045Q1E1G01a1
Method	BLASTX
NCBI GI	g2129581
BLAST score	211
E value	9.0e-17
Match length	91
% identity	46
NCBI Description	envelope Ca2+-ATPase precursor - Arabidopsis thaliana >gi_471089_dbj_BAA03091_ (D13984) chloroplast envelope Ca2+-ATPase precursor [Arabidopsis thaliana] >gi_4165448_emb_CAA49558_ (X69940) envelope Ca2+-ATPase [Arabidopsis thaliana]
Seq. No.	134580
Contig ID	105649_1.R1010
5'-most EST	jC-atXmonuni25Ac08b1
Seq. No.	134581
Contig ID	105656_1.R1010
5'-most EST	jC-alX25046Q1E1A11a1
Method	BLASTN
NCBI GI	g2191157
BLAST score	388
E value	0.0e+00
Match length	409
% identity	88
NCBI Description	Arabidopsis thaliana BAC IG002P16
Seq. No.	134582
Contig ID	105669_1.R1010
5'-most EST	jC-atXmonuni25Ce11b1
Method	BLASTN
NCBI GI	g2979540
BLAST score	330
E value	0.0e+00

Match length	387
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F17K2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134583
Contig ID	105672_1.R1010
5'-most EST	jC-atXmonuni25Ce09b1
Method	BLASTN
NCBI GI	g3702736
BLAST score	198
E value	1.0e-107
Match length	308
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRI1, complete sequence [Arabidopsis thaliana]

Seq. No.	134584
Contig ID	105680_1.R1010
5'-most EST	g2062895
Method	BLASTX
NCBI GI	g2160176
BLAST score	294
E value	2.0e-26
Match length	83
% identity	67
NCBI Description	(AC000132) F21M12.25 gene product [Arabidopsis thaliana]

Seq. No.	134585
Contig ID	105693_1.R1010
5'-most EST	jC-alX25047Q1E1B01a1
Method	BLASTN
NCBI GI	g2656026
BLAST score	385
E value	0.0e+00
Match length	413
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDF20

Seq. No.	134586
Contig ID	105704_1.R1010
5'-most EST	jC-atXmonuni25Ae06a1
Method	BLASTN
NCBI GI	g2760169
BLAST score	234
E value	1.0e-129
Match length	401
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFB13, complete sequence [Arabidopsis thaliana]

Seq. No.	134587
Contig ID	105721_1.R1010
5'-most EST	jC-atXmonuni25Cf11b1

Seq. No. 134588

Contig ID	105732_1.R1010
5'-most EST	jC-alX25049Q1E1B02a1
Method	BLASTN
NCBI GI	g2645198
BLAST score	327
E value	0.0e+00
Match length	501
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC T26J12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134589
Contig ID	105743_1.R1010
5'-most EST	jC-atXmonuni25Ce05b1
Method	BLASTN
NCBI GI	g4589427
BLAST score	324
E value	0.0e+00
Match length	328
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFG13, complete sequence

Seq. No.	134590
Contig ID	105752_1.R1010
5'-most EST	jC-alX25048Q1E1G06a1

Seq. No.	134591
Contig ID	105756_1.R1010
5'-most EST	g957476
Method	BLASTX
NCBI GI	g2493495
BLAST score	513
E value	1.0e-54
Match length	134
% identity	79
NCBI Description	SERINE CARBOXYPEPTIDASE-LIKE >gi_2129878_pir__S72370 carboxypeptidase - garden pea (fragment) >gi_1089904_emb_CAA92216_ (Z68130) carboxypeptidase [Pisum sativum] >gi_1587217_prf__2206338A Ser carboxypeptidase [Pisum sativum]

Seq. No.	134592
Contig ID	105756_2.R1010
5'-most EST	jC-alX25048Q1E1G09a1
Method	BLASTX
NCBI GI	g2493495
BLAST score	324
E value	4.0e-30
Match length	78
% identity	71
NCBI Description	SERINE CARBOXYPEPTIDASE-LIKE >gi_2129878_pir__S72370 carboxypeptidase - garden pea (fragment) >gi_1089904_emb_CAA92216_ (Z68130) carboxypeptidase [Pisum sativum] >gi_1587217_prf__2206338A Ser carboxypeptidase [Pisum sativum]

Seq. No.	134593
Contig ID	105757_1.R1010
5'-most EST	jC-alX25048Q1E1H02a1
Method	BLASTN
NCBI GI	g4006815
BLAST score	323
E value	0.0e+00
Match length	331
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T6P5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134594
Contig ID	105762_1.R1010
5'-most EST	jC-alX25048Q1E1H12a1
Method	BLASTX
NCBI GI	g1934730
BLAST score	303
E value	1.0e-27
Match length	82
% identity	71
NCBI Description	(U95036) germin-like protein [Arabidopsis thaliana]

Seq. No.	134595
Contig ID	105764_1.R1010
5'-most EST	jC-atXmonuni25Ad05a1
Method	BLASTN
NCBI GI	g3510338
BLAST score	384
E value	0.0e+00
Match length	384
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21I16, complete sequence [Arabidopsis thaliana]

Seq. No.	134596
Contig ID	105774_1.R1010
5'-most EST	jC-atXP5C89H23T7038a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	43
E value	1.0e-14
Match length	51
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	134597
Contig ID	105793_1.R1010
5'-most EST	jC-atXmonuni25Ae10a1
Method	BLASTN
NCBI GI	g3046854
BLAST score	388
E value	0.0e+00
Match length	420
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRG7, complete sequence [Arabidopsis thaliana]

Seq. No.	134598
Contig ID	105795_1.R1010
5'-most EST	jC-atXmonuni25Ag07a1
Method	BLASTN
NCBI GI	g2351066
BLAST score	332
E value	0.0e+00
Match length	372
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOP9, complete sequence [Arabidopsis thaliana]

Seq. No.	134599
Contig ID	105812_1.R1010
5'-most EST	jC-alX25049Q1E1G02a1

Seq. No.	134600
Contig ID	105825_1.R1010
5'-most EST	g586966

Seq. No.	134601
Contig ID	105826_1.R1010
5'-most EST	g2062948
Method	BLASTN
NCBI GI	g4539378
BLAST score	336
E value	0.0e+00
Match length	462
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28A21 (ESSA project)

Seq. No.	134602
Contig ID	105837_1.R1010
5'-most EST	jC-atX25050Q1E1C03a1

Seq. No.	134603
Contig ID	105844_1.R1010
5'-most EST	g453761
Method	BLASTX
NCBI GI	g3328221
BLAST score	203
E value	2.0e-39
Match length	94
% identity	90
NCBI Description	(AF076920) thioredoxin peroxidase [Secale cereale]

Seq. No.	134604
Contig ID	105847_1.R1010
5'-most EST	jC-alX25051Q1E1A03a1
Method	BLASTN
NCBI GI	g4753195
BLAST score	67
E value	3.0e-29
Match length	311
% identity	85

NCBI Description	Arabidopsis thaliana BAC F15A18 from chromosome V near 68.5 cM, complete sequence
Seq. No.	134605
Contig ID	105851_1.R1010
5'-most EST	jC-atXmonuni25Ag09a1
Method	BLASTN
NCBI GI	g4589423
BLAST score	322
E value	0.0e+00
Match length	405
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K7B16, complete sequence
Seq. No.	134606
Contig ID	105856_1.R1010
5'-most EST	jC-alX25051Q1E1B12a1
Method	BLASTX
NCBI GI	g3660187
BLAST score	221
E value	5.0e-18
Match length	58
% identity	67
NCBI Description	Chain A, E2-C, An Ubiquitin Conjugating Enzyme Required For The Destruction Of Mitotic Cyclins >gi_3660188_pdb_1E2C_B Chain B, E2-C, An Ubiquitin Conjugating Enzyme Required For The Destruction Of Mitotic Cyclins >gi_3660189_pdb_1E2C_C Chain C, E2-C, An Ubiquitin Conjugating Enzyme Required For The Destruction Of Mitotic Cyclins >gi_4388942_pdb_2E2C_ E2-C, An Ubiquitin Conjugating Enzyme Required For The Destruction Of Mitotic Cyclins
Seq. No.	134607
Contig ID	105861_1.R1010
5'-most EST	jC-atXmonuni25Cg07b1
Method	BLASTN
NCBI GI	g2832667
BLAST score	358
E value	0.0e+00
Match length	553
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T10I14 (ESSAII project)
Seq. No.	134608
Contig ID	105866_1.R1010
5'-most EST	jC-atXmonuni25Cg09b1
Seq. No.	134609
Contig ID	105870_1.R1010
5'-most EST	jC-atXmonuni25Ah04a1
Method	BLASTN
NCBI GI	g3510337
BLAST score	209
E value	1.0e-114
Match length	381

% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E20, complete sequence [Arabidopsis thaliana]
Seq. No.	134610
Contig ID	105880_1.R1010
5'-most EST	jC-alX25051Q1E1E10a1
Seq. No.	134611
Contig ID	105889_1.R1010
5'-most EST	jC-alX25052Q1E1A11a1
Method	BLASTX
NCBI GI	g3297815
BLAST score	244
E value	1.0e-33
Match length	71
% identity	92
NCBI Description	(AL031032) putative protein [Arabidopsis thaliana]
Seq. No.	134612
Contig ID	105909_1.R1010
5'-most EST	jC-atXmonuni25Ch05b1
Method	BLASTN
NCBI GI	g3510336
BLAST score	344
E value	0.0e+00
Match length	479
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18J17, complete sequence [Arabidopsis thaliana]
Seq. No.	134613
Contig ID	105913_1.R1010
5'-most EST	jC-atXmonuni25Dg01a1
Method	BLASTN
NCBI GI	g3492855
BLAST score	349
E value	0.0e+00
Match length	401
% identity	90
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F20N2, complete sequence [Arabidopsis thaliana]
Seq. No.	134614
Contig ID	105945_1.R1010
5'-most EST	jC-alX25071Q1E1F11a1
Method	BLASTN
NCBI GI	g2583106
BLAST score	317
E value	1.0e-178
Match length	431
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F4L23 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	134615
Contig ID	106271_1.R1010

5'-most EST	g2763960
Method	BLASTN
NCBI GI	g3298532
BLAST score	354
E value	0.0e+00
Match length	402
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T26B15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134616
Contig ID	106393_1.R1010
5'-most EST	g2722930
Method	BLASTN
NCBI GI	g2264304
BLAST score	164
E value	5.0e-87
Match length	338
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBG8, complete sequence [Arabidopsis thaliana]

Seq. No.	134617
Contig ID	106401_1.R1010
5'-most EST	g2749256
Method	BLASTX
NCBI GI	g3341672
BLAST score	213
E value	6.0e-17
Match length	60
% identity	77
NCBI Description	(AC003672) putative heme A:farnesyltransferase, 5' partial [Arabidopsis thaliana]

Seq. No.	134618
Contig ID	106422_1.R1010
5'-most EST	jC-alX25113Q1E1F11a1
Method	BLASTX
NCBI GI	g3152557
BLAST score	90
E value	3.0e-10
Match length	80
% identity	50
NCBI Description	(AC002986) Contains similarity to S. cerevisiae hypothetical protein YOR197w, gb_Z75105. EST gb_T76227 comes from this gene. [Arabidopsis thaliana]

Seq. No.	134619
Contig ID	106428_1.R1010
5'-most EST	jC-atXP12C103C7T7052a1
Method	BLASTN
NCBI GI	g2618605
BLAST score	482
E value	0.0e+00
Match length	482
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUK11, complete sequence [Arabidopsis thaliana]

Seq. No.	134620
Contig ID	106462_1.R1010
5'-most EST	g398682
Method	BLASTN
NCBI GI	g2618605
BLAST score	234
E value	1.0e-129
Match length	393
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUK11, complete sequence [Arabidopsis thaliana]

Seq. No.	134621
Contig ID	106464_1.R1010
5'-most EST	jC-alX25114Q1E1G12a1

Seq. No.	134622
Contig ID	106575_1.R1010
5'-most EST	jC-atXmonuni26Ch08a1
Method	BLASTX
NCBI GI	g2245107
BLAST score	578
E value	7.0e-60
Match length	111
% identity	59
NCBI Description	(Z97343) thioesterase homolog [Arabidopsis thaliana]

Seq. No.	134623
Contig ID	106596_1.R1010
5'-most EST	jC-atXP20C115G18T7031a1
Method	BLASTN
NCBI GI	g3241917
BLAST score	46
E value	2.0e-16
Match length	74
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19B1, complete sequence [Arabidopsis thaliana]

Seq. No.	134624
Contig ID	106654_1.R1010
5'-most EST	g671782
Method	BLASTN
NCBI GI	g2570223
BLAST score	237
E value	1.0e-130
Match length	408
% identity	96
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F20D22 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134625
Contig ID	106868_1.R1010
5'-most EST	jC-atXP58C192E21T7s3
Method	BLASTX

NCBI GI	g3386603
BLAST score	923
E value	1.0e-100
Match length	194
% identity	94
NCBI Description	(AC004665) unknown protein [Arabidopsis thaliana]

Seq. No.	134626
Contig ID	106869_1.R1010
5'-most EST	g2748347
Method	BLASTN
NCBI GI	g4325340
BLAST score	312
E value	1.0e-175
Match length	422
% identity	93
NCBI Description	Arabidopsis thaliana BAC T1J1

Seq. No.	134627
Contig ID	106912_1.R1010
5'-most EST	jC-atXP64C205P8T7s1
Method	BLASTN
NCBI GI	g4678705
BLAST score	400
E value	0.0e+00
Match length	421
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7 (ESSA project)

Seq. No.	134628
Contig ID	106933_1.R1010
5'-most EST	g506544

Seq. No.	134629
Contig ID	106949_1.R1010
5'-most EST	g510802
Method	BLASTX
NCBI GI	g2129655
BLAST score	235
E value	1.0e-19
Match length	46
% identity	100
NCBI Description	OBP32pep protein - Arabidopsis thaliana (fragment) >gi_1022799 (U37698) OBP32pep [Arabidopsis thaliana]

Seq. No.	134630
Contig ID	106991_1.R1010
5'-most EST	jC-atX22012Q1E1C06a1
Method	BLASTN
NCBI GI	g2924768
BLAST score	231
E value	1.0e-127
Match length	263
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F25I18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134631
Contig ID	107012_1.R1010
5'-most EST	g2749305
Method	BLASTX
NCBI GI	g1707857
BLAST score	50
E value	7.0e-31
Match length	85
% identity	80
NCBI Description	(Y09291) obtusifoliol 14-alpha-demethylase [Triticum aestivum]

Seq. No.	134632
Contig ID	107066_1.R1010
5'-most EST	jC-atXZ4109Q1E1B06a1
Method	BLASTX
NCBI GI	g4510342
BLAST score	409
E value	4.0e-40
Match length	98
% identity	83
NCBI Description	(AC006921) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	134633
Contig ID	107125_1.R1010
5'-most EST	jC-atXP123C117C18T7067a1
Method	BLASTX
NCBI GI	g4580471
BLAST score	335
E value	5.0e-31
Match length	65
% identity	92
NCBI Description	(AC006081) unknown protein [Arabidopsis thaliana]

Seq. No.	134634
Contig ID	107125_2.R1010
5'-most EST	jC-atXP123C162E13T7073a1
Method	BLASTN
NCBI GI	g4580454
BLAST score	193
E value	1.0e-104
Match length	401
% identity	87
NCBI Description	Arabidopsis thaliana chromosome II BAC T2G17 genomic sequence, complete sequence

Seq. No.	134635
Contig ID	107135_1.R1010
5'-most EST	jC-atXP112C132G21T7a1
Method	BLASTN
NCBI GI	g3212846
BLAST score	317
E value	1.0e-178
Match length	579
% identity	99

NCBI Description	Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	134636
Contig ID	107135_3.R1010
5'-most EST	jC-atXP49C178N3T7023a1
Method	BLASTN
NCBI GI	g3212846
BLAST score	331
E value	0.0e+00
Match length	594
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	134637
Contig ID	107146_1.R1010
5'-most EST	jC-atX22016Q1E1B07a1
Method	BLASTX
NCBI GI	g3193301
BLAST score	90
E value	2.0e-37
Match length	89
% identity	99
NCBI Description	(AF069298) Arabidopsis putative chloroplast outer envelope 86-like protein T10P11.19 (GB: AC002330) [Arabidopsis thaliana]
Seq. No.	134638
Contig ID	107217_1.R1010
5'-most EST	jC-atXP3C85B2T7093a1
Method	BLASTN
NCBI GI	g3128143
BLAST score	593
E value	0.0e+00
Match length	635
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTI20, complete sequence [Arabidopsis thaliana]
Seq. No.	134639
Contig ID	107281_1.R1010
5'-most EST	g2580671
Method	BLASTX
NCBI GI	g2492782
BLAST score	249
E value	5.0e-21
Match length	93
% identity	55
NCBI Description	ALPHA-GALACTOSIDASE PRECURSOR (MELIBIASE) (ALPHA-D-GALACTOSIDE GALACTOHYDROLASE) >gi_504489 (L27992) alpha-galactosidase [Coffea arabica]
Seq. No.	134640
Contig ID	107301_1.R1010
5'-most EST	jC-atX22021Q1E1D03a1
Method	BLASTX

NCBI GI	g2462836
BLAST score	270
E value	8.0e-24
Match length	60
% identity	85
NCBI Description	(AF000657) beta-glucanase [Arabidopsis thaliana]

Seq. No.	134641
Contig ID	107377_1.R1010
5'-most EST	g902611
Method	BLASTX
NCBI GI	g1706739
BLAST score	417
E value	1.0e-40
Match length	146
% identity	53
NCBI Description	FLAVONOL 3-SULFOTRANSFERASE (F3-ST) >gi_285285_pir__B40216 flavonol 3'-sulfotransferase - Flaveria chloraefolia

Seq. No.	134642
Contig ID	107433_1.R1010
5'-most EST	g935698
Method	BLASTN
NCBI GI	g4454022
BLAST score	379
E value	0.0e+00
Match length	422
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16 (ESSAII project)

Seq. No.	134643
Contig ID	107438_1.R1010
5'-most EST	jC-atXP52C182L13T7s2
Method	BLASTX
NCBI GI	g2832632
BLAST score	149
E value	2.0e-09
Match length	54
% identity	54
NCBI Description	(AL021711) hypothetical protein [Arabidopsis thaliana]

Seq. No.	134644
Contig ID	107449_1.R1010
5'-most EST	jC-atX25024Q1E1C05a1

Seq. No.	134645
Contig ID	107472_1.R1010
5'-most EST	jC-atXP20C114A14T7075a1
Method	BLASTX
NCBI GI	g2245037
BLAST score	400
E value	2.0e-38
Match length	214
% identity	40
NCBI Description	(Z97342) nuclear antigen homolog [Arabidopsis thaliana]

Seq. No. 134646
Contig ID 107495_1.R1010
5'-most EST jC-atX22029Q1E1A08a1

Seq. No. 134647
Contig ID 107496_1.R1010
5'-most EST g2749166
Method BLASTX
NCBI GI g3298545
BLAST score 241
E value 3.0e-20
Match length 42
% identity 100
NCBI Description (AC004681) unknown protein [Arabidopsis thaliana]

Seq. No. 134648
Contig ID 107499_1.R1010
5'-most EST jC-atX25002Q1E1F10a1

Seq. No. 134649
Contig ID 107514_1.R1010
5'-most EST g1103350
Method BLASTX
NCBI GI g3831453
BLAST score 475
E value 1.0e-47
Match length 111
% identity 71
NCBI Description (AC005700) unknown protein [Arabidopsis thaliana]

Seq. No. 134650
Contig ID 107530_1.R1010
5'-most EST jC-atX22031Q1E1A01a1
Method BLASTN
NCBI GI g2435510
BLAST score 349
E value 0.0e+00
Match length 571
% identity 87
NCBI Description Arabidopsis thaliana BAC TM017A05

Seq. No. 134651
Contig ID 107546_1.R1010
5'-most EST jC-atXP122C117M22T7036a1
Method BLASTN
NCBI GI g3510247
BLAST score 541
E value 0.0e+00
Match length 657
% identity 95
NCBI Description Arabidopsis thaliana chromosome II BAC F19D11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 134652
Contig ID 107554_1.R1010
5'-most EST g2722604
Method BLASTX

NCBI GI	g3249084
BLAST score	401
E value	4.0e-39
Match length	87
% identity	84
NCBI Description	(AC004473) Similar to red-1 (related to thioredoxin) gene gb_X92750 from Mus musculus. ESTs gb_AA712687 and gb_Z37223 come from this gene [Arabidopsis thaliana]

Seq. No.	134653
Contig ID	107566_1.R1010
5'-most EST	jC-atX25004Q1E1F05a1

Seq. No.	134654
Contig ID	107575_1.R1010
5'-most EST	jC-atX22033Q1E1F03a1

Seq. No.	134655
Contig ID	107581_1.R1010
5'-most EST	jC-atX25012Q1E1F08a1

Seq. No.	134656
Contig ID	107611_1.R1010
5'-most EST	jC-atX22034Q1E2E03a1
Method	BLASTN
NCBI GI	g3241920
BLAST score	198
E value	1.0e-107
Match length	329
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAE1, complete sequence [Arabidopsis thaliana]

Seq. No.	134657
Contig ID	107808_2.R1010
5'-most EST	jC-atX22052Q1E1B08a1
Method	BLASTN
NCBI GI	g4584531
BLAST score	303
E value	1.0e-170
Match length	347
% identity	59
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9E8 (ESSA project)

Seq. No.	134658
Contig ID	107812_1.R1010
5'-most EST	g2748926

Seq. No.	134659
Contig ID	107819_1.R1010
5'-most EST	jC-atX22052Q1E1C09b1

Seq. No.	134660
Contig ID	107821_1.R1010
5'-most EST	g2413479

Seq. No.	134661
Contig ID	107870_1.R1010
5'-most EST	jC-atX22055Q1E1D04a1

Seq. No.	134662
Contig ID	107900_1.R1010
5'-most EST	jC-atX22056Q1E1F06a1
Method	BLASTN
NCBI GI	g2656025
BLAST score	337
E value	0.0e+00
Match length	353
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCD7

Seq. No.	134663
Contig ID	107972_1.R1010
5'-most EST	jC-atX22060Q1E1F04a1

Seq. No.	134664
Contig ID	108048_1.R1010
5'-most EST	g2393691

Seq. No.	134665
Contig ID	108058_1.R1010
5'-most EST	jC-atX22066Q1E1G02a1
Method	BLASTN
NCBI GI	g3399678
BLAST score	333
E value	0.0e+00
Match length	333
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F13M7 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134666
Contig ID	108083_1.R1010
5'-most EST	jC-atX22068Q1E1B05a1
Method	BLASTN
NCBI GI	g4220644
BLAST score	83
E value	8.0e-39
Match length	251
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXL8, complete sequence [Arabidopsis thaliana]

Seq. No.	134667
Contig ID	108086_1.R1010
5'-most EST	jC-atX22068Q1E1B12a1

Seq. No.	134668
Contig ID	108093_1.R1010
5'-most EST	jC-atXP25C125M21T7024a1
Method	BLASTN
NCBI GI	g2760165

BLAST score	314
E value	1.0e-176
Match length	505
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC9, complete sequence [Arabidopsis thaliana]

Seq. No.	134669
Contig ID	108109_1.R1010
5'-most EST	jC-atX22069Q1E1F07a1
Method	BLASTN
NCBI GI	g3250673
BLAST score	291
E value	1.0e-163
Match length	311
% identity	75
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T16H5 (ESSAII project)

Seq. No.	134670
Contig ID	108161_1.R1010
5'-most EST	g937668
Method	BLASTX
NCBI GI	g232202
BLAST score	321
E value	1.0e-29
Match length	150
% identity	46
NCBI Description	GLUTATHIONE S-TRANSFERASE PARB (CLASS-PHI) >gi_285295_pir__A41789 glutathione transferase (EC 2.5.1.18) - common tobacco >gi_218294_dbj_BAA01394_ (D10524) glutathione S-transferase [Nicotiana tabacum]

Seq. No.	134671
Contig ID	108181_1.R1010
5'-most EST	g2446048
Method	BLASTN
NCBI GI	g3702731
BLAST score	310
E value	1.0e-174
Match length	388
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFC19, complete sequence [Arabidopsis thaliana]

Seq. No.	134672
Contig ID	108218_1.R1010
5'-most EST	g2062878
Method	BLASTN
NCBI GI	g3641835
BLAST score	168
E value	1.0e-89
Match length	168
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T4L20 (ESSAII project)

Seq. No.	134673
Contig ID	108235_1.R1010
5'-most EST	g2048814
Method	BLASTX
NCBI GI	g4455220
BLAST score	1032
E value	1.0e-112
Match length	276
% identity	60
NCBI Description	(AL035440) putative aconitase [Arabidopsis thaliana]

Seq. No.	134674
Contig ID	108297_1.R1010
5'-most EST	g2048818
Method	BLASTN
NCBI GI	g2618602
BLAST score	336
E value	0.0e+00
Match length	391
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	134675
Contig ID	108332_1.R1010
5'-most EST	g2062908
Method	BLASTX
NCBI GI	g2911059
BLAST score	576
E value	2.0e-59
Match length	122
% identity	96
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	134676
Contig ID	108355_1.R1010
5'-most EST	g2749201
Method	BLASTN
NCBI GI	g2924734
BLAST score	299
E value	1.0e-167
Match length	447
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXE10, complete sequence [Arabidopsis thaliana]

Seq. No.	134677
Contig ID	108501_1.R1010
5'-most EST	jC-atX22088Q1E1C05a1
Method	BLASTN
NCBI GI	g3608126
BLAST score	400
E value	0.0e+00
Match length	445
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T32F12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134678
Contig ID	108547_1.R1010
5'-most EST	jC-atXmonuni27De10b1

Seq. No.	134679
Contig ID	108647_1.R1010
5'-most EST	jC-atXmonuni27Bh10a1
Method	BLASTX
NCBI GI	g4587589
BLAST score	300
E value	3.0e-27
Match length	121
% identity	47
NCBI Description	(AC007232) hypothetical protein [Arabidopsis thaliana]

Seq. No.	134680
Contig ID	108675_1.R1010
5'-most EST	jC-atXmonuni27Bh08a1
Method	BLASTN
NCBI GI	g4662609
BLAST score	405
E value	0.0e+00
Match length	437
% identity	98
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10A5, complete sequence

Seq. No.	134681
Contig ID	108720_1.R1010
5'-most EST	jC-atX23007Q1E1H05a1

Seq. No.	134682
Contig ID	108743_1.R1010
5'-most EST	jC-atXP3C83G12T7070a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	55
E value	8.0e-22
Match length	55
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	134683
Contig ID	108823_1.R1010
5'-most EST	g1033247
Method	BLASTX
NCBI GI	g2129753
BLAST score	846
E value	6.0e-91
Match length	193
% identity	84
NCBI Description	threonine synthase (EC 4.2.99.2) precursor - Arabidopsis thaliana (fragment) >gi_1448917 (L41666) threonine synthase [Arabidopsis thaliana]

Seq. No. 134684

Contig ID	108961_1.R1010
5'-most EST	jC-atXP94CH5G7T7b1
Method	BLASTN
NCBI GI	g4454587
BLAST score	234
E value	1.0e-129
Match length	331
% identity	97
NCBI Description	Arabidopsis thaliana BAC F21A20 from chromosome V near 61 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	134685
Contig ID	108984_1.R1010
5'-most EST	g3450472
Method	BLASTX
NCBI GI	g1699024
BLAST score	52
E value	7.0e-16
Match length	85
% identity	55
NCBI Description	(U78866) gene1000 [Arabidopsis thaliana] >gi_1699057 (U78870) unknown [Arabidopsis thaliana]

Seq. No.	134686
Contig ID	109099_1.R1010
5'-most EST	jC-atXP52C181L9T7s2
Method	BLASTN
NCBI GI	g4589442
BLAST score	262
E value	1.0e-145
Match length	431
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MVP2, complete sequence

Seq. No.	134687
Contig ID	109110_1.R1010
5'-most EST	jC-atX23026Q1E1D07a1

Seq. No.	134688
Contig ID	109123_1.R1010
5'-most EST	jC-atX24001Q1E1B02a1
Method	BLASTX
NCBI GI	g1731990
BLAST score	218
E value	4.0e-34
Match length	108
% identity	67
NCBI Description	(Y09602) serine carboxypeptidase II, CP-MII [Hordeum vulgare]

Seq. No.	134689
Contig ID	109127_1.R1010
5'-most EST	jC-atXP26C124P8T7044a1
Method	BLASTN
NCBI GI	g3065834
BLAST score	763

E value	0.0e+00
Match length	836
% identity	98
NCBI Description	Arabidopsis thaliana putative methyltransferase gene, complete cds

Seq. No.	134690
Contig ID	109275_1.R1010
5'-most EST	jC-atX24007Q1E1D06a1
Method	BLASTX
NCBI GI	g3152618
BLAST score	253
E value	1.0e-21
Match length	97
% identity	52
NCBI Description	(AC004482) putative pectinesterase [Arabidopsis thaliana] >gi_3242724 (AC003040) putative pectinesterase [Arabidopsis thaliana]

Seq. No.	134691
Contig ID	109314_1.R1010
5'-most EST	jC-atX24009Q1E1D12a1
Method	BLASTN
NCBI GI	g3128136
BLAST score	300
E value	1.0e-168
Match length	344
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1F13, complete sequence [Arabidopsis thaliana]

Seq. No.	134692
Contig ID	109332_1.R1010
5'-most EST	jC-atX24061Q1E1D08a2

Seq. No.	134693
Contig ID	109466_1.R1010
5'-most EST	jC-atX24015Q1E1A01a1
Method	BLASTN
NCBI GI	g4757409
BLAST score	394
E value	0.0e+00
Match length	394
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MVC8, complete sequence

Seq. No.	134694
Contig ID	109542_1.R1010
5'-most EST	jC-atXP2C76D6T7041a1
Method	BLASTN
NCBI GI	g3341671
BLAST score	541
E value	0.0e+00
Match length	621
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F16B22 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134695
Contig ID	109600_1.R1010
5'-most EST	g3450410
Method	BLASTN
NCBI GI	g409704
BLAST score	378
E value	0.0e+00
Match length	390
% identity	99
NCBI Description	Arabidopsis thaliana ETR1 gene, complete cds. >gi_3011559_gb_I75418_I75418 Sequence 1 from patent US

Seq. No.	134696
Contig ID	109631_1.R1010
5'-most EST	jC-atX24022Q1E1D07a1

Seq. No.	134697
Contig ID	109667_1.R1010
5'-most EST	jC-atX24023Q1E1F07a1
Method	BLASTN
NCBI GI	g1402915
BLAST score	35
E value	3.0e-10
Match length	51
% identity	92
NCBI Description	A.thaliana mRNA for peroxidase, prxr7

Seq. No.	134698
Contig ID	109693_1.R1010
5'-most EST	g1103339
Method	BLASTN
NCBI GI	g4587582
BLAST score	152
E value	8.0e-80
Match length	506
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T16B14 genomic sequence, complete sequence

Seq. No.	134699
Contig ID	109788_1.R1010
5'-most EST	jC-atXP15C106G5T7021a1

Seq. No.	134700
Contig ID	109839_1.R1010
5'-most EST	jC-atX24028Q1E1C08a1

Seq. No.	134701
Contig ID	109844_1.R1010
5'-most EST	jC-atX24028Q1E1D01a1
Method	BLASTN
NCBI GI	g2351071
BLAST score	292
E value	1.0e-163
Match length	336

% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MVA3, complete sequence [Arabidopsis thaliana]

Seq. No.	134702
Contig ID	109881_1.R1010
5'-most EST	g2062778
Method	BLASTN
NCBI GI	g3128135
BLAST score	302
E value	1.0e-169
Match length	343
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E1, complete sequence [Arabidopsis thaliana]

Seq. No.	134703
Contig ID	109918_1.R1010
5'-most EST	g2062931
Method	BLASTX
NCBI GI	g2316022
BLAST score	328
E value	2.0e-30
Match length	68
% identity	97
NCBI Description	(U96399) MRP-like ABC transporter [Arabidopsis thaliana]

Seq. No.	134704
Contig ID	109931_1.R1010
5'-most EST	g3450174
Method	BLASTX
NCBI GI	g4467122
BLAST score	408
E value	8.0e-40
Match length	83
% identity	95
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]

Seq. No.	134705
Contig ID	110019_1.R1010
5'-most EST	jC-atX24037Q1E2A03a1

Seq. No.	134706
Contig ID	110035_1.R1010
5'-most EST	jC-atX24106Q1E1C12b1
Method	BLASTN
NCBI GI	g3702735
BLAST score	101
E value	2.0e-49
Match length	422
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQL5, complete sequence [Arabidopsis thaliana]

Seq. No.	134707
Contig ID	110098_1.R1010
5'-most EST	jC-atX24040Q1E1F03b1

Method	BLASTX
NCBI GI	g1361155
BLAST score	146
E value	3.0e-09
Match length	84
% identity	44
NCBI Description	hypothetical protein o215b - Escherichia coli >gi_537235 (U14003) Kenn Rudd identifies as gpmB [Escherichia coli] >gi_1790856 (AE000509) phosphoglyceromutase 2 [Escherichia coli]

Seq. No.	134708
Contig ID	110195_1.R1010
5'-most EST	jC-atXP27C133D24T7s2
Method	BLASTX
NCBI GI	g2129941
BLAST score	280
E value	8.0e-25
Match length	69
% identity	75
NCBI Description	zeaxanthin epoxidase precursor - curled-leaved tobacco >gi_1370274_emb_CAA65048_ (X95732) zeaxanthin epoxidase [Nicotiana plumbaginifolia]

Seq. No.	134709
Contig ID	110267_1.R1010
5'-most EST	g2747534
Method	BLASTN
NCBI GI	g4519195
BLAST score	384
E value	0.0e+00
Match length	692
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MQC12, complete sequence

Seq. No.	134710
Contig ID	110346_1.R1010
5'-most EST	jC-atX24051Q1E1C06a1
Method	BLASTX
NCBI GI	g3033398
BLAST score	47
E value	5.0e-24
Match length	77
% identity	81
NCBI Description	(AC004238) putative phosphoribosylaminoimidazolecarboxamide formyltransferase [Arabidopsis thaliana]

Seq. No.	134711
Contig ID	110413_1.R1010
5'-most EST	g2393340
Method	BLASTN
NCBI GI	g4567237
BLAST score	96
E value	2.0e-46
Match length	473
% identity	94

NCBI Description	Arabidopsis thaliana chromosome II BAC T22F11 genomic sequence, complete sequence
Seq. No.	134712
Contig ID	110418_1.R1010
5'-most EST	jC-atXP47C17204T7s2
Method	BLASTN
NCBI GI	g2337888
BLAST score	225
E value	1.0e-123
Match length	527
% identity	95
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14J16, complete sequence [Arabidopsis thaliana]
Seq. No.	134713
Contig ID	110423_1.R1010
5'-most EST	g1215987
Method	BLASTN
NCBI GI	g2145357
BLAST score	313
E value	1.0e-176
Match length	394
% identity	97
NCBI Description	A.thaliana ATHB-9 gene
Seq. No.	134714
Contig ID	110430_1.R1010
5'-most EST	jC-atXP98CH8C11T7b1
Method	BLASTN
NCBI GI	g3123718
BLAST score	41
E value	1.0e-13
Match length	57
% identity	93
NCBI Description	Homo sapiens gene for 24-kDa subunit of complex I, exon
Seq. No.	134715
Contig ID	110454_1.R1010
5'-most EST	g2048218
Method	BLASTN
NCBI GI	g3176693
BLAST score	269
E value	1.0e-150
Match length	372
% identity	93
NCBI Description	Arabidopsis thaliana chromosome I BAC T27I1 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	134716
Contig ID	110468_1.R1010
5'-most EST	g2763164
Method	BLASTX
NCBI GI	g4455359
BLAST score	234
E value	2.0e-19
Match length	50

% identity	88
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	134717
Contig ID	110470_1.R1010
5'-most EST	g3450356
Method	BLASTN
NCBI GI	g4159700
BLAST score	317
E value	1.0e-178
Match length	530
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1L20, complete sequence

Seq. No.	134718
Contig ID	110525_1.R1010
5'-most EST	g2749454
Method	BLASTX
NCBI GI	g3334144
BLAST score	76
E value	2.0e-38
Match length	132
% identity	64
NCBI Description	G1/S-SPECIFIC CYCLIN C-TYPE >gi_1695698_dbj_BAA13181_ (D86925) C-type cyclin [Oryza sativa]

Seq. No.	134719
Contig ID	110560_1.R1010
5'-most EST	g507037
Method	BLASTN
NCBI GI	g3985958
BLAST score	346
E value	0.0e+00
Match length	540
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZN1, complete sequence [Arabidopsis thaliana]

Seq. No.	134720
Contig ID	110568_1.R1010
5'-most EST	jC-atX24060Q1E1H02a1

Seq. No.	134721
Contig ID	110675_1.R1010
5'-most EST	jC-atX24075Q1E1A09a1
Method	BLASTX
NCBI GI	g4678230
BLAST score	380
E value	1.0e-36
Match length	74
% identity	100
NCBI Description	(AC007135) putative kinesin related protein [Arabidopsis thaliana]

Seq. No.	134722
Contig ID	110707_1.R1010

5'-most EST	jC-atX24066Q1E1A05a1
Seq. No.	134723
Contig ID	110716_1.R1010
5'-most EST	jC-atX24066Q1E1B10a1
Seq. No.	134724
Contig ID	110724_1.R1010
5'-most EST	g2048493
Method	BLASTN
NCBI GI	g3600045
BLAST score	419
E value	0.0e+00
Match length	466
% identity	98
NCBI Description	Arabidopsis thaliana BAC F2P3
Seq. No.	134725
Contig ID	110756_1.R1010
5'-most EST	g2047950
Method	BLASTX
NCBI GI	g4507075
BLAST score	256
E value	2.0e-28
Match length	149
% identity	47
NCBI Description	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5 >gi_2967452_dbj_BAA25173_ (AB010882) hSNF2H [Homo sapiens]
Seq. No.	134726
Contig ID	110786_1.R1010
5'-most EST	g4714006
Method	BLASTN
NCBI GI	g2191157
BLAST score	302
E value	1.0e-169
Match length	445
% identity	99
NCBI Description	Arabidopsis thaliana BAC IG002P16
Seq. No.	134727
Contig ID	110790_1.R1010
5'-most EST	g1215844
Seq. No.	134728
Contig ID	110856_1.R1010
5'-most EST	jC-atX24075Q1E1G12a1
Method	BLASTX
NCBI GI	g4314359
BLAST score	125
E value	5.0e-45
Match length	110
% identity	84
NCBI Description	(AC006340) hypothetical protein [Arabidopsis thaliana]
Seq. No.	134729

Contig ID	110922_1.R1010
5'-most EST	jC-atX24082Q1E1C11a1
Seq. No.	134730
Contig ID	110929_1.R1010
5'-most EST	jC-atX24082Q1E1G04a1
Method	BLASTX
NCBI GI	g3688528
BLAST score	333
E value	4.0e-31
Match length	86
% identity	70
NCBI Description	(AJ004958) pre-pro-TPE4A protein [Pisum sativum]
Seq. No.	134731
Contig ID	111043_1.R1010
5'-most EST	jC-atX24103Q1E2G11a1
Method	BLASTX
NCBI GI	g4325368
BLAST score	254
E value	1.0e-39
Match length	79
% identity	94
NCBI Description	(AF128396) Arabidopsis thaliana flavin-type blue-light photoreceptor (SW:Q43125) (Pfam: PF00875, Score=765.2, E=2.6e-226, N=1) [Arabidopsis thaliana]
Seq. No.	134732
Contig ID	111053_1.R1010
5'-most EST	g509454
Method	BLASTN
NCBI GI	g2264309
BLAST score	422
E value	0.0e+00
Match length	426
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJJ3, complete sequence [Arabidopsis thaliana]
Seq. No.	134733
Contig ID	111056_1.R1010
5'-most EST	g2062862
Method	BLASTN
NCBI GI	g4756963
BLAST score	411
E value	0.0e+00
Match length	444
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23 (ESSA project)
Seq. No.	134734
Contig ID	111066_1.R1010
5'-most EST	g2048246
Seq. No.	134735
Contig ID	111073_1.R1010

5'-most EST	g17155
Method	BLASTN
NCBI GI	g4538895
BLAST score	108
E value	1.0e-53
Match length	263
% identity	86
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17A8 (ESSA project)

Seq. No.	134736
Contig ID	111077_1.R1010
5'-most EST	jC-atX24106Q1E1B06a2
Method	BLASTX
NCBI GI	g2275202
BLAST score	368
E value	3.0e-35
Match length	75
% identity	99
NCBI Description	(AC002337) acyl-CoA synthetase isolog [Arabidopsis thaliana]

Seq. No.	134737
Contig ID	111122_1.R1010
5'-most EST	g398623
Method	BLASTX
NCBI GI	g2569938
BLAST score	365
E value	1.0e-34
Match length	93
% identity	73
NCBI Description	(Y15193) GAI [Arabidopsis thaliana]

Seq. No.	134738
Contig ID	111145_1.R1010
5'-most EST	jC-atXP90C246H11T7s2
Method	BLASTX
NCBI GI	g3281849
BLAST score	632
E value	6.0e-66
Match length	120
% identity	100
NCBI Description	(AL031004) methyltransferase - like protein [Arabidopsis thaliana]

Seq. No.	134739
Contig ID	111159_1.R1010
5'-most EST	jC-atX24109Q1E1B06a2
Method	BLASTX
NCBI GI	g2191165
BLAST score	51
E value	1.0e-21
Match length	113
% identity	53
NCBI Description	(AF007270) A_IG002P16.14 gene product [Arabidopsis thaliana]

Seq. No.	134740
Contig ID	111191_1.R1010
5'-most EST	g2580629

Seq. No.	134741
Contig ID	111205_1.R1010
5'-most EST	g2749355

Seq. No.	134742
Contig ID	111222_1.R1010
5'-most EST	jC-atX24111Q1E1B12a1
Method	BLASTN
NCBI GI	g3128143
BLAST score	256
E value	1.0e-142
Match length	263
% identity	60
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTI20, complete sequence [Arabidopsis thaliana]

Seq. No.	134743
Contig ID	111228_1.R1010
5'-most EST	jC-atXP117C141N5T7a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	3.0e-21
Match length	54
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	134744
Contig ID	111246_1.R1010
5'-most EST	jC-atXP22C122D21T7008a1
Method	BLASTX
NCBI GI	g3236240
BLAST score	381
E value	2.0e-36
Match length	100
% identity	70
NCBI Description	(AC004684) unknown protein [Arabidopsis thaliana]

Seq. No.	134745
Contig ID	111246_2.R1010
5'-most EST	g3157655
Method	BLASTX
NCBI GI	g3236240
BLAST score	211
E value	2.0e-16
Match length	128
% identity	43
NCBI Description	(AC004684) unknown protein [Arabidopsis thaliana]

Seq. No.	134746
Contig ID	111252_1.R1010
5'-most EST	g2748810
Method	BLASTN

NCBI GI g4760411
BLAST score 241
E value 1.0e-133
Match length 340
% identity 98
NCBI Description Arabidopsis thaliana chromosome 1 BAC F25C20 sequence, complete sequence

Seq. No. 134747
Contig ID 111331_1.R1010
5'-most EST g1053286
Method BLASTX
NCBI GI g4455293
BLAST score 520
E value 2.0e-64
Match length 162
% identity 90
NCBI Description (AL035528) putative protein [Arabidopsis thaliana]

Seq. No. 134748
Contig ID 111331_2.R1010
5'-most EST g2749717
Method BLASTN
NCBI GI g4455290
BLAST score 155
E value 1.0e-81
Match length 452
% identity 99
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F18A5 (ESSAII project)

Seq. No. 134749
Contig ID 111531_1.R1010
5'-most EST jC-atX25053Q1E1H11a1
Method BLASTN
NCBI GI g4115930
BLAST score 360
E value 0.0e+00
Match length 397
% identity 97
NCBI Description Arabidopsis thaliana BAC T4B21

Seq. No. 134750
Contig ID 111544_1.R1010
5'-most EST g2413369
Method BLASTN
NCBI GI g4646215
BLAST score 382
E value 0.0e+00
Match length 457
% identity 97
NCBI Description Arabidopsis thaliana chromosome II BAC T22O13 genomic sequence, complete sequence

Seq. No. 134751
Contig ID 111568_1.R1010
5'-most EST g4933266

Seq. No.	134752
Contig ID	111806_1.R1010
5'-most EST	g2763318
Method	BLASTN
NCBI GI	g4589434
BLAST score	369
E value	0.0e+00
Match length	476
% identity	78
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNJ7, complete sequence

Seq. No.	134753
Contig ID	111970_1.R1010
5'-most EST	g1932875
Method	BLASTN
NCBI GI	g2827513
BLAST score	210
E value	1.0e-114
Match length	273
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F8F16 (ESSAII project)

Seq. No.	134754
Contig ID	112083_1.R1010
5'-most EST	g17632

Seq. No.	134755
Contig ID	112109_1.R1010
5'-most EST	g1215841

Seq. No.	134756
Contig ID	112294_1.R1010
5'-most EST	jC-atX25027Q1E1B01a1
Method	BLASTN
NCBI GI	g3176695
BLAST score	470
E value	0.0e+00
Match length	538
% identity	97
NCBI Description	Arabidopsis thaliana chromosome I BAC F14J9 genomic sequence contains phyA marker, complete sequence [Arabidopsis thaliana]

Seq. No.	134757
Contig ID	112307_1.R1010
5'-most EST	jC-atX25027Q1E1F03a1

Seq. No.	134758
Contig ID	112331_1.R1010
5'-most EST	jC-atX25029Q1E1B12a1
Method	BLASTX
NCBI GI	g4680318
BLAST score	134
E value	5.0e-69

Match length	151
% identity	95
NCBI Description	(AF124376) 30S ribosomal protein S7 [Brassica napus]

Seq. No.	134759
Contig ID	112346_1.R1010
5'-most EST	jC-atX25031Q1E1A09a1
Method	BLASTN
NCBI GI	g4538990
BLAST score	185
E value	1.0e-99
Match length	350
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T5L19 (ESSA project)

Seq. No.	134760
Contig ID	112362_1.R1010
5'-most EST	g2763881

Seq. No.	134761
Contig ID	112384_1.R1010
5'-most EST	jC-atXP110C119G10T7058a1
Method	BLASTN
NCBI GI	g2760168
BLAST score	242
E value	1.0e-133
Match length	500
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MEE6, complete sequence [Arabidopsis thaliana]

Seq. No.	134762
Contig ID	112384_2.R1010
5'-most EST	jC-atXP13C104A8T7d2
Method	BLASTN
NCBI GI	g2760168
BLAST score	271
E value	1.0e-151
Match length	472
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MEE6, complete sequence [Arabidopsis thaliana]

Seq. No.	134763
Contig ID	112424_1.R1010
5'-most EST	jC-atX25034Q1E1B02a1
Method	BLASTN
NCBI GI	g1707006
BLAST score	345
E value	0.0e+00
Match length	417
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T1B8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 134764

Contig ID	112520_1.R1010
5'-most EST	jC-atX25038Q1E1E11a1
Seq. No.	134765
Contig ID	112604_1.R1010
5'-most EST	jC-atX25041Q1E1F12a2
Method	BLASTX
NCBI GI	g1769891
BLAST score	209
E value	1.0e-16
Match length	40
% identity	97
NCBI Description	(X99747) bZIP transcription factor [Arabidopsis thaliana] >gi_1865679_emb_CAB04795_ (Z82043) ATB2 [Arabidopsis thaliana]
Seq. No.	134766
Contig ID	112703_1.R1010
5'-most EST	jC-atXmonuni26Ca01a1
Method	BLASTN
NCBI GI	g4589437
BLAST score	252
E value	1.0e-140
Match length	308
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPN9, complete sequence
Seq. No.	134767
Contig ID	112708_1.R1010
5'-most EST	jC-atXmonuni26Ca06a1
Method	BLASTX
NCBI GI	g3128188
BLAST score	274
E value	3.0e-25
Match length	97
% identity	59
NCBI Description	(AC004521) putative beta-glucosidase [Arabidopsis thaliana]
Seq. No.	134768
Contig ID	112776_1.R1010
5'-most EST	jC-atX25057Q1E1B05b1
Method	BLASTN
NCBI GI	g3859658
BLAST score	183
E value	1.0e-98
Match length	215
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1 (ESSAII project)
Seq. No.	134769
Contig ID	112852_1.R1010
5'-most EST	jC-atX25060Q1E1H09a1
Seq. No.	134770
Contig ID	112897_1.R1010

5'-most EST	jC-atXP14C105N12T7s1
Method	BLASTN
NCBI GI	g2262135
BLAST score	240
E value	1.0e-132
Match length	499
% identity	100
NCBI Description	Arabidopsis thaliana BAC T10P11 from chromosome IV, near 15 cM, complete sequence

Seq. No.	134771
Contig ID	113035_1.R1010
5'-most EST	jC-atXL1031Q1E1E04a1
Method	BLASTN
NCBI GI	g4519195
BLAST score	118
E value	1.0e-59
Match length	281
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MQC12, complete sequence

Seq. No.	134772
Contig ID	113100_1.R1010
5'-most EST	jC-atX25071Q1E1E03a1
Method	BLASTN
NCBI GI	g4589419
BLAST score	502
E value	0.0e+00
Match length	582
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2I5, complete sequence

Seq. No.	134773
Contig ID	113119_1.R1010
5'-most EST	jC-atX25073Q1E1B033a1
Method	BLASTX
NCBI GI	g4455366
BLAST score	189
E value	3.0e-14
Match length	50
% identity	72
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	134774
Contig ID	113137_1.R1010
5'-most EST	jC-atXP122C118G17T7074a1
Method	BLASTN
NCBI GI	g4580745
BLAST score	583
E value	0.0e+00
Match length	620
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F10O3 sequence, complete sequence

Seq. No.	134775
Contig ID	113172_1.R1010
5'-most EST	jC-atX25074Q1E1F06a1
Seq. No.	134776
Contig ID	113238_1.R1010
5'-most EST	jC-atXP123C159O16T7065a1
Method	BLASTN
NCBI GI	g4589445
BLAST score	215
E value	1.0e-117
Match length	462
% identity	66
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWL2, complete sequence
Seq. No.	134777
Contig ID	113538_1.R1010
5'-most EST	jC-atXP5C90D4T7085a1
Method	BLASTX
NCBI GI	g4056505
BLAST score	1088
E value	1.0e-119
Match length	237
% identity	91
NCBI Description	(AC005896) nodulin-like protein [Arabidopsis thaliana]
Seq. No.	134778
Contig ID	113709_1.R1010
5'-most EST	jC-atX25102Q1E1E06a1
Seq. No.	134779
Contig ID	113757_1.R1010
5'-most EST	jC-atX25103Q1E1E11a1
Method	BLASTX
NCBI GI	g114339
BLAST score	413
E value	2.0e-40
Match length	81
% identity	100
NCBI Description	PLASMA MEMBRANE ATPASE 3 (PROTON PUMP) >gi_67974_pir__PXMUP3 H+-transporting ATPase (EC 3.6.1.35) type 3, plasma membrane - Arabidopsis thaliana >gi_166625 (J04737) ATPase [Arabidopsis thaliana]
Seq. No.	134780
Contig ID	113971_1.R1010
5'-most EST	jC-atX25114Q1E1E02a1
Method	BLASTX
NCBI GI	g2467274
BLAST score	228
E value	2.0e-18
Match length	99
% identity	56
NCBI Description	(Z99759) rna binding protein [Schizosaccharomyces pombe]
Seq. No.	134781

Contig ID	114018_1.R1010
5'-most EST	jC-atX25116Q1E1C05a1
Method	BLASTN
NCBI GI	g3869075
BLAST score	450
E value	0.0e+00
Match length	454
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence [Arabidopsis thaliana]

Seq. No.	134782
Contig ID	114068_1.R1010
5'-most EST	jC-atXmonuni26Cc06a1
Method	BLASTN
NCBI GI	g2244829
BLAST score	293
E value	1.0e-164
Match length	436
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	134783
Contig ID	114074_1.R1010
5'-most EST	jC-atXmonuni26Cb11a1
Method	BLASTN
NCBI GI	g3738313
BLAST score	292
E value	1.0e-163
Match length	453
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T29E15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134784
Contig ID	114093_1.R1010
5'-most EST	g2412884
Method	BLASTX
NCBI GI	g3377673
BLAST score	233
E value	3.0e-19
Match length	86
% identity	57
NCBI Description	(AF078079) UDP-glucose:flavonoid 3-O-glucosyltransferase [Forsythia x intermedia]

Seq. No.	134785
Contig ID	114098_1.R1010
5'-most EST	jC-atXmonuni26Ce01a1

Seq. No.	134786
Contig ID	114101_1.R1010
5'-most EST	jC-atX35005Q1E1G04a1
Method	BLASTX
NCBI GI	g3242721
BLAST score	450

E value	6.0e-45
Match length	90
% identity	94
NCBI Description	(AC003040) putative acetone-cyanohydrin lyase [Arabidopsis thaliana]

Seq. No.	134787
Contig ID	114130_1.R1010
5'-most EST	jC-atXmonuni26Cf03a1
Method	BLASTN
NCBI GI	g4490324
BLAST score	166
E value	3.0e-88
Match length	387
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14 (ESSA project)

Seq. No.	134788
Contig ID	114188_1.R1010
5'-most EST	jC-atXmonuni27Bb05a1
Method	BLASTN
NCBI GI	g2656031
BLAST score	301
E value	1.0e-169
Match length	384
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC20

Seq. No.	134789
Contig ID	114208_1.R1010
5'-most EST	jC-atXmonuni26Ch02a1
Method	BLASTX
NCBI GI	g3249077
BLAST score	217
E value	3.0e-49
Match length	117
% identity	83
NCBI Description	(AC004473) Similar to prunasin hydrolase precursor gb_U50201 from Prunus serotina. ESTs gb_T21225 and gb_AA586305 come from this gene. [Arabidopsis thaliana]

Seq. No.	134790
Contig ID	114234_1.R1010
5'-most EST	jC-atXmonuni27Aa06a1
Method	BLASTX
NCBI GI	g132942
BLAST score	139
E value	1.0e-08
Match length	40
% identity	60
NCBI Description	60S RIBOSOMAL PROTEIN L35A (L32) >gi_71348_pir__R5XL32 ribosomal protein L35a - African clawed frog >gi_65064_emb_CAA38849_ (X55030) ribosomal protein L32 [Xenopus laevis]

Seq. No.	134791
Contig ID	114255_1.R1010
5'-most EST	jC-atXmonuni27Bb10a1
Method	BLASTN
NCBI GI	g2924728
BLAST score	278
E value	1.0e-155
Match length	419
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXH1, complete sequence [Arabidopsis thaliana]

Seq. No.	134792
Contig ID	114326_1.R1010
5'-most EST	jC-atXmonuni27Bd09a1

Seq. No.	134793
Contig ID	114427_1.R1010
5'-most EST	jC-atX35033Q1E1H05a1
Method	BLASTN
NCBI GI	g4512656
BLAST score	135
E value	5.0e-70
Match length	213
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	134794
Contig ID	114429_1.R1010
5'-most EST	jC-atXP80C240F24T7s1
Method	BLASTN
NCBI GI	g4713943
BLAST score	93
E value	1.0e-44
Match length	185
% identity	90
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8K14 sequence, complete sequence

Seq. No.	134795
Contig ID	114619_1.R1010
5'-most EST	g2763413
Method	BLASTN
NCBI GI	g3355463
BLAST score	182
E value	1.0e-97
Match length	404
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134796
Contig ID	114631_1.R1010
5'-most EST	g3449804
Method	BLASTN
NCBI GI	g4589415

BLAST score	250
E value	1.0e-138
Match length	496
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K14A3, complete sequence

Seq. No.	134797
Contig ID	114637_1.R1010
5'-most EST	jC-atX35053Q1E1B10a2
Method	BLASTN
NCBI GI	g3241923
BLAST score	440
E value	0.0e+00
Match length	464
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMN10, complete sequence [Arabidopsis thaliana]

Seq. No.	134798
Contig ID	114648_1.R1010
5'-most EST	jC-atX35054Q1E1F12a1
Method	BLASTX
NCBI GI	g3763918
BLAST score	203
E value	5.0e-50
Match length	123
% identity	79
NCBI Description	(AC004450) putative isopropylmalate dehydratase [Arabidopsis thaliana]

Seq. No.	134799
Contig ID	114720_1.R1010
5'-most EST	jC-atXL1024Q1B1D01b1
Method	BLASTX
NCBI GI	g2462827
BLAST score	395
E value	2.0e-38
Match length	100
% identity	82
NCBI Description	(AF000657) probable thiamin biosynthetic enzyme [Arabidopsis thaliana]

Seq. No.	134800
Contig ID	114722_1.R1010
5'-most EST	g2048827
Method	BLASTN
NCBI GI	g452815
BLAST score	356
E value	0.0e+00
Match length	444
% identity	96
NCBI Description	A.thaliana phyE gene

Seq. No.	134801
Contig ID	114739_1.R1010
5'-most EST	g2047808

Method	BLASTX
NCBI GI	g4510348
BLAST score	247
E value	7.0e-21
Match length	94
% identity	48
NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]

Seq. No.	134802
Contig ID	114749_1.R1010
5'-most EST	jC-atXP107C40F2T7s1
Method	BLASTX
NCBI GI	g2281086
BLAST score	349
E value	6.0e-33
Match length	114
% identity	59
NCBI Description	(AC002333) indole-3-acetate beta-glucosyltransferase isolog [Arabidopsis thaliana]

Seq. No.	134803
Contig ID	114753_1.R1010
5'-most EST	g1033249
Method	BLASTN
NCBI GI	g4512656
BLAST score	340
E value	0.0e+00
Match length	407
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	134804
Contig ID	114763_1.R1010
5'-most EST	g2393247

Seq. No.	134805
Contig ID	114798_1.R1010
5'-most EST	jC-atXP29C135I12T7001d1
Method	BLASTX
NCBI GI	g2245144
BLAST score	502
E value	2.0e-50
Match length	177
% identity	58
NCBI Description	(Y10846) O-acetylserine(thiol) lyase [Brassica juncea]

Seq. No.	134806
Contig ID	114798_2.R1010
5'-most EST	jC-atXL1030Q1B1D05b1
Method	BLASTX
NCBI GI	g2245144
BLAST score	252
E value	1.0e-21
Match length	81
% identity	67
NCBI Description	(Y10846) O-acetylserine(thiol) lyase [Brassica juncea]

Seq. No.	134807
Contig ID	114928_1.R1010
5'-most EST	jC-atXL1040Q1E1C07a1
Method	BLASTN
NCBI GI	g2459406
BLAST score	363
E value	0.0e+00
Match length	470
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F4P9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134808
Contig ID	115337_1.R1010
5'-most EST	jC-atXP100C251I2T7d1

Seq. No.	134809
Contig ID	115339_1.R1010
5'-most EST	jC-atXP100C251P4T7b1
Method	BLASTX
NCBI GI	g2244797
BLAST score	431
E value	5.0e-45
Match length	128
% identity	82
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	134810
Contig ID	115339_2.R1010
5'-most EST	jC-atXP100C251J8T7d1
Method	BLASTN
NCBI GI	g4589414
BLAST score	164
E value	6.0e-87
Match length	596
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K14B15, complete sequence

Seq. No.	134811
Contig ID	115340_1.R1010
5'-most EST	jC-atXP100C268B11T7b1
Method	BLASTX
NCBI GI	g4455319
BLAST score	111
E value	8.0e-05
Match length	187
% identity	10
NCBI Description	(AL035528) putative disease resistance protein [Arabidopsis thaliana]

Seq. No.	134812
Contig ID	115341_1.R1010
5'-most EST	jC-atXP100CE3D5T7b1
Method	BLASTX
NCBI GI	g1705678

BLAST score	276
E value	3.0e-24
Match length	178
% identity	21
NCBI Description	CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING PROTEIN HOMOLOG) (VCP) >gi_862480 (U20213) valosin-containing protein [Glycine max]

Seq. No.	134813
Contig ID	115385_1.R1010
5'-most EST	jC-atXP107C107F5T7s1
Method	BLASTN
NCBI GI	g4115370
BLAST score	273
E value	1.0e-152
Match length	366
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC F27D4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134814
Contig ID	115399_1.R1010
5'-most EST	jC-atXP107C113K21T7s1
Method	BLASTX
NCBI GI	g2213595
BLAST score	503
E value	6.0e-51
Match length	101
% identity	98
NCBI Description	(AC000348) T7N9.15 [Arabidopsis thaliana]

Seq. No.	134815
Contig ID	115409_1.R1010
5'-most EST	g2048684
Method	BLASTX
NCBI GI	g3880353
BLAST score	241
E value	6.0e-20
Match length	153
% identity	39
NCBI Description	(Z82285) predicted using Genefinder [Caenorhabditis elegans]

Seq. No.	134816
Contig ID	115444_1.R1010
5'-most EST	jC-atXP107C123C17T7d1
Method	BLASTX
NCBI GI	g3874563
BLAST score	293
E value	6.0e-30
Match length	128
% identity	54
NCBI Description	(Z81042) similar to Yeast hypothetical protein YEY6 like; cDNA EST yk206h5.3 comes from this gene; cDNA EST yk206h5.5 comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5 comes from this gene; cDNA ... >gi_3924825_emb_CAB05549_ (Z83113) similar to Yeast

hypothetical protein YEY6 like; cDNA EST yk206h5.3 comes from this gene; cDNA EST yk206h5.5 comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5 comes from this gene; cDNA

Seq. No.	134817
Contig ID	115473_1.R1010
5'-most EST	jC-atXP108C168L4T7092d1
Method	BLASTX
NCBI GI	g584741
BLAST score	214
E value	9.0e-17
Match length	104
% identity	20
NCBI Description	ANKYRIN REPEAT PROTEIN (AKRP) >gi_322461_pir__JQ1729 ankyrin-repeat protein - Arabidopsis thaliana >gi_166744 (M82883) ankyrin repeat-containing protein [Arabidopsis thaliana]

Seq. No.	134818
Contig ID	115476_1.R1010
5'-most EST	jC-atXP108C150L7T7s1
Method	BLASTX
NCBI GI	g4115916
BLAST score	270
E value	1.0e-23
Match length	93
% identity	59
NCBI Description	(AF118222) F3H7.9 gene product [Arabidopsis thaliana] >gi_4539441_emb_CAB40029.1_ (AL049523) putative protein [Arabidopsis thaliana]

Seq. No.	134819
Contig ID	115479_1.R1010
5'-most EST	jC-atXP108C157G23T7035d1
Method	BLASTX
NCBI GI	g4510371
BLAST score	531
E value	5.0e-54
Match length	179
% identity	62
NCBI Description	(AC007017) putative harpin-induced protein [Arabidopsis thaliana]

Seq. No.	134820
Contig ID	115481_1.R1010
5'-most EST	jC-atXP108C161K24T7s1

Seq. No.	134821
Contig ID	115497_1.R1010
5'-most EST	jC-atXP109C91B11T7s1
Method	BLASTN
NCBI GI	g2828186
BLAST score	473
E value	0.0e+00
Match length	505
% identity	99

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18I23, complete sequence [Arabidopsis thaliana]
Seq. No.	134822
Contig ID	115501_1.R1010
5'-most EST	jC-atXP108C184O24T7s1
Method	BLASTX
NCBI GI	g4835232
BLAST score	368
E value	2.0e-41
Match length	140
% identity	75
NCBI Description	(AL049862) putative protein [Arabidopsis thaliana]
Seq. No.	134823
Contig ID	115535_1.R1010
5'-most EST	g1053980
Seq. No.	134824
Contig ID	115545_1.R1010
5'-most EST	jC-atXP109C204J8T7d1
Method	BLASTX
NCBI GI	g3608154
BLAST score	691
E value	5.0e-73
Match length	166
% identity	89
NCBI Description	(AC005314) unknown protein [Arabidopsis thaliana]
Seq. No.	134825
Contig ID	115546_1.R1010
5'-most EST	g2445957
Method	BLASTX
NCBI GI	g3608154
BLAST score	114
E value	2.0e-36
Match length	94
% identity	88
NCBI Description	(AC005314) unknown protein [Arabidopsis thaliana]
Seq. No.	134826
Contig ID	115549_1.R1010
5'-most EST	g3719140
Method	BLASTN
NCBI GI	g2264316
BLAST score	420
E value	0.0e+00
Match length	740
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRO11, complete sequence [Arabidopsis thaliana]
Seq. No.	134827
Contig ID	115555_1.R1010
5'-most EST	g936979
Method	BLASTX
NCBI GI	g4218987

09554705.040500

BLAST score	446
E value	4.0e-44
Match length	111
% identity	89
NCBI Description	(AF098630) putative cell wall-plasma membrane disconnecting CLCT protein [Arabidopsis thaliana] >gi_4725954_emb_CAB41725.1_ (AL049730) putative cell wall-plasma membrane disconnecting CLCT protein (AIR1A) [Arabidopsis thaliana]

Seq. No.	134828
Contig ID	115560_1.R1010
5'-most EST	jC-atXP109C205P11T7s1
Method	BLASTN
NCBI GI	g3510346
BLAST score	120
E value	8.0e-61
Match length	456
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNL12, complete sequence [Arabidopsis thaliana]

Seq. No.	134829
Contig ID	115561_1.R1010
5'-most EST	g936229
Method	BLASTN
NCBI GI	g4581138
BLAST score	319
E value	1.0e-179
Match length	458
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F1O11 genomic sequence, complete sequence

Seq. No.	134830
Contig ID	115562_1.R1010
5'-most EST	jC-atXP109C206E11T7s1
Method	BLASTN
NCBI GI	g4581138
BLAST score	405
E value	0.0e+00
Match length	484
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F1O11 genomic sequence, complete sequence

Seq. No.	134831
Contig ID	115580_1.R1010
5'-most EST	g2763397
Method	BLASTN
NCBI GI	g2264302
BLAST score	328
E value	0.0e+00
Match length	623
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC12, complete sequence [Arabidopsis thaliana]

Seq. No.	134832
Contig ID	115596_1.R1010
5'-most EST	jC-atXP109C215B3T7d1
Method	BLASTN
NCBI GI	g2924653
BLAST score	124
E value	4.0e-63
Match length	527
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDA7, complete sequence [Arabidopsis thaliana]

Seq. No.	134833
Contig ID	115646_1.R1010
5'-most EST	jC-atXP109C91C14T7d1
Method	BLASTX
NCBI GI	g4585901
BLAST score	309
E value	1.0e-37
Match length	156
% identity	52
NCBI Description	(AC007133) hypothetical protein [Arabidopsis thaliana]

Seq. No.	134834
Contig ID	115674_1.R1010
5'-most EST	jC-atXP109C95E3T7d1
Method	BLASTX
NCBI GI	g2565009
BLAST score	331
E value	8.0e-31
Match length	68
% identity	81
NCBI Description	(AC002983) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	134835
Contig ID	115705_1.R1010
5'-most EST	jC-atXP10C94M1T7d2
Method	BLASTX
NCBI GI	g3269291
BLAST score	591
E value	7.0e-99
Match length	183
% identity	100
NCBI Description	(AL030978) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	134836
Contig ID	115721_1.R1010
5'-most EST	g2757102
Method	BLASTX
NCBI GI	g3885334
BLAST score	708
E value	5.0e-75
Match length	147
% identity	94

NCBI Description	(AC005623) putative argonaute protein [Arabidopsis thaliana]
Seq. No.	134837
Contig ID	115723_1.R1010
5'-most EST	jC-atXP10C95A9T7s2
Method	BLASTN
NCBI GI	g3885325
BLAST score	370
E value	0.0e+00
Match length	417
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T20P8 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	134838
Contig ID	115728_1.R1010
5'-most EST	jC-atXP10C95K14T7s1
Method	BLASTX
NCBI GI	g4678221
BLAST score	191
E value	3.0e-14
Match length	129
% identity	38
NCBI Description	(AC007135) hypothetical protein [Arabidopsis thaliana]
Seq. No.	134839
Contig ID	115728_2.R1010
5'-most EST	g2048855
Seq. No.	134840
Contig ID	115761_1.R1010
5'-most EST	jC-atXP10C95M15T7d1
Method	BLASTX
NCBI GI	g4099076
BLAST score	149
E value	2.0e-09
Match length	65
% identity	43
NCBI Description	(U82510) IAP [Choristoneura fumiferana nucleopolyhedrovirus]
Seq. No.	134841
Contig ID	115765_1.R1010
5'-most EST	jC-atXP10C95M21T7d2
Method	BLASTN
NCBI GI	g4580522
BLAST score	278
E value	1.0e-155
Match length	310
% identity	99
NCBI Description	Arabidopsis thaliana scarecrow-like 8 (SCL8) mRNA, partial cds
Seq. No.	134842
Contig ID	115767_1.R1010
5'-most EST	g2581747

Method	BLASTX
NCBI GI	g4580523
BLAST score	54
E value	8.0e-41
Match length	95
% identity	92
NCBI Description	(AF036305) scarecrow-like 8 [Arabidopsis thaliana]

Seq. No.	134843
Contig ID	115767_2.R1010
5'-most EST	jC-atXP61C201A2T7d1
Method	BLASTX
NCBI GI	g4580523
BLAST score	277
E value	2.0e-52
Match length	160
% identity	83
NCBI Description	(AF036305) scarecrow-like 8 [Arabidopsis thaliana]

Seq. No.	134844
Contig ID	115771_1.R1010
5'-most EST	g2048794
Method	BLASTX
NCBI GI	g2160185
BLAST score	644
E value	3.0e-67
Match length	247
% identity	54
NCBI Description	(AC000132) Similar to S. pombe ISP4 (gb_D83992). [Arabidopsis thaliana]

Seq. No.	134845
Contig ID	115773_1.R1010
5'-most EST	g2048870
Method	BLASTX
NCBI GI	g2160185
BLAST score	351
E value	4.0e-33
Match length	90
% identity	70
NCBI Description	(AC000132) Similar to S. pombe ISP4 (gb_D83992). [Arabidopsis thaliana]

Seq. No.	134846
Contig ID	115792_1.R1010
5'-most EST	g502324
Method	BLASTX
NCBI GI	g3928100
BLAST score	324
E value	3.0e-30
Match length	62
% identity	100
NCBI Description	(AC005770) putative protease inhibitor [Arabidopsis thaliana]

Seq. No.	134847
Contig ID	115793_1.R1010

5'-most EST	jC-atXP10C96B2T7d1
Method	BLASTN
NCBI GI	g3080352
BLAST score	201
E value	1.0e-109
Match length	371
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T5K18 (ESSAII project)

Seq. No.	134848
Contig ID	115795_1.R1010
5'-most EST	g2048873
Method	BLASTN
NCBI GI	g3080352
BLAST score	291
E value	1.0e-162
Match length	454
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T5K18 (ESSAII project)

Seq. No.	134849
Contig ID	115807_1.R1010
5'-most EST	g2048875
Method	BLASTN
NCBI GI	g2264318
BLAST score	335
E value	0.0e+00
Match length	384
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUP24, complete sequence [Arabidopsis thaliana]

Seq. No.	134850
Contig ID	115817_1.R1010
5'-most EST	jC-atXP10C96I11T7d1
Method	BLASTN
NCBI GI	g3046853
BLAST score	170
E value	2.0e-90
Match length	574
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRA19, complete sequence [Arabidopsis thaliana]

Seq. No.	134851
Contig ID	115819_1.R1010
5'-most EST	jC-atXP10C96I11T7s2
Method	BLASTN
NCBI GI	g3046853
BLAST score	217
E value	1.0e-118
Match length	463
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRA19, complete sequence [Arabidopsis thaliana]

Seq. No.	134852
Contig ID	115833_1.R1010
5'-most EST	jC-atXP10C96L18T7d2
Method	BLASTN
NCBI GI	g4732168
BLAST score	299
E value	1.0e-167
Match length	323
% identity	98
NCBI Description	Arabidopsis thaliana BAC T1J24

Seq. No.	134853
Contig ID	115843_1.R1010
5'-most EST	jC-atXP10C96P17T7d2

Seq. No.	134854
Contig ID	115848_1.R1010
5'-most EST	jC-atXP33C151A11T7s2

Seq. No.	134855
Contig ID	115854_1.R1010
5'-most EST	jC-atXP10C97A3T7d1
Method	BLASTN
NCBI GI	g2760169
BLAST score	304
E value	1.0e-170
Match length	550
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFB13, complete sequence [Arabidopsis thaliana]

Seq. No.	134856
Contig ID	115905_1.R1010
5'-most EST	jC-atXP10C97C23T7d2
Method	BLASTN
NCBI GI	g2760170
BLAST score	423
E value	0.0e+00
Match length	945
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIO24, complete sequence [Arabidopsis thaliana]

Seq. No.	134857
Contig ID	115937_1.R1010
5'-most EST	jC-atXP10C97D3T7s2

Seq. No.	134858
Contig ID	115941_1.R1010
5'-most EST	jC-atXP110C119E4T7d1

Seq. No.	134859
Contig ID	115942_1.R1010
5'-most EST	g2759874
Method	BLASTN
NCBI GI	g2351069

BLAST score	349
E value	0.0e+00
Match length	850
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSH12, complete sequence [Arabidopsis thaliana]

Seq. No.	134860
Contig ID	115946_1.R1010
5'-most EST	jC-atXP110C105L21T7d1
Method	BLASTX
NCBI GI	g4678950
BLAST score	504
E value	4.0e-51
Match length	163
% identity	67
NCBI Description	(AL049711) putative protein [Arabidopsis thaliana]

Seq. No.	134861
Contig ID	115950_1.R1010
5'-most EST	g2757018
Method	BLASTN
NCBI GI	g3236234
BLAST score	441
E value	0.0e+00
Match length	482
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F13M22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134862
Contig ID	115951_1.R1010
5'-most EST	jC-atXP110C119D20T7025a1
Method	BLASTX
NCBI GI	g4262185
BLAST score	641
E value	6.0e-67
Match length	123
% identity	99
NCBI Description	(AC005508) 64038 [Arabidopsis thaliana]

Seq. No.	134863
Contig ID	115952_1.R1010
5'-most EST	g933511
Method	BLASTX
NCBI GI	g1617270
BLAST score	520
E value	6.0e-53
Match length	154
% identity	64
NCBI Description	(X94624) acyl-CoA synthetase [Brassica napus]

Seq. No.	134864
Contig ID	115967_1.R1010
5'-most EST	jC-atXP110C119G23T7d1

Seq. No.	134865

Contig ID	115979_1.R1010
5'-most EST	jC-atXP98CH8A11T7b1
Method	BLASTX
NCBI GI	g3341680
BLAST score	71
E value	2.0e-28
Match length	185
% identity	50
NCBI Description	(AC003672) unknown protein [Arabidopsis thaliana]

Seq. No.	134866
Contig ID	115981_1.R1010
5'-most EST	jC-atXP121C96C18T7092d1
Method	BLASTN
NCBI GI	g3702735
BLAST score	238
E value	1.0e-131
Match length	357
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQL5, complete sequence [Arabidopsis thaliana]

Seq. No.	134867
Contig ID	115983_1.R1010
5'-most EST	jC-atXP121C96L4T7029d1
Method	BLASTX
NCBI GI	g1703153
BLAST score	281
E value	1.0e-24
Match length	226
% identity	38
NCBI Description	ACTIN >gi_2147076_pir__S65079 actin - Cyanidioschyzon merolae >gi_1167501_dbj_BAA06866_ (D32140) actin [Cyanidioschyzon merolae]

Seq. No.	134868
Contig ID	115988_1.R1010
5'-most EST	jC-atXP111C105M8T7s1
Method	BLASTX
NCBI GI	g4417298
BLAST score	798
E value	3.0e-85
Match length	184
% identity	92
NCBI Description	(AC007019) putative RAS-related protein RAB7 [Arabidopsis thaliana]

Seq. No.	134869
Contig ID	115994_1.R1010
5'-most EST	jC-atXP111C106L5T7s1
Method	BLASTX
NCBI GI	g3894171
BLAST score	512
E value	5.0e-52
Match length	106
% identity	92
NCBI Description	(AC005312) putative glutathione s-transferase [Arabidopsis

thaliana]

Seq. No.	134870
Contig ID	115997_1.R1010
5'-most EST	g2597278
Method	BLASTX
NCBI GI	g1621461
BLAST score	183
E value	2.0e-13
Match length	117
% identity	34
NCBI Description	(U73103) laccase [Liriodendron tulipifera]

Seq. No.	134871
Contig ID	116010_1.R1010
5'-most EST	g2393229
Method	BLASTX
NCBI GI	g1621465
BLAST score	352
E value	3.0e-33
Match length	98
% identity	61
NCBI Description	(U73105) laccase [Liriodendron tulipifera]

Seq. No.	134872
Contig ID	116011_1.R1010
5'-most EST	jC-atXP111C119L1T7d1
Method	BLASTN
NCBI GI	g3985949
BLAST score	229
E value	1.0e-126
Match length	272
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOB24, complete sequence [Arabidopsis thaliana]

Seq. No.	134873
Contig ID	116013_1.R1010
5'-most EST	jC-atXP111C116J23T7d1
Method	BLASTX
NCBI GI	g3046815
BLAST score	335
E value	1.0e-65
Match length	128
% identity	91
NCBI Description	(AL021687) cytochrome P450 [Arabidopsis thaliana]

Seq. No.	134874
Contig ID	116016_1.R1010
5'-most EST	jC-atXP111C116L23T7s1
Method	BLASTN
NCBI GI	g2335089
BLAST score	346
E value	0.0e+00
Match length	433
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T11A7 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134875
Contig ID	116017_1.R1010
5'-most EST	g2048060
Method	BLASTN
NCBI GI	g4376087
BLAST score	245
E value	1.0e-135
Match length	715
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	134876
Contig ID	116018_1.R1010
5'-most EST	g2048483

Seq. No.	134877
Contig ID	116026_1.R1010
5'-most EST	jC-atXP111C116P22T7d1
Method	BLASTX
NCBI GI	g3152613
BLAST score	299
E value	5.0e-27
Match length	162
% identity	42
NCBI Description	(AC004482) hypothetical protein [Arabidopsis thaliana]

Seq. No.	134878
Contig ID	116035_1.R1010
5'-most EST	g2048476

Seq. No.	134879
Contig ID	116037_1.R1010
5'-most EST	jC-atXP111C119I23T7d1
Method	BLASTX
NCBI GI	g3786011
BLAST score	611
E value	1.0e-63
Match length	118
% identity	100
NCBI Description	(AC005499) putative elongation factor [Arabidopsis thaliana]

Seq. No.	134880
Contig ID	116039_1.R1010
5'-most EST	g947802
Method	BLASTX
NCBI GI	g4584110
BLAST score	209
E value	2.0e-16
Match length	100
% identity	46
NCBI Description	(AJ133639) SAH7 protein [Arabidopsis thaliana]

Seq. No. 134881

Contig ID	116042_1.R1010
5'-most EST	g2758268
Seq. No.	134882
Contig ID	116046_1.R1010
5'-most EST	g2048473
Method	BLASTN
NCBI GI	g3785992
BLAST score	284
E value	1.0e-158
Match length	356
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T6A23 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	134883
Contig ID	116048_1.R1010
5'-most EST	jC-atXP111C119K22T7s1
Seq. No.	134884
Contig ID	116052_1.R1010
5'-most EST	jC-atXP111C119L1T7s1
Seq. No.	134885
Contig ID	116057_1.R1010
5'-most EST	jC-atXP111C122I17T7d1
Method	BLASTX
NCBI GI	g3334133
BLAST score	562
E value	5.0e-58
Match length	196
% identity	59
NCBI Description	CYTOCHROME P450 89A2 (CYPLXXXIX) (ATH 6-1) >gi_1432145 (U61231) cytochrome P450 [Arabidopsis thaliana]
Seq. No.	134886
Contig ID	116063_1.R1010
5'-most EST	jC-atXP111C122M18T7d1
Method	BLASTX
NCBI GI	g3881820
BLAST score	131
E value	3.0e-09
Match length	93
% identity	43
NCBI Description	(Z73898) similar to dehydrogenase [Caenorhabditis elegans] >gi_3881832_emb_CAA98083_ (Z73899) similar to dehydrogenase [Caenorhabditis elegans]
Seq. No.	134887
Contig ID	116067_1.R1010
5'-most EST	jC-atXP111C122M20T7d1
Method	BLASTN
NCBI GI	g4220635
BLAST score	653
E value	0.0e+00
Match length	653
% identity	100

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDB19, complete sequence [Arabidopsis thaliana]
Seq. No.	134888
Contig ID	116071_1.R1010
5'-most EST	jC-atXP111C122021T7d1
Seq. No.	134889
Contig ID	116073_1.R1010
5'-most EST	g2048622
Seq. No.	134890
Contig ID	116084_1.R1010
5'-most EST	jC-atXP111C124D7T7d1
Seq. No.	134891
Contig ID	116091_1.R1010
5'-most EST	jC-atXP111C124H12T7d1
Method	BLASTX
NCBI GI	g3258569
BLAST score	615
E value	4.0e-64
Match length	157
% identity	80
NCBI Description	(U89959) Similar to yeast general negative regulator of transcription subunit 1 [Arabidopsis thaliana]
Seq. No.	134892
Contig ID	116103_1.R1010
5'-most EST	jC-atXP111C124K5T7d1
Seq. No.	134893
Contig ID	116106_1.R1010
5'-most EST	g957822
Method	BLASTX
NCBI GI	g2447107
BLAST score	196
E value	7.0e-15
Match length	98
% identity	44
NCBI Description	(U42580) A638R [Paramecium bursaria Chlorella virus 1]
Seq. No.	134894
Contig ID	116106_2.R1010
5'-most EST	g2393231
Seq. No.	134895
Contig ID	116109_1.R1010
5'-most EST	jC-atXP111C124L22T7d1
Method	BLASTN
NCBI GI	g3461885
BLAST score	41
E value	1.0e-13
Match length	53
% identity	94
NCBI Description	Arabidopsis thaliana gene for phosphoribosyl-ATP pyrophosphohydrolase, complete cds

Seq. No.	134896
Contig ID	116112_1.R1010
5'-most EST	jC-atXP25C125K19T7063a1
Method	BLASTX
NCBI GI	g2618699
BLAST score	760
E value	6.0e-81
Match length	149
% identity	97
NCBI Description	(AC002510) unknown protein [Arabidopsis thaliana]

Seq. No.	134897
Contig ID	116125_1.R1010
5'-most EST	g1216040

Seq. No.	134898
Contig ID	116132_1.R1010
5'-most EST	jC-atXP111C125J19T7d1
Method	BLASTN
NCBI GI	g2335089
BLAST score	277
E value	1.0e-154
Match length	493
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC T11A7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134899
Contig ID	116134_1.R1010
5'-most EST	jC-atXP111C125J6T7d1
Method	BLASTX
NCBI GI	g3935176
BLAST score	599
E value	3.0e-62
Match length	151
% identity	81
NCBI Description	(AC004557) F17L21.19 [Arabidopsis thaliana]

Seq. No.	134900
Contig ID	116136_1.R1010
5'-most EST	jC-atXP111C125L15T7d1
Method	BLASTX
NCBI GI	g4314366
BLAST score	226
E value	2.0e-18
Match length	91
% identity	65
NCBI Description	(AC006340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	134901
Contig ID	116137_1.R1010
5'-most EST	jC-atXP111C125L24T7d1
Method	BLASTN
NCBI GI	g2618600
BLAST score	126
E value	2.0e-64

Match length	407
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDC12, complete sequence [Arabidopsis thaliana]

Seq. No.	134902
Contig ID	116144_1.R1010
5'-most EST	g2048673
Method	BLASTX
NCBI GI	g4417286
BLAST score	357
E value	8.0e-34
Match length	99
% identity	76
NCBI Description	(AC007019) putative shikimate kinase [Arabidopsis thaliana]

Seq. No.	134903
Contig ID	116148_1.R1010
5'-most EST	jC-atXP111C126H21T7d1
Method	BLASTX
NCBI GI	g2190558
BLAST score	385
E value	2.0e-67
Match length	136
% identity	96
NCBI Description	(AC001229) F5I14.14 [Arabidopsis thaliana]

Seq. No.	134904
Contig ID	116152_1.R1010
5'-most EST	jC-atXP111C126K2T7d1
Method	BLASTX
NCBI GI	g2864613
BLAST score	598
E value	4.0e-62
Match length	157
% identity	76
NCBI Description	(AL021811) S-receptor kinase -like protein [Arabidopsis thaliana] >gi_4049333_emb_CAA22558_ (AL034567) S-receptor kinase-like protein [Arabidopsis thaliana]

Seq. No.	134905
Contig ID	116155_1.R1010
5'-most EST	g2048681
Method	BLASTN
NCBI GI	g4159700
BLAST score	299
E value	1.0e-167
Match length	382
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1L20, complete sequence

Seq. No.	134906
Contig ID	116157_1.R1010
5'-most EST	jC-atXP111C126M5T7s1

Seq. No.	134907

Contig ID	116158_1.R1010
5'-most EST	jC-atXP111C126M8T7d1
Method	BLASTX
NCBI GI	g119745
BLAST score	73
E value	3.0e-12
Match length	139
% identity	44
NCBI Description	FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi_67242_pir__PAWTF fructose-bisphosphatase (EC 3.1.3.11) precursor, chloroplast - wheat >gi_21737_emb_CAA30612_ (X07780) pre-FBPase [Triticum aestivum] >gi_21741_emb_CAA37908_ (X53957) fructose-bisphosphatase [Triticum aestivum]

Seq. No.	134908
Contig ID	116163_1.R1010
5'-most EST	jC-atXP113C125C9T7d1
Method	BLASTX
NCBI GI	g4115383
BLAST score	470
E value	2.0e-47
Match length	95
% identity	95
NCBI Description	(AC005967) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	134909
Contig ID	116164_1.R1010
5'-most EST	jC-atXP98CH8A4T7b1
Method	BLASTX
NCBI GI	g3643604
BLAST score	106
E value	4.0e-04
Match length	101
% identity	6
NCBI Description	(AC005395) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	134910
Contig ID	116167_1.R1010
5'-most EST	g934161
Method	BLASTN
NCBI GI	g4589440
BLAST score	107
E value	5.0e-53
Match length	428
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSD21, complete sequence

Seq. No.	134911
Contig ID	116172_1.R1010
5'-most EST	g2762283
Method	BLASTN
NCBI GI	g3510347

BLAST score	85
E value	5.0e-40
Match length	305
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]

Seq. No.	134912
Contig ID	116174_1.R1010
5'-most EST	jC-atXP113C134I5T7d1
Method	BLASTN
NCBI GI	g4589437
BLAST score	279
E value	1.0e-155
Match length	401
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPN9, complete sequence

Seq. No.	134913
Contig ID	116186_1.R1010
5'-most EST	jC-atXP113C221P16T7d1
Method	BLASTN
NCBI GI	g3337347
BLAST score	266
E value	1.0e-148
Match length	289
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F13P17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134914
Contig ID	116193_1.R1010
5'-most EST	g1216849
Method	BLASTX
NCBI GI	g3236253
BLAST score	294
E value	1.0e-26
Match length	104
% identity	58
NCBI Description	(AC004684) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	134915
Contig ID	116201_1.R1010
5'-most EST	jC-atXP113C230D16T7d1

Seq. No.	134916
Contig ID	116217_1.R1010
5'-most EST	g957536
Method	BLASTX
NCBI GI	g2281109
BLAST score	835
E value	8.0e-90
Match length	151
% identity	100
NCBI Description	(AC002333) endochitinase isolog [Arabidopsis thaliana]

Seq. No.	134917
Contig ID	116217_2.R1010
5'-most EST	jC-atXP14C105O10T7s1
Method	BLASTX
NCBI GI	g2281109
BLAST score	526
E value	1.0e-53
Match length	111
% identity	89
NCBI Description	(AC002333) endochitinase isolog [Arabidopsis thaliana]

Seq. No.	134918
Contig ID	116222_1.R1010
5'-most EST	g2723003
Method	BLASTX
NCBI GI	g2864613
BLAST score	165
E value	3.0e-11
Match length	72
% identity	46
NCBI Description	(AL021811) S-receptor kinase -like protein [Arabidopsis thaliana] >gi_4049333_emb_CAA22558_ (AL034567) S-receptor kinase-like protein [Arabidopsis thaliana]

Seq. No.	134919
Contig ID	116231_1.R1010
5'-most EST	g934740
Method	BLASTX
NCBI GI	g3420054
BLAST score	258
E value	5.0e-22
Match length	112
% identity	50
NCBI Description	(AC004680) unknown protein [Arabidopsis thaliana]

Seq. No.	134920
Contig ID	116235_1.R1010
5'-most EST	g1217129
Method	BLASTX
NCBI GI	g3212867
BLAST score	496
E value	5.0e-50
Match length	150
% identity	65
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	134921
Contig ID	116238_1.R1010
5'-most EST	g1269347
Method	BLASTX
NCBI GI	g3982576
BLAST score	195
E value	7.0e-15
Match length	39
% identity	100
NCBI Description	(AF023140) imidazoleglycerol phosphate dehydratase [Thlaspi

goesingense]

Seq. No.	134922
Contig ID	116239_1.R1010
5'-most EST	g906702
Method	BLASTN
NCBI GI	g4589425
BLAST score	36
E value	2.0e-10
Match length	68
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBA10, complete sequence

Seq. No.	134923
Contig ID	116245_1.R1010
5'-most EST	jC-atXP114C231C23T7d1
Method	BLASTN
NCBI GI	g2264367
BLAST score	600
E value	0.0e+00
Match length	658
% identity	98
NCBI Description	Arabidopsis thaliana BAC F6P23 from chromosome IV, top arm, complete sequence [Arabidopsis thaliana]

Seq. No.	134924
Contig ID	116246_1.R1010
5'-most EST	g2749394
Method	BLASTN
NCBI GI	g2264367
BLAST score	226
E value	1.0e-124
Match length	399
% identity	98
NCBI Description	Arabidopsis thaliana BAC F6P23 from chromosome IV, top arm, complete sequence [Arabidopsis thaliana]

Seq. No.	134925
Contig ID	116257_1.R1010
5'-most EST	g1217170
Method	BLASTX
NCBI GI	g4753650
BLAST score	554
E value	6.0e-57
Match length	106
% identity	100
NCBI Description	(AL049751) putative protein [Arabidopsis thaliana]

Seq. No.	134926
Contig ID	116259_1.R1010
5'-most EST	jC-atXP114C231J12T7d1
Method	BLASTN
NCBI GI	g2494106
BLAST score	517
E value	0.0e+00
Match length	521

% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134927
Contig ID	116267_1.R1010
5'-most EST	g2580666

Seq. No.	134928
Contig ID	116277_1.R1010
5'-most EST	jC-atXP114C231L24T7d1
Method	BLASTN
NCBI GI	g2760170
BLAST score	524
E value	0.0e+00
Match length	593
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIO24, complete sequence [Arabidopsis thaliana]

Seq. No.	134929
Contig ID	116289_1.R1010
5'-most EST	g1217183
Method	BLASTX
NCBI GI	g4558678
BLAST score	160
E value	1.0e-10
Match length	60
% identity	47
NCBI Description	(AC006586) unknown protein [Arabidopsis thaliana]

Seq. No.	134930
Contig ID	116291_1.R1010
5'-most EST	g1217407
Method	BLASTX
NCBI GI	g3193318
BLAST score	341
E value	6.0e-32
Match length	111
% identity	62
NCBI Description	(AF069299) No definition line found [Arabidopsis thaliana]

Seq. No.	134931
Contig ID	116297_1.R1010
5'-most EST	g1217413

Seq. No.	134932
Contig ID	116299_1.R1010
5'-most EST	jC-atXP114C232F4T7d1
Method	BLASTX
NCBI GI	g1903367
BLAST score	596
E value	5.0e-74
Match length	177
% identity	86
NCBI Description	(AC000104) ESTs gb_N65789,gb_T04628 come from this gene. [Arabidopsis thaliana]

Seq. No.	134933
Contig ID	116300_1.R1010
5'-most EST	g2596171
Method	BLASTN
NCBI GI	g2341023
BLAST score	249
E value	1.0e-138
Match length	336
% identity	99
NCBI Description	Sequence of BAC F19P19 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	134934
Contig ID	116315_1.R1010
5'-most EST	jC-atXP19C111K12T7d2
Method	BLASTX
NCBI GI	g4006827
BLAST score	959
E value	1.0e-104
Match length	193
% identity	98
NCBI Description	(AC005970) subtilisin-like protease [Arabidopsis thaliana]

Seq. No.	134935
Contig ID	116323_1.R1010
5'-most EST	g936304
Method	BLASTX
NCBI GI	g4220454
BLAST score	590
E value	1.0e-76
Match length	157
% identity	62
NCBI Description	(AC006216) Similar to gi_3413714 T19L18.21 putative myrosinase-binding protein from Arabidopsis thaliana BAC gb_AC004747. ESTs gb_65870 and gb_T20812 come from this gene. [Arabidopsis thaliana]

Seq. No.	134936
Contig ID	116323_2.R1010
5'-most EST	jC-atXP114C240G22T7d1
Method	BLASTX
NCBI GI	g4220454
BLAST score	362
E value	2.0e-34
Match length	70
% identity	56
NCBI Description	(AC006216) Similar to gi_3413714 T19L18.21 putative myrosinase-binding protein from Arabidopsis thaliana BAC gb_AC004747. ESTs gb_65870 and gb_T20812 come from this gene. [Arabidopsis thaliana]

Seq. No.	134937
Contig ID	116335_1.R1010
5'-most EST	g1217274
Method	BLASTN
NCBI GI	g3928074

BLAST score	203
E value	1.0e-110
Match length	407
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T7F6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134938
Contig ID	116337_1.R1010
5'-most EST	g1217276

Seq. No.	134939
Contig ID	116358_1.R1010
5'-most EST	g2762981
Method	BLASTN
NCBI GI	g4757402
BLAST score	46
E value	2.0e-16
Match length	298
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MIG5, complete sequence

Seq. No.	134940
Contig ID	116365_1.R1010
5'-most EST	jC-atXP115C244E9T7d1
Method	BLASTN
NCBI GI	g2098816
BLAST score	411
E value	0.0e+00
Match length	500
% identity	97
NCBI Description	Arabidopsis thaliana BAC F19G10, complete sequence

Seq. No.	134941
Contig ID	116376_1.R1010
5'-most EST	jC-atXP115C248F7T7d1
Method	BLASTX
NCBI GI	g3080418
BLAST score	641
E value	7.0e-67
Match length	143
% identity	87
NCBI Description	(AL022604) putative protein [Arabidopsis thaliana]

Seq. No.	134942
Contig ID	116380_1.R1010
5'-most EST	g2762308
Method	BLASTN
NCBI GI	g2570223
BLAST score	621
E value	0.0e+00
Match length	625
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F20D22 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134943
Contig ID	116381_1.R1010
5'-most EST	g934224
Method	BLASTN
NCBI GI	g4589432
BLAST score	453
E value	0.0e+00
Match length	537
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MMJ24, complete sequence

Seq. No.	134944
Contig ID	116394_1.R1010
5'-most EST	g2762872
Method	BLASTX
NCBI GI	g2924517
BLAST score	498
E value	2.0e-53
Match length	124
% identity	90
NCBI Description	(AL022023) putative protein [Arabidopsis thaliana]

Seq. No.	134945
Contig ID	116399_1.R1010
5'-most EST	g2762782
Method	BLASTX
NCBI GI	g4587540
BLAST score	177
E value	1.0e-18
Match length	136
% identity	45
NCBI Description	(AC006577) Belongs to the PF_00657 Lipase/Acylhydrolase with GDSL-motif family. [Arabidopsis thaliana]

Seq. No.	134946
Contig ID	116418_1.R1010
5'-most EST	g506907
Method	BLASTX
NCBI GI	g2347188
BLAST score	313
E value	1.0e-28
Match length	57
% identity	96
NCBI Description	(AC002338) laccase isolog [Arabidopsis thaliana] >gi_3150401 (AC004165) putative laccase [Arabidopsis thaliana]

Seq. No.	134947
Contig ID	116420_1.R1010
5'-most EST	jC-atXP115C249O8T7s1
Method	BLASTN
NCBI GI	g2244788
BLAST score	204
E value	1.0e-111
Match length	375
% identity	90

NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No
Seq. No.	134948
Contig ID	116424_1.R1010
5'-most EST	jC-atXP115C250G24T7s1
Seq. No.	134949
Contig ID	116426_1.R1010
5'-most EST	g2762878
Method	BLASTN
NCBI GI	g2252848
BLAST score	178
E value	2.0e-95
Match length	407
% identity	97
NCBI Description	Arabidopsis thaliana BAC TM018A10
Seq. No.	134950
Contig ID	116427_1.R1010
5'-most EST	g2062769
Method	BLASTN
NCBI GI	g2252848
BLAST score	311
E value	1.0e-174
Match length	439
% identity	98
NCBI Description	Arabidopsis thaliana BAC TM018A10
Seq. No.	134951
Contig ID	116429_1.R1010
5'-most EST	jC-atXP115C251B22T7d1
Seq. No.	134952
Contig ID	116431_1.R1010
5'-most EST	jC-atXP115C251D4T7d1
Method	BLASTN
NCBI GI	g3985931
BLAST score	366
E value	0.0e+00
Match length	410
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21H1, complete sequence [Arabidopsis thaliana]
Seq. No.	134953
Contig ID	116442_1.R1010
5'-most EST	g1269420
Method	BLASTX
NCBI GI	g2494144
BLAST score	134
E value	1.0e-07
Match length	116
% identity	5
NCBI Description	(AC002329) predicted leucine-rich protein [Arabidopsis thaliana]

Seq. No.	134954
Contig ID	116464_1.R1010
5'-most EST	jC-atXP94CG11D3T7b1

Seq. No.	134955
Contig ID	116470_1.R1010
5'-most EST	jC-atXP115C248O19T7029d1
Method	BLASTX
NCBI GI	g2739010
BLAST score	62
E value	1.0e-75
Match length	185
% identity	73
NCBI Description	(AF022464) CYP77A3p [Glycine max]

Seq. No.	134956
Contig ID	116472_1.R1010
5'-most EST	jC-atXP115C248O20T7037d1
Method	BLASTX
NCBI GI	g2632254
BLAST score	303
E value	3.0e-27
Match length	166
% identity	39
NCBI Description	(Y12465) serine/threonine kinase [Sorghum bicolor]

Seq. No.	134957
Contig ID	116475_1.R1010
5'-most EST	g1217236
Method	BLASTN
NCBI GI	g3869069
BLAST score	145
E value	1.0e-75
Match length	417
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence [Arabidopsis thaliana]

Seq. No.	134958
Contig ID	116495_1.R1010
5'-most EST	jC-atXP116C136F20T7d1
Method	BLASTN
NCBI GI	g3355463
BLAST score	343
E value	0.0e+00
Match length	347
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134959
Contig ID	116496_1.R1010
5'-most EST	jC-atXP115C248G24T7012d1
Method	BLASTX
NCBI GI	g4587529
BLAST score	445
E value	7.0e-44

Match length	188
% identity	46
NCBI Description	(AC007060) Strong similarity to F19I3.2 gi_3033375 putative berberine bridge enzyme from Arabidopsis thaliana BAC gb_AC004238. EST gb_H76902 comes from this gene

Seq. No.	134960
Contig ID	116503_1.R1010
5'-most EST	jC-atXP115C248I24T7036d1
Method	BLASTX
NCBI GI	g4454019
BLAST score	969
E value	1.0e-105
Match length	189
% identity	100
NCBI Description	(AL035396) SRG1-like protein [Arabidopsis thaliana]

Seq. No.	134961
Contig ID	116528_1.R1010
5'-most EST	g2445860

Seq. No.	134962
Contig ID	116537_1.R1010
5'-most EST	jC-atXP115C249L1T7006d1
Method	BLASTN
NCBI GI	g17818
BLAST score	57
E value	6.0e-23
Match length	216
% identity	88
NCBI Description	B.napus BnGRP10 gene encoding glycine-rich RNA-binding protein

Seq. No.	134963
Contig ID	116537_2.R1010
5'-most EST	g2412827
Method	BLASTN
NCBI GI	g17818
BLAST score	57
E value	3.0e-23
Match length	149
% identity	89
NCBI Description	B.napus BnGRP10 gene encoding glycine-rich RNA-binding protein

Seq. No.	134964
Contig ID	116545_1.R1010
5'-most EST	jC-atXP115C249O8T7046d1
Method	BLASTX
NCBI GI	g4056421
BLAST score	1252
E value	1.0e-138
Match length	249
% identity	93
NCBI Description	(AC005322) Similar to gb_Z30094 basic transcripion factor 2, 44 kD subunit from Homo sapiens. EST gb_W43325 comes from this gene. [Arabidopsis thaliana]

Seq. No.	134965
Contig ID	116563_1.R1010
5'-most EST	g511214
Method	BLASTX
NCBI GI	g3033375
BLAST score	723
E value	2.0e-76
Match length	240
% identity	57
NCBI Description	(AC004238) putative berberine bridge enzyme [Arabidopsis thaliana]

Seq. No.	134966
Contig ID	116563_7.R1010
5'-most EST	jC-atXP48C178D14T7s2
Method	BLASTX
NCBI GI	g4587526
BLAST score	251
E value	1.0e-21
Match length	75
% identity	60
NCBI Description	(AC007060) Strong similarity to F19I3.2 gi_3033375 putative berberine bridge enzyme from Arabidopsis thaliana BAC gb_AC004238. ESTs gb_F19886, gb_Z30784 and gb_Z30785 come from this gene

Seq. No.	134967
Contig ID	116580_1.R1010
5'-most EST	jC-atXP117C140F7T7a1

Seq. No.	134968
Contig ID	116581_1.R1010
5'-most EST	jC-atXP117C140J18T7a1
Method	BLASTN
NCBI GI	g2351064
BLAST score	62
E value	8.0e-26
Match length	1008
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDJ22, complete sequence [Arabidopsis thaliana]

Seq. No.	134969
Contig ID	116583_1.R1010
5'-most EST	jC-atXP117C140K16T7d1

Seq. No.	134970
Contig ID	116584_1.R1010
5'-most EST	jC-atXP117C140L2T7a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	52
E value	5.0e-20
Match length	56
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	134971
Contig ID	116595_1.R1010
5'-most EST	jC-atXP117C141J1T7a1
Method	BLASTX
NCBI GI	g3242705
BLAST score	481
E value	4.0e-48
Match length	100
% identity	89
NCBI Description	(AC003040) putative nicotinate phosphoribosyltransferase [Arabidopsis thaliana]

Seq. No.	134972
Contig ID	116596_1.R1010
5'-most EST	jC-atXP117C141K23T7a1
Method	BLASTX
NCBI GI	g4587527
BLAST score	325
E value	7.0e-30
Match length	130
% identity	50
NCBI Description	(AC007060) Strong similarity to F19I3.2 gi_3033375 putative berberine bridge enzyme from Arabidopsis thaliana BAC gb_AC004238

Seq. No.	134973
Contig ID	116600_1.R1010
5'-most EST	jC-atXP117C141M18T7a1
Method	BLASTX
NCBI GI	g231660
BLAST score	465
E value	3.0e-46
Match length	153
% identity	61
NCBI Description	HYPOTHETICAL 226 KD PROTEIN (ORF 1901)

Seq. No.	134974
Contig ID	116605_1.R1010
5'-most EST	jC-atXP117C143A20T7a1
Method	BLASTN
NCBI GI	g3885325
BLAST score	403
E value	0.0e+00
Match length	507
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T20P8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134975
Contig ID	116609_1.R1010
5'-most EST	g936843
Method	BLASTN
NCBI GI	g2351062
BLAST score	331
E value	0.0e+00
Match length	429

% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAH20, complete sequence [Arabidopsis thaliana]
Seq. No.	134976
Contig ID	116612_1.R1010
5'-most EST	jC-atXP119C166H13T7024a1
Method	BLASTN
NCBI GI	g2582640
BLAST score	34
E value	3.0e-09
Match length	73
% identity	89
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40
Seq. No.	134977
Contig ID	116621_1.R1010
5'-most EST	jC-atXP11C97F18T7s1
Method	BLASTN
NCBI GI	g3702728
BLAST score	375
E value	0.0e+00
Match length	475
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M13, complete sequence [Arabidopsis thaliana]
Seq. No.	134978
Contig ID	116622_1.R1010
5'-most EST	g2048894
Method	BLASTX
NCBI GI	g4581111
BLAST score	217
E value	9.0e-18
Match length	81
% identity	55
NCBI Description	(AC005825) putative reverse transcriptase [Arabidopsis thaliana]
Seq. No.	134979
Contig ID	116627_1.R1010
5'-most EST	jC-atXP11C97O11T7s1
Method	BLASTX
NCBI GI	g4678356
BLAST score	189
E value	4.0e-23
Match length	76
% identity	71
NCBI Description	(AL049659) cytochrome P450-like protein [Arabidopsis thaliana]
Seq. No.	134980
Contig ID	116631_1.R1010
5'-most EST	jC-atXP16C109D21T7s1
Method	BLASTN
NCBI GI	g2564051

BLAST score	407
E value	0.0e+00
Match length	419
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD9, complete sequence [Arabidopsis thaliana]

Seq. No.	134981
Contig ID	116636_1.R1010
5'-most EST	jC-atXP11C98C15T7s1

Seq. No.	134982
Contig ID	116639_1.R1010
5'-most EST	g2048905
Method	BLASTN
NCBI GI	g3395421
BLAST score	194
E value	1.0e-105
Match length	374
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T19C21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134983
Contig ID	116648_1.R1010
5'-most EST	g936220
Method	BLASTX
NCBI GI	g1279598
BLAST score	391
E value	9.0e-38
Match length	108
% identity	64
NCBI Description	(Z71752) pectin methylesterase [Nicotiana plumbaginifolia]

Seq. No.	134984
Contig ID	116653_1.R1010
5'-most EST	jC-atXP122C158F2T7079a1
Method	BLASTX
NCBI GI	g2244893
BLAST score	665
E value	1.0e-102
Match length	375
% identity	56
NCBI Description	(Z97338) similarity to cytochrome P450 [Arabidopsis thaliana]

Seq. No.	134985
Contig ID	116655_1.R1010
5'-most EST	g2757310
Method	BLASTN
NCBI GI	g2262155
BLAST score	189
E value	1.0e-102
Match length	421
% identity	96
NCBI Description	DNA sequence of Arabidopsis thaliana BAC F5J6 from chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No.	134986
Contig ID	116668_1.R1010
5'-most EST	jC-atXP11C98N10T7s1
Method	BLASTN
NCBI GI	g2623294
BLAST score	213
E value	1.0e-116
Match length	321
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC T20B5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	134987
Contig ID	116672_1.R1010
5'-most EST	jC-atXP11C99A10T7s1
Method	BLASTN
NCBI GI	g3805839
BLAST score	238
E value	1.0e-131
Match length	506
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4B14 (ESSAII project)

Seq. No.	134988
Contig ID	116680_1.R1010
5'-most EST	g2758176
Method	BLASTX
NCBI GI	g3482925
BLAST score	223
E value	1.0e-31
Match length	151
% identity	48
NCBI Description	(AC003970) Highly similar to cinnamyl alcohol dehydrogenase, gi_1143445 [Arabidopsis thaliana]

Seq. No.	134989
Contig ID	116681_1.R1010
5'-most EST	g2758196

Seq. No.	134990
Contig ID	116688_1.R1010
5'-most EST	jC-atXP122C117J22T7d1

Seq. No.	134991
Contig ID	116690_1.R1010
5'-most EST	jC-atXP122C117J5T7d1
Method	BLASTN
NCBI GI	g1946354
BLAST score	329
E value	0.0e+00
Match length	429
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T06B20 genomic sequence, complete sequence

Seq. No.	134992
Contig ID	116692_1.R1010
5'-most EST	jC-atXP122C117K20T7d1
Method	BLASTN
NCBI GI	g2245073
BLAST score	302
E value	1.0e-169
Match length	451
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	134993
Contig ID	116693_1.R1010
5'-most EST	g2758219
Method	BLASTN
NCBI GI	g3510346
BLAST score	258
E value	1.0e-143
Match length	278
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNL12, complete sequence [Arabidopsis thaliana]

Seq. No.	134994
Contig ID	116697_1.R1010
5'-most EST	jC-atXP122C118F20T7034a1
Method	BLASTN
NCBI GI	g2264312
BLAST score	411
E value	0.0e+00
Match length	504
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK16, complete sequence [Arabidopsis thaliana]

Seq. No.	134995
Contig ID	116700_1.R1010
5'-most EST	g2758256
Method	BLASTX
NCBI GI	g3776576
BLAST score	283
E value	9.0e-25
Match length	94
% identity	56
NCBI Description	(AC005388) ESTs gb_Z25669 and gb_Z33817 come from this gene. [Arabidopsis thaliana]

Seq. No.	134996
Contig ID	116703_1.R1010
5'-most EST	jC-atXP122C118H3T7d1
Method	BLASTN
NCBI GI	g3335356
BLAST score	242
E value	1.0e-133
Match length	336
% identity	99

NCBI Description	Arabidopsis thaliana chromosome II BAC F16M14 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	134997
Contig ID	116704_1.R1010
5'-most EST	jC-atXP122C118I13T7d1
Seq. No.	134998
Contig ID	116706_1.R1010
5'-most EST	g2722487
Method	BLASTN
NCBI GI	g2264318
BLAST score	328
E value	0.0e+00
Match length	356
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUP24, complete sequence [Arabidopsis thaliana]
Seq. No.	134999
Contig ID	116707_1.R1010
5'-most EST	g2747431
Seq. No.	135000
Contig ID	116708_1.R1010
5'-most EST	jC-atXP122C152H15T7094a1
Method	BLASTN
NCBI GI	g3399678
BLAST score	406
E value	0.0e+00
Match length	458
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F13M7 sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	135001
Contig ID	116708_2.R1010
5'-most EST	jC-atXP122C152H15T7d1
Method	BLASTN
NCBI GI	g3399678
BLAST score	433
E value	0.0e+00
Match length	577
% identity	96
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F13M7 sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	135002
Contig ID	116712_1.R1010
5'-most EST	g936001
Seq. No.	135003
Contig ID	116713_1.R1010
5'-most EST	jC-atXP122C158F2T7d1
Method	BLASTX
NCBI GI	g2244893
BLAST score	155

E value	5.0e-18
Match length	68
% identity	71
NCBI Description	(Z97338) similarity to cytochrome P450 [Arabidopsis thaliana]

Seq. No.	135004
Contig ID	116716_2.R1010
5'-most EST	jC-atXP122C159H19T7d1
Method	BLASTN
NCBI GI	g3540210
BLAST score	399
E value	0.0e+00
Match length	441
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC F5A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135005
Contig ID	116717_1.R1010
5'-most EST	jC-atXP122C159H23T7d1
Method	BLASTX
NCBI GI	g2499812
BLAST score	588
E value	2.0e-60
Match length	135
% identity	83
NCBI Description	PROFILIN 3 >gi_1353765 (U43323) profilin 3 [Arabidopsis thaliana]

Seq. No.	135006
Contig ID	116722_1.R1010
5'-most EST	g2763951
Method	BLASTX
NCBI GI	g3912922
BLAST score	311
E value	5.0e-28
Match length	88
% identity	65
NCBI Description	(AF001308) hypothetical protein [Arabidopsis thaliana]

Seq. No.	135007
Contig ID	116723_1.R1010
5'-most EST	g2759562
Method	BLASTX
NCBI GI	g4263787
BLAST score	693
E value	4.0e-83
Match length	166
% identity	96
NCBI Description	(AC006068) unknown protein [Arabidopsis thaliana]

Seq. No.	135008
Contig ID	116724_1.R1010
5'-most EST	jC-atXP124C118M17T7d1
Method	BLASTN
NCBI GI	g2160132

BLAST score	199
E value	1.0e-108
Match length	369
% identity	100
NCBI Description	Sequence of BAC F19K23 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	135009
Contig ID	116731_1.R1010
5'-most EST	jC-atXP124C118N2T7d1
Method	BLASTX
NCBI GI	g1172019
BLAST score	222
E value	5.0e-18
Match length	95
% identity	45
NCBI Description	PEROXISOME BIOSYNTHESIS PROTEIN PAS1 (PEROXIN-1) >gi_1076972_pir__A55152 PAS1 protein - yeast (Pichia pastoris) >gi_537420_emb_CAA85450_ (Z36987) PAS1 [Pichia pastoris]

Seq. No.	135010
Contig ID	116739_1.R1010
5'-most EST	g2758688
Method	BLASTN
NCBI GI	g4159701
BLAST score	115
E value	9.0e-58
Match length	516
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K22G18, complete sequence

Seq. No.	135011
Contig ID	116748_1.R1010
5'-most EST	g2758702

Seq. No.	135012
Contig ID	116754_1.R1010
5'-most EST	g938006
Method	BLASTX
NCBI GI	g3695383
BLAST score	379
E value	2.0e-36
Match length	73
% identity	97
NCBI Description	(AF096370) similar to inorganic pyrophosphatase (Pfam: PF00719 Pyrophosphatase, E-value: 2.7e-88) [Arabidopsis thaliana]

Seq. No.	135013
Contig ID	116756_1.R1010
5'-most EST	jC-atXP124C121B23T7d1
Method	BLASTN
NCBI GI	g4467094
BLAST score	311
E value	1.0e-174

Match length	984
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10 (ESSA project)

Seq. No.	135014
Contig ID	116757_1.R1010
5'-most EST	jC-atXP124C121B9T7d1
Method	BLASTX
NCBI GI	g4760370
BLAST score	369
E value	4.0e-35
Match length	187
% identity	36
NCBI Description	(AF082565) ATP dependent copper transporter [Arabidopsis thaliana] >gi_4760380_gb_AAD29115.1_ (AF091112) ATP dependent copper transporter [Arabidopsis thaliana]

Seq. No.	135015
Contig ID	116776_1.R1010
5'-most EST	g2758825
Method	BLASTX
NCBI GI	g3935180
BLAST score	585
E value	2.0e-60
Match length	132
% identity	87
NCBI Description	(AC004557) F17L21.23 [Arabidopsis thaliana]

Seq. No.	135016
Contig ID	116780_1.R1010
5'-most EST	g2758441
Method	BLASTX
NCBI GI	g1208497
BLAST score	335
E value	7.0e-31
Match length	192
% identity	41
NCBI Description	(D38125) EREBP-4 [Nicotiana tabacum]

Seq. No.	135017
Contig ID	116780_2.R1010
5'-most EST	g936643
Method	BLASTX
NCBI GI	g1208497
BLAST score	150
E value	4.0e-12
Match length	119
% identity	44
NCBI Description	(D38125) EREBP-4 [Nicotiana tabacum]

Seq. No.	135018
Contig ID	116784_2.R1010
5'-most EST	g2758455
Method	BLASTX
NCBI GI	g2997593
BLAST score	276

E value	3.0e-24
Match length	124
% identity	51
NCBI Description	(AF020816) glucose-6-phosphate/phosphate-translocator precursor [Solanum tuberosum]

Seq. No.	135019
Contig ID	116797_1.R1010
5'-most EST	jC-atXP124C122B2T7d1
Method	BLASTX
NCBI GI	g2506277
BLAST score	241
E value	2.0e-31
Match length	130
% identity	58
NCBI Description	RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT PRECURSOR (60 KD CHAPERONIN BETA SUBUNIT) (CPN-60 BETA) >gi_806808 (U21139) chaperonin precursor [Pisum sativum]

Seq. No.	135020
Contig ID	116807_1.R1010
5'-most EST	jC-atXP125C125N19T7d2
Method	BLASTX
NCBI GI	g3913435
BLAST score	279
E value	1.0e-24
Match length	97
% identity	49
NCBI Description	PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE F56D2.6 >gi_532106 (U13644) similar to S. cerevisiae pre-mRNA splicing factor RNA helicase PRP22 and other DEAD box family helicases (DEAH subfamily) [Caenorhabditis elegans]

Seq. No.	135021
Contig ID	116810_1.R1010
5'-most EST	g2413992
Method	BLASTX
NCBI GI	g4490733
BLAST score	731
E value	1.0e-77
Match length	139
% identity	99
NCBI Description	(AL035709) putative protein [Arabidopsis thaliana]

Seq. No.	135022
Contig ID	116811_1.R1010
5'-most EST	g2762251
Method	BLASTX
NCBI GI	g731456
BLAST score	175
E value	2.0e-12
Match length	75
% identity	41
NCBI Description	HYPOTHETICAL 27.7 KD PROTEIN IN PIP1-GLN3 INTERGENIC REGION >gi_1077649_pir__S50542 hypothetical protein YER039c - yeast (Saccharomyces cerevisiae) >gi_603272 (U18796)

Yer039cp [Saccharomyces cerevisiae]

Seq. No.	135023
Contig ID	116813_1.R1010
5'-most EST	jC-atXP125C133H7T7d1

Seq. No.	135024
Contig ID	116814_1.R1010
5'-most EST	jC-atXP125C133H9T7d1

Seq. No.	135025
Contig ID	116819_1.R1010
5'-most EST	g2763262
Method	BLASTX
NCBI GI	g1001355
BLAST score	146
E value	3.0e-09
Match length	81
% identity	40
NCBI Description	(D64006) auxin-induced protein [Synechocystis sp.]

Seq. No.	135026
Contig ID	116836_1.R1010
5'-most EST	jC-atXP125C193P6T7d1
Method	BLASTX
NCBI GI	g2494143
BLAST score	628
E value	4.0e-73
Match length	149
% identity	97
NCBI Description	(AC002329) Mlo-like protein [Arabidopsis thaliana]

Seq. No.	135027
Contig ID	116840_1.R1010
5'-most EST	g1216605
Method	BLASTX
NCBI GI	g4581123
BLAST score	270
E value	5.0e-44
Match length	113
% identity	84
NCBI Description	(AC005825) unknown protein [Arabidopsis thaliana]

Seq. No.	135028
Contig ID	116855_1.R1010
5'-most EST	jC-atXP12C103G5T7069a1
Method	BLASTX
NCBI GI	g1709925
BLAST score	359
E value	5.0e-35
Match length	97
% identity	71
NCBI Description	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE CYCLO-LIGASE PRECURSOR (AIRS) (PHOSPHORIBOSYL-AMINOIMIDAZOLE SYNTHETASE) (AIR SYNTHASE) >gi_945060 (U30895) aminoimidazole ribonucleotide (AIRS) synthetase [Vigna unguiculata]

Seq. No.	135029
Contig ID	116861_1.R1010
5'-most EST	jC-atXP12C103D21T7d2
Method	BLASTX
NCBI GI	g2982283
BLAST score	483
E value	2.0e-48
Match length	191
% identity	55
NCBI Description	(AF051226) PREG-like protein [Picea mariana]

Seq. No.	135030
Contig ID	116861_2.R1010
5'-most EST	g2048149
Method	BLASTX
NCBI GI	g2982283
BLAST score	327
E value	3.0e-30
Match length	114
% identity	54
NCBI Description	(AF051226) PREG-like protein [Picea mariana]

Seq. No.	135031
Contig ID	116866_1.R1010
5'-most EST	jC-atXP12C103M24T7094a1
Method	BLASTN
NCBI GI	g1865682
BLAST score	310
E value	1.0e-174
Match length	503
% identity	99
NCBI Description	A.thaliana 16 kb chromosome 1 DNA fragment

Seq. No.	135032
Contig ID	116870_1.R1010
5'-most EST	g2596534
Method	BLASTN
NCBI GI	g2264312
BLAST score	408
E value	0.0e+00
Match length	514
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK16, complete sequence [Arabidopsis thaliana]

Seq. No.	135033
Contig ID	116873_1.R1010
5'-most EST	g2596541
Method	BLASTN
NCBI GI	g3193311
BLAST score	302
E value	1.0e-169
Match length	430
% identity	97
NCBI Description	Arabidopsis thaliana BAC F6N15

Seq. No.	135034

Contig ID	116874_1.R1010
5'-most EST	jC-atXP12C103K22T7d2
Method	BLASTN
NCBI GI	g2979540
BLAST score	403
E value	0.0e+00
Match length	563
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F17K2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135035
Contig ID	116875_1.R1010
5'-most EST	g2596544
Method	BLASTX
NCBI GI	g4726110
BLAST score	274
E value	9.0e-24
Match length	181
% identity	26
NCBI Description	(AC006436) unknown protein [Arabidopsis thaliana]

Seq. No.	135036
Contig ID	116879_1.R1010
5'-most EST	g2596549
Method	BLASTX
NCBI GI	g2541876
BLAST score	264
E value	3.0e-24
Match length	142
% identity	46
NCBI Description	(D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]

Seq. No.	135037
Contig ID	116880_1.R1010
5'-most EST	g576968
Method	BLASTX
NCBI GI	g3874433
BLAST score	231
E value	7.0e-19
Match length	152
% identity	36
NCBI Description	(Z81038) predicted using Genefinder; Similarity to Yeast ABD1 protein (SW:P32783); cDNA EST EMBL:T01105 comes from this gene [Caenorhabditis elegans]

Seq. No.	135038
Contig ID	116895_1.R1010
5'-most EST	g2596863
Method	BLASTX
NCBI GI	g2832642
BLAST score	461
E value	7.0e-78
Match length	178
% identity	82
NCBI Description	(AL021710) putative protein [Arabidopsis thaliana]

Seq. No.	135039
Contig ID	116898_1.R1010
5'-most EST	jC-atXP12C99M14T7d2
Method	BLASTX
NCBI GI	g4689473
BLAST score	157
E value	2.0e-10
Match length	40
% identity	68
NCBI Description	(AC007213) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	135040
Contig ID	116900_1.R1010
5'-most EST	jC-atXP12C99M18T7d2

Seq. No.	135041
Contig ID	116901_1.R1010
5'-most EST	jC-atXP12C99M20T7d2
Method	BLASTX
NCBI GI	g2281103
BLAST score	599
E value	4.0e-62
Match length	111
% identity	99
NCBI Description	(AC002333) Glucan endo-1,3-beta glucosidase isolog [Arabidopsis thaliana]

Seq. No.	135042
Contig ID	116903_1.R1010
5'-most EST	jC-atXP12C99M23T7d2
Method	BLASTX
NCBI GI	g3377517
BLAST score	213
E value	4.0e-17
Match length	100
% identity	41
NCBI Description	(AF073361) nitrate transporter NTL1 [Arabidopsis thaliana]

Seq. No.	135043
Contig ID	116921_1.R1010
5'-most EST	g2596947

Seq. No.	135044
Contig ID	116933_1.R1010
5'-most EST	g2596583
Method	BLASTX
NCBI GI	g2911067
BLAST score	400
E value	6.0e-39
Match length	114
% identity	71
NCBI Description	(AL021960) UV-damaged DNA-binding protein-like [Arabidopsis thaliana]

Seq. No. 135045

Contig ID	116942_1.R1010
5'-most EST	jC-atXP13C104E2T7d2
Method	BLASTX
NCBI GI	g3702314
BLAST score	378
E value	2.0e-36
Match length	144
% identity	62
NCBI Description	(AC002535) similar to SWI/SNF complex subunit BAF170 [Arabidopsis thaliana]

Seq. No.	135046
Contig ID	116945_1.R1010
5'-most EST	jC-atXP13C104G18T7d2
Method	BLASTX
NCBI GI	g1653395
BLAST score	386
E value	3.0e-37
Match length	170
% identity	49
NCBI Description	(D90913) PET112 [Synechocystis sp.]

Seq. No.	135047
Contig ID	116947_1.R1010
5'-most EST	jC-atXP13C104G23T7d2
Method	BLASTX
NCBI GI	g3341695
BLAST score	562
E value	1.0e-105
Match length	221
% identity	89
NCBI Description	(AC003672) putative thiamin pyrophosphokinase [Arabidopsis thaliana]

Seq. No.	135048
Contig ID	116951_1.R1010
5'-most EST	g2596602
Method	BLASTX
NCBI GI	g4468984
BLAST score	345
E value	2.0e-32
Match length	90
% identity	74
NCBI Description	(AL035605) putative protein [Arabidopsis thaliana]

Seq. No.	135049
Contig ID	116960_1.R1010
5'-most EST	jC-atXP13C104K22T7d2
Method	BLASTN
NCBI GI	g4580454
BLAST score	342
E value	0.0e+00
Match length	470
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T2G17 genomic sequence, complete sequence

Seq. No.	135050
Contig ID	116961_1.R1010
5'-most EST	jC-atXP13C104L10T7d2
Method	BLASTX
NCBI GI	g4097547
BLAST score	369
E value	3.0e-35
Match length	113
% identity	38
NCBI Description	(U64906) ATFP3 [Arabidopsis thaliana]

Seq. No.	135051
Contig ID	116971_1.R1010
5'-most EST	jC-atXP13C104N12T7d2
Method	BLASTX
NCBI GI	g2262116
BLAST score	627
E value	2.0e-65
Match length	124
% identity	99
NCBI Description	(AC002343) cellulose synthase isolog [Arabidopsis thaliana]

Seq. No.	135052
Contig ID	116977_1.R1010
5'-most EST	jC-atXP13C104O14T7d2
Method	BLASTN
NCBI GI	g4713943
BLAST score	181
E value	4.0e-97
Match length	332
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8K14 sequence, complete sequence

Seq. No.	135053
Contig ID	116978_1.R1010
5'-most EST	jC-atXP13C104O15T7d2
Method	BLASTX
NCBI GI	g4586045
BLAST score	55
E value	1.0e-52
Match length	169
% identity	67
NCBI Description	(AC007020) putative ankyrin protein [Arabidopsis thaliana]

Seq. No.	135054
Contig ID	116979_1.R1010
5'-most EST	g1269447
Method	BLASTX
NCBI GI	g2244859
BLAST score	556
E value	7.0e-57
Match length	143
% identity	80
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 135055

Contig ID	116980_1.R1010
5'-most EST	g2596676
Method	BLASTN
NCBI GI	g4662647
BLAST score	203
E value	1.0e-110
Match length	416
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F3K12 genomic sequence, complete sequence

Seq. No.	135056
Contig ID	116984_1.R1010
5'-most EST	jC-atXP14C104P22T7d1
Method	BLASTX
NCBI GI	g4455206
BLAST score	58
E value	4.0e-35
Match length	148
% identity	53
NCBI Description	(AL035440) putative beta-1, 3-glucanase [Arabidopsis thaliana]

Seq. No.	135057
Contig ID	116988_1.R1010
5'-most EST	jC-atXP14C104P2T7d1
Method	BLASTX
NCBI GI	g3021506
BLAST score	820
E value	7.0e-88
Match length	207
% identity	77
NCBI Description	(X96727) isocitrate dehydrogenase (NAD+) [Nicotiana tabacum]

Seq. No.	135058
Contig ID	116992_1.R1010
5'-most EST	jC-atXP14C105A3T7d1
Method	BLASTN
NCBI GI	g2245031
BLAST score	477
E value	0.0e+00
Match length	517
% identity	38
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	135059
Contig ID	116994_1.R1010
5'-most EST	g2597025
Method	BLASTX
NCBI GI	g2342687
BLAST score	230
E value	1.0e-32
Match length	147
% identity	52
NCBI Description	(AC000106) Similar to Beta integral membrane protein

(gb_U43629). EST gb_W43122 comes from this gene.
[Arabidopsis thaliana]

Seq. No.	135060
Contig ID	116997_1.R1010
5'-most EST	g2597035
Method	BLASTX
NCBI GI	g1495804
BLAST score	429
E value	2.0e-42
Match length	113
% identity	73
NCBI Description	(X96406) 13-lipoxygenase [Solanum tuberosum]

Seq. No.	135061
Contig ID	116999_1.R1010
5'-most EST	jC-atXP14C105C12T7d1
Method	BLASTX
NCBI GI	g4115381
BLAST score	191
E value	8.0e-15
Match length	45
% identity	78
NCBI Description	(AC005967) putative limonene cyclase [Arabidopsis thaliana]

Seq. No.	135062
Contig ID	117008_1.R1010
5'-most EST	g3450085

Seq. No.	135063
Contig ID	117013_1.R1010
5'-most EST	jC-atXP14C105E9T7d1
Method	BLASTN
NCBI GI	g4159703
BLAST score	289
E value	1.0e-161
Match length	417
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K5F14, complete sequence

Seq. No.	135064
Contig ID	117017_1.R1010
5'-most EST	jC-atXP14C105H16T7d1

Seq. No.	135065
Contig ID	117027_1.R1010
5'-most EST	jC-atXP14C105K12T7d1

Seq. No.	135066
Contig ID	117031_1.R1010
5'-most EST	jC-atXP14C105K19T7s1
Method	BLASTN
NCBI GI	g3522932
BLAST score	271
E value	1.0e-151
Match length	398

% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135067
Contig ID	117042_1.R1010
5'-most EST	g2597223
Method	BLASTN
NCBI GI	g2262135
BLAST score	316
E value	1.0e-178
Match length	328
% identity	99
NCBI Description	Arabidopsis thaliana BAC T10P11 from chromosome IV, near 15 cM, complete sequence

Seq. No.	135068
Contig ID	117048_1.R1010
5'-most EST	jC-atXP14C105N24T7d1

Seq. No.	135069
Contig ID	117050_1.R1010
5'-most EST	jC-atXP14C105N3T7d1
Method	BLASTX
NCBI GI	g4835225
BLAST score	493
E value	7.0e-50
Match length	121
% identity	84
NCBI Description	(AL049862) UTP-glucose glucosyltransferase like protein [Arabidopsis thaliana]

Seq. No.	135070
Contig ID	117051_1.R1010
5'-most EST	g3450100
Method	BLASTN
NCBI GI	g4835223
BLAST score	441
E value	0.0e+00
Match length	498
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F18B3 (ESSA project)

Seq. No.	135071
Contig ID	117052_1.R1010
5'-most EST	jC-atXP14C105O10T7d1
Method	BLASTX
NCBI GI	g2281109
BLAST score	556
E value	4.0e-57
Match length	159
% identity	69
NCBI Description	(AC002333) endochitinase isolog [Arabidopsis thaliana]

Seq. No.	135072
Contig ID	117062_1.R1010

5'-most EST	jC-atXP14C105P24T7d1
Method	BLASTX
NCBI GI	g1351203
BLAST score	502
E value	1.0e-73
Match length	187
% identity	80
NCBI Description	TUBULIN BETA CHAIN

Seq. No.	135073
Contig ID	117064_1.R1010
5'-most EST	g2597241
Method	BLASTX
NCBI GI	g4455276
BLAST score	321
E value	2.0e-30
Match length	137
% identity	52
NCBI Description	(AL035527) peptide transporter-like protein [Arabidopsis thaliana]

Seq. No.	135074
Contig ID	117068_1.R1010
5'-most EST	g3450107
Method	BLASTN
NCBI GI	g4262221
BLAST score	262
E value	1.0e-145
Match length	438
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135075
Contig ID	117076_1.R1010
5'-most EST	jC-atXP14C106C5T7s1
Method	BLASTN
NCBI GI	g3046856
BLAST score	289
E value	1.0e-161
Match length	508
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXI22, complete sequence [Arabidopsis thaliana]

Seq. No.	135076
Contig ID	117079_1.R1010
5'-most EST	g2596732
Method	BLASTX
NCBI GI	g4646203
BLAST score	256
E value	5.0e-22
Match length	143
% identity	37
NCBI Description	(AC007230) Belongs to PF_00026 Eukaryotic aspartyl protease family. [Arabidopsis thaliana]

Seq. No.	135077
Contig ID	117081_1.R1010
5'-most EST	g2597490
Method	BLASTN
NCBI GI	g3080352
BLAST score	313
E value	1.0e-176
Match length	465
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T5K18 (ESSAII project)

Seq. No.	135078
Contig ID	117085_1.R1010
5'-most EST	g2597246

Seq. No.	135079
Contig ID	117090_1.R1010
5'-most EST	g2596753
Method	BLASTX
NCBI GI	g3152563
BLAST score	691
E value	4.0e-94
Match length	213
% identity	84
NCBI Description	(AC002986) Similar to myb-related transcription factors e.g., gb_X98308. EST gb_T22093 and gb_T22697 come from this gene. [Arabidopsis thaliana]

Seq. No.	135080
Contig ID	117109_1.R1010
5'-most EST	jC-atXP15C108A20T7d1
Method	BLASTX
NCBI GI	g3128185
BLAST score	226
E value	4.0e-18
Match length	164
% identity	41
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	135081
Contig ID	117114_1.R1010
5'-most EST	g2597422

Seq. No.	135082
Contig ID	117129_1.R1010
5'-most EST	g2048194
Method	BLASTN
NCBI GI	g4220632
BLAST score	249
E value	1.0e-137
Match length	460
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K6M13, complete sequence [Arabidopsis thaliana]

Seq. No.	135083

Contig ID 117129_2.R1010
5'-most EST jC-atXP80C240G12T7d1
Method BLASTN
NCBI GI g4220632
BLAST score 471
E value 0.0e+00
Match length 637
% identity 100
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K6M13, complete sequence [Arabidopsis thaliana]

Seq. No. 135084
Contig ID 117136_1.R1010
5'-most EST g3450153
Method BLASTN
NCBI GI g2244901
BLAST score 297
E value 1.0e-166
Match length 553
% identity 97
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No. 135085
Contig ID 117137_1.R1010
5'-most EST jC-atXP16C108K11T7d1
Method BLASTX
NCBI GI g3129952
BLAST score 368
E value 6.0e-35
Match length 125
% identity 45
NCBI Description (AJ006052) copper amine oxidase [Cicer arietinum]

Seq. No. 135086
Contig ID 117163_1.R1010
5'-most EST g634488

Seq. No. 135087
Contig ID 117172_1.R1010
5'-most EST g3450198
Method BLASTX
NCBI GI g3763919
BLAST score 479
E value 4.0e-48
Match length 96
% identity 98
NCBI Description (AC004450) putative isopropylmalate dehydratase [Arabidopsis thaliana] >gi_4531436_gb_AAD22121.1_AC006224_3 (AC006224) putative isopropylmalate dehydratase [Arabidopsis thaliana]

Seq. No. 135088
Contig ID 117174_1.R1010
5'-most EST g2048240

Seq. No. 135089

Contig ID	117177_1.R1010
5'-most EST	g2393261
Seq. No.	135090
Contig ID	117180_1.R1010
5'-most EST	g634615
Method	BLASTX
NCBI GI	g4406759
BLAST score	395
E value	3.0e-38
Match length	134
% identity	60
NCBI Description	(AC006836) hypothetical protein [Arabidopsis thaliana]
Seq. No.	135091
Contig ID	117201_1.R1010
5'-most EST	g2393267
Method	BLASTX
NCBI GI	g3334162
BLAST score	223
E value	6.0e-18
Match length	102
% identity	43
NCBI Description	DOWN SYNDROME CRITICAL REGION PROTEIN A >gi_2588993_dbj_BAA23270_ (AB001990) Dcra [Mus musculus]
Seq. No.	135092
Contig ID	117205_1.R1010
5'-most EST	g1268399
Method	BLASTX
NCBI GI	g3540181
BLAST score	203
E value	1.0e-15
Match length	130
% identity	42
NCBI Description	(AC004122) Unknown protein [Arabidopsis thaliana]
Seq. No.	135093
Contig ID	117215_1.R1010
5'-most EST	jC-atXP17C110F15T7s3
Method	BLASTX
NCBI GI	g2911073
BLAST score	226
E value	6.0e-28
Match length	123
% identity	51
NCBI Description	(AL021960) putative protein [Arabidopsis thaliana]
Seq. No.	135094
Contig ID	117218_1.R1010
5'-most EST	jC-atXP17C110F21T7d3
Method	BLASTX
NCBI GI	g4567283
BLAST score	486
E value	8.0e-49
Match length	152
% identity	72

NCBI Description	(AC006841) unknown protein [Arabidopsis thaliana]
Seq. No.	135095
Contig ID	117230_1.R1010
5'-most EST	jC-atXP17C110G3T7d3
Method	BLASTX
NCBI GI	g2827665
BLAST score	653
E value	2.0e-68
Match length	183
% identity	53
NCBI Description	(AL021637) vacuolar sorting receptor-like protein [Arabidopsis thaliana]
Seq. No.	135096
Contig ID	117232_1.R1010
5'-most EST	jC-atXP17C110G6T7d3
Method	BLASTN
NCBI GI	g4589430
BLAST score	470
E value	0.0e+00
Match length	514
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLD14, complete sequence
Seq. No.	135097
Contig ID	117233_1.R1010
5'-most EST	jC-atXP17C110G6T7s3
Method	BLASTX
NCBI GI	g3046694
BLAST score	346
E value	2.0e-32
Match length	112
% identity	62
NCBI Description	(AL022224) vacuolar sorting receptor-like protein [Arabidopsis thaliana]
Seq. No.	135098
Contig ID	117235_1.R1010
5'-most EST	jC-atXP17C110G7T7s3
Method	BLASTX
NCBI GI	g2827699
BLAST score	146
E value	4.0e-09
Match length	46
% identity	63
NCBI Description	(AL021684) predicted protein [Arabidopsis thaliana]
Seq. No.	135099
Contig ID	117236_1.R1010
5'-most EST	jC-atXP17C110H10T7d3
Method	BLASTN
NCBI GI	g4159707
BLAST score	212
E value	1.0e-115
Match length	368

% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJK13, complete sequence

Seq. No.	135100
Contig ID	117237_1.R1010
5'-most EST	jC-atXP17C110H10T7s3
Method	BLASTX
NCBI GI	g2244796
BLAST score	466
E value	1.0e-46
Match length	130
% identity	75
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	135101
Contig ID	117240_1.R1010
5'-most EST	g2757502
Method	BLASTN
NCBI GI	g4406776
BLAST score	295
E value	1.0e-165
Match length	398
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F14H20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135102
Contig ID	117241_1.R1010
5'-most EST	g2446103
Method	BLASTX
NCBI GI	g2129661
BLAST score	349
E value	7.0e-33
Match length	67
% identity	97
NCBI Description	OR23 protein - Arabidopsis thaliana (fragment) >gi_1022809 (U37704) OR23peptide [Arabidopsis thaliana]

Seq. No.	135103
Contig ID	117274_1.R1010
5'-most EST	jC-atXP17C110L6T7d3
Method	BLASTN
NCBI GI	g4519192
BLAST score	211
E value	1.0e-115
Match length	447
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MBK21, complete sequence

Seq. No.	135104
Contig ID	117283_1.R1010
5'-most EST	g2446044
Method	BLASTX
NCBI GI	g3426039
BLAST score	153

E value	7.0e-10
Match length	109
% identity	37
NCBI Description	(AC005168) unknown protein [Arabidopsis thaliana]

Seq. No.	135105
Contig ID	117286_1.R1010
5'-most EST	jC-atXP17C110N24T7d3
Method	BLASTX
NCBI GI	g3024893
BLAST score	151
E value	1.0e-09
Match length	160
% identity	13
NCBI Description	HYPOTHETICAL WD-REPEAT PROTEIN SLR0143 >gi_1653631_dbj_BAA18543_ (D90915) beta transducin-like protein [Synechocystis sp.]

Seq. No.	135106
Contig ID	117297_1.R1010
5'-most EST	g634772
Method	BLASTX
NCBI GI	g2570515
BLAST score	250
E value	3.0e-21
Match length	120
% identity	47
NCBI Description	(AF022740) glycolate oxidase [Oryza sativa]

Seq. No.	135107
Contig ID	117311_1.R1010
5'-most EST	jC-atXP17C110P5T7s3

Seq. No.	135108
Contig ID	117318_2.R1010
5'-most EST	jC-atXP17C113F6T7s3
Method	BLASTN
NCBI GI	g2656026
BLAST score	244
E value	1.0e-135
Match length	462
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDF20

Seq. No.	135109
Contig ID	117328_1.R1010
5'-most EST	g2048270
Method	BLASTN
NCBI GI	g2828186
BLAST score	288
E value	1.0e-161
Match length	440
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18I23, complete sequence [Arabidopsis thaliana]

Seq. No.	135110
Contig ID	117341_1.R1010
5'-most EST	jC-atXP18C108N14T7d2
Method	BLASTX
NCBI GI	g2130473
BLAST score	153
E value	5.0e-10
Match length	78
% identity	44
NCBI Description	RAD8 protein - fission yeast (Schizosaccharomyces pombe) (fragment) >gi_1008986_emb_CAA91094_ (Z54308) DNA helicase [Schizosaccharomyces pombe]

Seq. No.	135111
Contig ID	117342_1.R1010
5'-most EST	g2048201
Method	BLASTX
NCBI GI	g3420051
BLAST score	126
E value	2.0e-41
Match length	92
% identity	90
NCBI Description	(AC004680) unknown protein [Arabidopsis thaliana]

Seq. No.	135112
Contig ID	117342_2.R1010
5'-most EST	jC-atXP18C108N16T7d2
Method	BLASTX
NCBI GI	g3420051
BLAST score	367
E value	2.0e-38
Match length	113
% identity	76
NCBI Description	(AC004680) unknown protein [Arabidopsis thaliana]

Seq. No.	135113
Contig ID	117345_1.R1010
5'-most EST	jC-atXP18C108N4T7d2

Seq. No.	135114
Contig ID	117347_1.R1010
5'-most EST	jC-atXP18C108P20T7d2
Method	BLASTN
NCBI GI	g2696018
BLAST score	243
E value	1.0e-134
Match length	459
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC9, complete sequence [Arabidopsis thaliana]

Seq. No.	135115
Contig ID	117353_1.R1010
5'-most EST	jC-atXP18C111B23T7d2
Method	BLASTX
NCBI GI	g2660668
BLAST score	223

E value	2.0e-32
Match length	84
% identity	85
NCBI Description	(AC002342) unknown protein [Arabidopsis thaliana]

Seq. No.	135116
Contig ID	117359_1.R1010
5'-most EST	g2393297

Seq. No.	135117
Contig ID	117359_2.R1010
5'-most EST	g634809

Seq. No.	135118
Contig ID	117363_1.R1010
5'-most EST	jC-atXP18C111E17T7d2
Method	BLASTX
NCBI GI	g3915866
BLAST score	762
E value	5.0e-81
Match length	190
% identity	75
NCBI Description	GLUTAMINYL-TRNA SYNTHETASE (GLUTAMINE--TRNA LIGASE) (GLNRS) >gi_2995455_emb_CAA62901_ (X91787) tRNA-glutamine synthetase [Lupinus luteus]

Seq. No.	135119
Contig ID	117366_1.R1010
5'-most EST	jC-atXP18C111F3T7d2
Method	BLASTX
NCBI GI	g3228664
BLAST score	221
E value	2.0e-27
Match length	113
% identity	58
NCBI Description	(AF069986) nitrilase and fragile histidine triad fusion protein NitFhit [Caenorhabditis elegans]

Seq. No.	135120
Contig ID	117369_1.R1010
5'-most EST	g2757778
Method	BLASTN
NCBI GI	g2760165
BLAST score	39
E value	1.0e-12
Match length	123
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC9, complete sequence [Arabidopsis thaliana]

Seq. No.	135121
Contig ID	117371_1.R1010
5'-most EST	jC-atXP40C162L8T7046a1
Method	BLASTN
NCBI GI	g4371278
BLAST score	230
E value	1.0e-126

Match length 607
% identity 99
NCBI Description Arabidopsis thaliana chromosome II BAC T2N18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 135122
Contig ID 117371_2.R1010
5'-most EST g2749233
Method BLASTN
NCBI GI g4371278
BLAST score 189
E value 1.0e-102
Match length 352
% identity 99
NCBI Description Arabidopsis thaliana chromosome II BAC T2N18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 135123
Contig ID 117374_1.R1010
5'-most EST g635077

Seq. No. 135124
Contig ID 117383_1.R1010
5'-most EST jC-atXP18C113N14T7d2
Method BLASTX
NCBI GI g3746060
BLAST score 298
E value 5.0e-27
Match length 67
% identity 78
NCBI Description (AC005311) unknown protein [Arabidopsis thaliana]

Seq. No. 135125
Contig ID 117390_1.R1010
5'-most EST g2597071
Method BLASTX
NCBI GI g1806140
BLAST score 503
E value 1.0e-58
Match length 132
% identity 82
NCBI Description (X97314) cdc2MsC [Medicago sativa]

Seq. No. 135126
Contig ID 117393_1.R1010
5'-most EST jC-atXP18C113P14T7d2
Method BLASTN
NCBI GI g2583106
BLAST score 475
E value 0.0e+00
Match length 495
% identity 99
NCBI Description Arabidopsis thaliana chromosome II BAC F4L23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 135127
Contig ID 117403_1.R1010

5'-most EST	jC-atXP18C115B8T7d2
Seq. No.	135128
Contig ID	117409_1.R1010
5'-most EST	jC-atXP19C111O14T7d2
Method	BLASTX
NCBI GI	g3033374
BLAST score	1074
E value	1.0e-118
Match length	213
% identity	100
NCBI Description	(AC004238) unknown protein [Arabidopsis thaliana]
Seq. No.	135129
Contig ID	117424_1.R1010
5'-most EST	jC-atXP19C113C5T7096a1
Method	BLASTN
NCBI GI	g4455262
BLAST score	197
E value	1.0e-106
Match length	365
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22 (ESSAII project)
Seq. No.	135130
Contig ID	117424_2.R1010
5'-most EST	jC-atXP19C111H14T7d2
Method	BLASTN
NCBI GI	g4455262
BLAST score	172
E value	1.0e-91
Match length	513
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22 (ESSAII project)
Seq. No.	135131
Contig ID	117448_1.R1010
5'-most EST	jC-atXP19C111N8T7d2
Method	BLASTX
NCBI GI	g2245137
BLAST score	239
E value	2.0e-94
Match length	202
% identity	91
NCBI Description	(Z97344) MYB transcription factor homolog [Arabidopsis thaliana]
Seq. No.	135132
Contig ID	117457_1.R1010
5'-most EST	g931295
Method	BLASTX
NCBI GI	g132714
BLAST score	524
E value	3.0e-53
Match length	104

% identity	94
NCBI Description	CHLOROPLAST 50S RIBOSOMAL PROTEIN L16 (RIBOSOMAL PROTEIN CS-L24) >gi_71248_pir__R5SP16 ribosomal protein L16 - spinach chloroplast >gi_12311_emb_CAA31716_ (X13336) ribosomal protein L16 [Spinacia oleracea]

Seq. No.	135133
Contig ID	117462_1.R1010
5'-most EST	g576983
Method	BLASTX
NCBI GI	g2245048
BLAST score	245
E value	1.0e-20
Match length	67
% identity	78
NCBI Description	(Z97342) resistance gene homolog [Arabidopsis thaliana]

Seq. No.	135134
Contig ID	117470_1.R1010
5'-most EST	g2393490

Seq. No.	135135
Contig ID	117473_1.R1010
5'-most EST	g931315
Method	BLASTN
NCBI GI	g4733953
BLAST score	287
E value	1.0e-160
Match length	392
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC F13O11 genomic sequence, complete sequence

Seq. No.	135136
Contig ID	117474_1.R1010
5'-most EST	jC-atXP1C63C2T7s2
Method	BLASTN
NCBI GI	g4733953
BLAST score	259
E value	1.0e-144
Match length	419
% identity	93
NCBI Description	Arabidopsis thaliana chromosome I BAC F13O11 genomic sequence, complete sequence

Seq. No.	135137
Contig ID	117478_1.R1010
5'-most EST	g2393493
Method	BLASTN
NCBI GI	g4589412
BLAST score	143
E value	2.0e-74
Match length	285
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F6N7, complete sequence

Seq. No.	135138
Contig ID	117488_1.R1010
5'-most EST	g931326
Seq. No.	135139
Contig ID	117498_1.R1010
5'-most EST	g931334
Method	BLASTX
NCBI GI	g1931641
BLAST score	147
E value	3.0e-09
Match length	98
% identity	72
NCBI Description	(U95973) unknown protein [Arabidopsis thaliana]
Seq. No.	135140
Contig ID	117499_1.R1010
5'-most EST	g2393496
Seq. No.	135141
Contig ID	117502_1.R1010
5'-most EST	jC-atXP1C64C8T7d1
Method	BLASTN
NCBI GI	g3241916
BLAST score	347
E value	0.0e+00
Match length	502
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15N18, complete sequence [Arabidopsis thaliana]
Seq. No.	135142
Contig ID	117516_1.R1010
5'-most EST	jC-atXP1C65F10T7d1
Seq. No.	135143
Contig ID	117517_1.R1010
5'-most EST	jC-atXP1C64F1T7s2
Seq. No.	135144
Contig ID	117518_1.R1010
5'-most EST	jC-atXP1C64F9T7d1
Method	BLASTX
NCBI GI	g3056583
BLAST score	161
E value	3.0e-12
Match length	86
% identity	51
NCBI Description	(AC004255) T1F9.4 [Arabidopsis thaliana]
Seq. No.	135145
Contig ID	117533_1.R1010
5'-most EST	g2722976
Seq. No.	135146
Contig ID	117538_1.R1010
5'-most EST	jC-atXP1C66E6T7d1

Method	BLASTX
NCBI GI	g2833499
BLAST score	63
E value	2.0e-15
Match length	109
% identity	45
NCBI Description	HYPOTHETICAL PROTEIN MJ0326 >gi_2128002_pir__F64340 hypothetical protein homolog MJ0326 - Methanococcus jannaschii >gi_1591045 (U67487) conserved hypothetical protein [Methanococcus jannaschii]

Seq. No.	135147
Contig ID	117543_1.R1010
5'-most EST	jC-atXP1C66F2T7s2
Method	BLASTN
NCBI GI	g4531433
BLAST score	294
E value	1.0e-164
Match length	492
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II P1 MFL8 genomic sequence, complete sequence

Seq. No.	135148
Contig ID	117552_1.R1010
5'-most EST	jC-atXP1C67A8T7d1
Method	BLASTX
NCBI GI	g2842484
BLAST score	358
E value	2.0e-37
Match length	135
% identity	51
NCBI Description	(AL021749) tyrosine transaminase-like protein [Arabidopsis thaliana]

Seq. No.	135149
Contig ID	117559_1.R1010
5'-most EST	jC-atXP1C67F2T7d1
Method	BLASTN
NCBI GI	g3075383
BLAST score	392
E value	0.0e+00
Match length	456
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T1D16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135150
Contig ID	117572_1.R1010
5'-most EST	g906622
Method	BLASTX
NCBI GI	g585165
BLAST score	722
E value	1.0e-76
Match length	163
% identity	85
NCBI Description	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CYTOPLASMIC ISOFORM

	(G6PD) >gi_2129985_pir__S60287 glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) - potato >gi_471345_emb_CAA52442_ (X74421) glucose-6-phosphate 1-dehydrogenase [Solanum tuberosum]
Seq. No.	135151
Contig ID	117572_2.R1010
5'-most EST	jC-atXP1C70E9T7s2
Method	BLASTX
NCBI GI	g3023815
BLAST score	170
E value	3.0e-12
Match length	35
% identity	83
NCBI Description	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CYTOPLASMIC ISOFORM (G6PD) >gi_1362053_pir__S57785 glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) - alfalfa >gi_603219 (U18238) glucose-6-phosphate dehydrogenase [Medicago sativa subsp. sativa]
Seq. No.	135152
Contig ID	117580_1.R1010
5'-most EST	jC-atXP1C70G8T7d1
Seq. No.	135153
Contig ID	117581_1.R1010
5'-most EST	jC-atXP1C70G8T7s2
Seq. No.	135154
Contig ID	117594_1.R1010
5'-most EST	g949384
Method	BLASTX
NCBI GI	g3426037
BLAST score	360
E value	4.0e-34
Match length	143
% identity	43
NCBI Description	(AC005168) putative ABC transporter protein [Arabidopsis thaliana]
Seq. No.	135155
Contig ID	117595_1.R1010
5'-most EST	g2748322
Method	BLASTN
NCBI GI	g3426033
BLAST score	464
E value	0.0e+00
Match length	500
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F12C20 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	135156
Contig ID	117595_2.R1010
5'-most EST	g2749544
Method	BLASTX
NCBI GI	g3426037

BLAST score	592
E value	6.0e-71
Match length	134
% identity	62
NCBI Description	(AC005168) putative ABC transporter protein [Arabidopsis thaliana]

Seq. No.	135157
Contig ID	117600_1.R1010
5'-most EST	g2733553

Seq. No.	135158
Contig ID	117601_1.R1010
5'-most EST	g2393515

Seq. No.	135159
Contig ID	117610_1.R1010
5'-most EST	jC-atXP1C72D2T7d1
Method	BLASTX
NCBI GI	g3128201
BLAST score	471
E value	3.0e-47
Match length	115
% identity	76
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	135160
Contig ID	117621_1.R1010
5'-most EST	g2733572
Method	BLASTN
NCBI GI	g4159703
BLAST score	74
E value	3.0e-33
Match length	378
% identity	45
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K5F14, complete sequence

Seq. No.	135161
Contig ID	117628_1.R1010
5'-most EST	jC-atXP20C113D19T7d2
Method	BLASTX
NCBI GI	g3176675
BLAST score	566
E value	4.0e-58
Match length	175
% identity	65
NCBI Description	(AC003671) F17O7.4 [Arabidopsis thaliana]

Seq. No.	135162
Contig ID	117630_1.R1010
5'-most EST	jC-atXP34C150N13T7d1
Method	BLASTN
NCBI GI	g3449330
BLAST score	880
E value	0.0e+00
Match length	1307

% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDJ14, complete sequence [Arabidopsis thaliana]
Seq. No.	135163
Contig ID	117632_1.R1010
5'-most EST	jC-atXP20C113G16T7d2
Method	BLASTN
NCBI GI	g2749918
BLAST score	178
E value	2.0e-95
Match length	375
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC F3I6 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	135164
Contig ID	117635_1.R1010
5'-most EST	jC-atXP20C113C18T7009a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	43
E value	1.0e-14
Match length	51
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.	135165
Contig ID	117635_2.R1010
5'-most EST	g2048264
Seq. No.	135166
Contig ID	117642_1.R1010
5'-most EST	jC-atXP20C114A24T7004a1
Method	BLASTN
NCBI GI	g3063690
BLAST score	285
E value	1.0e-159
Match length	611
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11 (ESSAII project)
Seq. No.	135167
Contig ID	117646_1.R1010
5'-most EST	g2757829
Seq. No.	135168
Contig ID	117658_1.R1010
5'-most EST	g2597580
Seq. No.	135169
Contig ID	117665_1.R1010
5'-most EST	g2581686
Method	BLASTN
NCBI GI	g3985949
BLAST score	495

E value	0.0e+00
Match length	889
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOB24, complete sequence [Arabidopsis thaliana]

Seq. No.	135170
Contig ID	117674_1.R1010
5'-most EST	jC-atXP20C115H3T7d2
Method	BLASTX
NCBI GI	g4006872
BLAST score	149
E value	2.0e-09
Match length	84
% identity	50
NCBI Description	(Z99707) methionyl aminopeptidase-like protein [Arabidopsis thaliana]

Seq. No.	135171
Contig ID	117675_1.R1010
5'-most EST	g2597671
Method	BLASTX
NCBI GI	g4204315
BLAST score	237
E value	1.0e-52
Match length	174
% identity	62
NCBI Description	(AC003027) Unknown protein [Arabidopsis thaliana]

Seq. No.	135172
Contig ID	117676_1.R1010
5'-most EST	g2597672
Method	BLASTN
NCBI GI	g4757678
BLAST score	291
E value	1.0e-163
Match length	345
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC F9H16 genomic sequence, complete sequence

Seq. No.	135173
Contig ID	117679_1.R1010
5'-most EST	jC-atXP20C116A10T7d2
Method	BLASTN
NCBI GI	g4467131
BLAST score	338
E value	0.0e+00
Match length	387
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20M13 (ESSA project)

Seq. No.	135174
Contig ID	117683_1.R1010
5'-most EST	g2759073

Seq. No. 135175
Contig ID 117686_1.R1010
5'-most EST g2757923

Seq. No. 135176
Contig ID 117687_1.R1010
5'-most EST g2576763

Seq. No. 135177
Contig ID 117693_1.R1010
5'-most EST g2048306
Method BLASTX
NCBI GI g4507703
BLAST score 146
E value 5.0e-09
Match length 62
% identity 45
NCBI Description tumor suppressing subtransferable candidate 1 >gi_2655037_gb_AAC51911_ (AF019952) tumor suppressing STF cDNA 1 [Homo sapiens]

Seq. No. 135178
Contig ID 117694_1.R1010
5'-most EST jC-atXP21C114I24T7d2
Method BLASTN
NCBI GI g3249094
BLAST score 294
E value 1.0e-164
Match length 468
% identity 94
NCBI Description Arabidopsis thaliana chromosome 1 BAC T12M4 sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 135179
Contig ID 117695_1.R1010
5'-most EST g2048307
Method BLASTN
NCBI GI g3249094
BLAST score 351
E value 0.0e+00
Match length 402
% identity 98
NCBI Description Arabidopsis thaliana chromosome 1 BAC T12M4 sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 135180
Contig ID 117697_1.R1010
5'-most EST jC-atXP21C114I3T7d2
Method BLASTX
NCBI GI g2459410
BLAST score 358
E value 8.0e-34
Match length 115
% identity 50
NCBI Description (AC002332) putative thioredoxin [Arabidopsis thaliana]

Seq. No. 135181

Contig ID	117715_1.R1010
5'-most EST	jC-atXP21C114K11T7d2
Method	BLASTN
NCBI GI	g4220631
BLAST score	349
E value	0.0e+00
Match length	384
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K5J14, complete sequence [Arabidopsis thaliana]

Seq. No.	135182
Contig ID	117716_1.R1010
5'-most EST	g3449413
Method	BLASTN
NCBI GI	g4220631
BLAST score	237
E value	1.0e-130
Match length	385
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K5J14, complete sequence [Arabidopsis thaliana]

Seq. No.	135183
Contig ID	117724_1.R1010
5'-most EST	g3450311
Method	BLASTN
NCBI GI	g4415905
BLAST score	42
E value	2.0e-14
Match length	179
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC F13K3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135184
Contig ID	117726_1.R1010
5'-most EST	g3450323
Method	BLASTX
NCBI GI	g4467147
BLAST score	59
E value	1.0e-08
Match length	43
% identity	81
NCBI Description	(AL035540) putative protein [Arabidopsis thaliana]

Seq. No.	135185
Contig ID	117736_1.R1010
5'-most EST	g3450327
Method	BLASTN
NCBI GI	g4544381
BLAST score	298
E value	1.0e-167
Match length	323
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F16F14 genomic sequence, complete sequence

Seq. No.	135186
Contig ID	117739_1.R1010
5'-most EST	jC-atXP21C115L21T7d2
Method	BLASTX
NCBI GI	g3377800
BLAST score	47
E value	1.0e-34
Match length	109
% identity	73
NCBI Description	(AF075597) similar to glycosyl hydrolases family 9 (PFam:glycosyl_hydro5.hmm, score: 100.70) [Arabidopsis thaliana]

Seq. No.	135187
Contig ID	117744_1.R1010
5'-most EST	g2757955
Method	BLASTN
NCBI GI	g4415928
BLAST score	202
E value	1.0e-110
Match length	266
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F13A10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135188
Contig ID	117791_1.R1010
5'-most EST	g2597643
Method	BLASTX
NCBI GI	g4758340
BLAST score	330
E value	2.0e-36
Match length	143
% identity	57
NCBI Description	phenylalanine-tRNA synthetase-like >gi_2102679 (U07424) putative tRNA synthetase-like protein [Homo sapiens] >gi_4104935_gb_AAD02221_ (AF042347) putative phenylalanyl-tRNA synthetase alpha-subunit; PheHA [Homo sapiens]

Seq. No.	135189
Contig ID	117793_1.R1010
5'-most EST	jC-atXP21C116H15T7d2
Method	BLASTX
NCBI GI	g4741188
BLAST score	157
E value	2.0e-10
Match length	43
% identity	67
NCBI Description	(AL049746) hypothetical protein [Arabidopsis thaliana]

Seq. No.	135190
Contig ID	117795_1.R1010
5'-most EST	g933370

Seq. No.	135191

Contig ID	117796_1.R1010
5'-most EST	jC-atXP22C114M6T7018a1
Method	BLASTX
NCBI GI	g1653333
BLAST score	294
E value	4.0e-26
Match length	92
% identity	60
NCBI Description	(D90912) ferredoxin [Synechocystis sp.]

Seq. No.	135192
Contig ID	117796_2.R1010
5'-most EST	g933372

Seq. No.	135193
Contig ID	117801_1.R1010
5'-most EST	g2597492
Method	BLASTX
NCBI GI	g3540219
BLAST score	155
E value	4.0e-10
Match length	104
% identity	37
NCBI Description	(D87686) KIAA0017 protein [Homo sapiens]

Seq. No.	135194
Contig ID	117804_1.R1010
5'-most EST	g2597497
Method	BLASTX
NCBI GI	g3335349
BLAST score	466
E value	1.0e-46
Match length	166
% identity	71
NCBI Description	(AC004512) Similar to gb_U46691 putative chromatin structure regulator (SUPT6H) from Homo sapiens. ESTs gb_T42908, gb_AA586170 and gb_AA395125 come from this gene. [Arabidopsis thaliana]

Seq. No.	135195
Contig ID	117808_1.R1010
5'-most EST	g2597507
Method	BLASTN
NCBI GI	g2244950
BLAST score	151
E value	3.0e-79
Match length	483
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	135196
Contig ID	117811_1.R1010
5'-most EST	g2597723
Method	BLASTN
NCBI GI	g3510336
BLAST score	183

E value	2.0e-98
Match length	436
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18J17, complete sequence [Arabidopsis thaliana]

Seq. No.	135197
Contig ID	117814_1.R1010
5'-most EST	g2597648
Method	BLASTX
NCBI GI	g2244779
BLAST score	308
E value	3.0e-28
Match length	111
% identity	65
NCBI Description	(Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No.	135198
Contig ID	117821_1.R1010
5'-most EST	g2597738
Method	BLASTX
NCBI GI	g2443887
BLAST score	128
E value	2.0e-09
Match length	102
% identity	45
NCBI Description	(AC002294) Similar to transcription factor gb_Z46606_1658307 and others [Arabidopsis thaliana]

Seq. No.	135199
Contig ID	117828_1.R1010
5'-most EST	g2758054
Method	BLASTN
NCBI GI	g4756963
BLAST score	122
E value	4.0e-62
Match length	296
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23 (ESSA project)

Seq. No.	135200
Contig ID	117831_1.R1010
5'-most EST	g2759090

Seq. No.	135201
Contig ID	117832_1.R1010
5'-most EST	jC-atXP22C119C5T7046a1

Seq. No.	135202
Contig ID	117836_1.R1010
5'-most EST	jC-atXP22C119D12T7d2

Seq. No.	135203
Contig ID	117837_1.R1010
5'-most EST	g933507
Method	BLASTN

NCBI GI	g2244950
BLAST score	269
E value	1.0e-149
Match length	403
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	135204
Contig ID	117838_1.R1010
5'-most EST	g2597779
Method	BLASTN
NCBI GI	g4165340
BLAST score	292
E value	1.0e-163
Match length	353
% identity	96
NCBI Description	Arabidopsis thaliana chromosome I BAC F11M15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135205
Contig ID	117840_1.R1010
5'-most EST	g2597554

Seq. No.	135206
Contig ID	117853_1.R1010
5'-most EST	jC-atXP22C122E6T7016a1
Method	BLASTX
NCBI GI	g629669
BLAST score	142
E value	6.0e-17
Match length	102
% identity	45
NCBI Description	hypothetical protein - tomato

Seq. No.	135207
Contig ID	117856_1.R1010
5'-most EST	jC-atXP22C114P21T7083a1
Method	BLASTN
NCBI GI	g4388714
BLAST score	381
E value	0.0e+00
Match length	541
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC F5K7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135208
Contig ID	117863_1.R1010
5'-most EST	jC-atXP23C120K21T7d2
Method	BLASTN
NCBI GI	g4753195
BLAST score	380
E value	0.0e+00
Match length	452
% identity	96
NCBI Description	Arabidopsis thaliana BAC F15A18 from chromosome V near 68.5

cM, complete sequence

Seq. No.	135209
Contig ID	117865_1.R1010
5'-most EST	jC-atXP23C121N4T7s2
Method	BLASTX
NCBI GI	g2661422
BLAST score	432
E value	1.0e-42
Match length	93
% identity	91
NCBI Description	(AJ001342) Putative S-phase-specific ribosomal protein [Arabidopsis thaliana] >gi_3096936_emb_CAA18846.1_ (AL023094) Putative S-phase-specific ribosomal protein [Arabidopsis thaliana]

Seq. No.	135210
Contig ID	117869_1.R1010
5'-most EST	g2758765
Method	BLASTX
NCBI GI	g2961373
BLAST score	331
E value	8.0e-31
Match length	103
% identity	38
NCBI Description	(AL022141) putative disease resistance protein [Arabidopsis thaliana]

Seq. No.	135211
Contig ID	117877_1.R1010
5'-most EST	g2048555
Method	BLASTX
NCBI GI	g3269297
BLAST score	171
E value	3.0e-12
Match length	58
% identity	57
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.	135212
Contig ID	117878_1.R1010
5'-most EST	g2048508
Method	BLASTN
NCBI GI	g3869069
BLAST score	288
E value	1.0e-161
Match length	403
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence [Arabidopsis thaliana]

Seq. No.	135213
Contig ID	117884_1.R1010
5'-most EST	g2758771

Seq. No.	135214
Contig ID	117886_1.R1010

5'-most EST	g2758773
Method	BLASTX
NCBI GI	g3241944
BLAST score	307
E value	5.0e-28
Match length	111
% identity	59
NCBI Description	(AC004625) DNA-(apurinic or apyrimidinic site) lyase, ARP [Arabidopsis thaliana]

Seq. No.	135215
Contig ID	117890_1.R1010
5'-most EST	g2758778
Method	BLASTX
NCBI GI	g4678322
BLAST score	395
E value	2.0e-38
Match length	154
% identity	76
NCBI Description	(AL049658) putative protein [Arabidopsis thaliana]

Seq. No.	135216
Contig ID	117900_1.R1010
5'-most EST	g2758382
Method	BLASTN
NCBI GI	g1871173
BLAST score	149
E value	5.0e-78
Match length	456
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC T06D20 genomic sequence, complete sequence

Seq. No.	135217
Contig ID	117902_1.R1010
5'-most EST	g2758793
Method	BLASTX
NCBI GI	g3193298
BLAST score	792
E value	1.0e-84
Match length	150
% identity	100
NCBI Description	(AF069298) T14P8.17 gene product [Arabidopsis thaliana]

Seq. No.	135218
Contig ID	117905_1.R1010
5'-most EST	g2576784
Method	BLASTN
NCBI GI	g4235150
BLAST score	115
E value	8.0e-58
Match length	446
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC T25B24 genomic sequence, complete sequence

Seq. No.	135219

Contig ID	117908_1.R1010
5'-most EST	g2758799
Method	BLASTN
NCBI GI	g4455321
BLAST score	763
E value	0.0e+00
Match length	903
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4I10 (ESSAII project)

Seq. No.	135220
Contig ID	117911_1.R1010
5'-most EST	g2758472
Method	BLASTX
NCBI GI	g7758
BLAST score	131
E value	2.0e-07
Match length	103
% identity	6
NCBI Description	(X58374) crn [Drosophila melanogaster]

Seq. No.	135221
Contig ID	117913_1.R1010
5'-most EST	g558156
Method	BLASTX
NCBI GI	g3377509
BLAST score	685
E value	6.0e-72
Match length	161
% identity	83
NCBI Description	(AF056027) auxin transport protein REH1 [Oryza sativa]

Seq. No.	135222
Contig ID	117915_1.R1010
5'-most EST	g572535
Method	BLASTN
NCBI GI	g3785968
BLAST score	278
E value	1.0e-155
Match length	376
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F2I9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135223
Contig ID	117918_1.R1010
5'-most EST	g948034
Method	BLASTX
NCBI GI	g3021265
BLAST score	294
E value	6.0e-42
Match length	153
% identity	66
NCBI Description	(AL022347) protein kinase - like protein [Arabidopsis thaliana] >gi_3292839_emb_CAA19829_ (AL031018) protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	135224
Contig ID	117920_1.R1010
5'-most EST	g2758482
Method	BLASTX
NCBI GI	g4585873
BLAST score	377
E value	5.0e-50
Match length	129
% identity	87
NCBI Description	(AC005850) Putative protein kinase [Arabidopsis thaliana]

Seq. No.	135225
Contig ID	117923_1.R1010
5'-most EST	g3449476
Method	BLASTN
NCBI GI	g3449312
BLAST score	179
E value	5.0e-96
Match length	318
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K16L22, complete sequence [Arabidopsis thaliana]

Seq. No.	135226
Contig ID	117929_1.R1010
5'-most EST	g2048580
Method	BLASTN
NCBI GI	g2351068
BLAST score	429
E value	0.0e+00
Match length	512
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRH10, complete sequence [Arabidopsis thaliana]

Seq. No.	135227
Contig ID	117936_1.R1010
5'-most EST	g2758505
Method	BLASTN
NCBI GI	g4580522
BLAST score	422
E value	0.0e+00
Match length	504
% identity	96
NCBI Description	Arabidopsis thaliana scarecrow-like 8 (SCL8) mRNA, partial cds

Seq. No.	135228
Contig ID	117938_1.R1010
5'-most EST	g2048512
Method	BLASTX
NCBI GI	g3241944
BLAST score	142
E value	1.0e-49
Match length	118
% identity	82

NCBI Description	(AC004625) DNA-(apurinic or apyrimidinic site) lyase, ARP [Arabidopsis thaliana]
Seq. No.	135229
Contig ID	117944_1.R1010
5'-most EST	jC-atXP23C122F9T7s2
Method	BLASTN
NCBI GI	g2245126
BLAST score	313
E value	1.0e-176
Match length	394
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No
Seq. No.	135230
Contig ID	117945_1.R1010
5'-most EST	g2758520
Seq. No.	135231
Contig ID	117963_1.R1010
5'-most EST	jC-atXP23C122H7T7s2
Method	BLASTN
NCBI GI	g2351069
BLAST score	513
E value	0.0e+00
Match length	517
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSH12, complete sequence [Arabidopsis thaliana]
Seq. No.	135232
Contig ID	117967_1.R1010
5'-most EST	g2758977
Seq. No.	135233
Contig ID	117978_1.R1010
5'-most EST	g2758559
Method	BLASTX
NCBI GI	g3540181
BLAST score	189
E value	4.0e-14
Match length	158
% identity	32
NCBI Description	(AC004122) Unknown protein [Arabidopsis thaliana]
Seq. No.	135234
Contig ID	117982_1.R1010
5'-most EST	g2758982
Seq. No.	135235
Contig ID	117984_1.R1010
5'-most EST	g5769799
Method	BLASTN
NCBI GI	g2264310
BLAST score	522
E value	0.0e+00

Match length	522
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKP11, complete sequence [Arabidopsis thaliana]

Seq. No.	135236
Contig ID	117985_1.R1010
5'-most EST	g2048583

Seq. No.	135237
Contig ID	117991_1.R1010
5'-most EST	g2758566
Method	BLASTX
NCBI GI	g2244772
BLAST score	315
E value	1.0e-79
Match length	196
% identity	75
NCBI Description	(Z97335) transport protein [Arabidopsis thaliana]

Seq. No.	135238
Contig ID	117995_1.R1010
5'-most EST	jC-atXP24C122J8T7s1
Method	BLASTX
NCBI GI	g2739373
BLAST score	148
E value	2.0e-12
Match length	175
% identity	31
NCBI Description	(AC002505) putative flavonol 3-o-glucosyltransferase [Arabidopsis thaliana]

Seq. No.	135239
Contig ID	118002_1.R1010
5'-most EST	jC-atXP25C122N16T7d1
Method	BLASTX
NCBI GI	g4263522
BLAST score	375
E value	9.0e-36
Match length	145
% identity	48
NCBI Description	(AC004044) hypothetical protein [Arabidopsis thaliana]

Seq. No.	135240
Contig ID	118012_1.R1010
5'-most EST	jC-atXP25C123O17T7d1
Method	BLASTN
NCBI GI	g3738275
BLAST score	403
E value	0.0e+00
Match length	466
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F17A22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135241
Contig ID	118013_1.R1010

5'-most EST	g2759108
Method	BLASTN
NCBI GI	g2264311
BLAST score	469
E value	0.0e+00
Match length	512
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLN1, complete sequence [Arabidopsis thaliana]

Seq. No.	135242
Contig ID	118016_1.R1010
5'-most EST	g2759536
Method	BLASTX
NCBI GI	g2827715
BLAST score	459
E value	2.0e-45
Match length	213
% identity	48
NCBI Description	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	135243
Contig ID	118032_1.R1010
5'-most EST	g507088
Method	BLASTX
NCBI GI	g3912917
BLAST score	561
E value	1.0e-57
Match length	169
% identity	73
NCBI Description	(AF001308) putative NAK-like ser/thr protein kinase [Arabidopsis thaliana]

Seq. No.	135244
Contig ID	118038_1.R1010
5'-most EST	g2759224
Method	BLASTN
NCBI GI	g2832667
BLAST score	179
E value	6.0e-96
Match length	378
% identity	54
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T10I14 (ESSAII project)

Seq. No.	135245
Contig ID	118039_1.R1010
5'-most EST	jC-atXP25C125E3T7d1

Seq. No.	135246
Contig ID	118046_1.R1010
5'-most EST	jC-atXP69C217G1T7065d1
Method	BLASTX
NCBI GI	g4039155
BLAST score	293
E value	2.0e-29

Match length	164
% identity	47
NCBI Description	(AF104258) putative copper-inducible 35.6 kDa protein [Festuca rubra]

Seq. No.	135247
Contig ID	118048_1.R1010
5'-most EST	jC-atXP25C125I16T7d1
Method	BLASTX
NCBI GI	g2760839
BLAST score	390
E value	2.0e-37
Match length	108
% identity	69
NCBI Description	(AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq. No.	135248
Contig ID	118057_1.R1010
5'-most EST	jC-atXP32C147H21T7d2
Method	BLASTX
NCBI GI	g3695379
BLAST score	1265
E value	1.0e-140
Match length	307
% identity	66
NCBI Description	(AF096370) contains similarity to a C. elegans hypothetical protein F44G4.1 (GB:Z49910) and several yeast hypothetical proteins such as 35.1 KD protein in NAM8-GAR1 intergenic region (SP:P38805) [Arabidopsis thaliana]

Seq. No.	135249
Contig ID	118058_1.R1010
5'-most EST	jC-atXP25C125N11T7d1

Seq. No.	135250
Contig ID	118059_1.R1010
5'-most EST	jC-atXP25C125N5T7d1
Method	BLASTX
NCBI GI	g2492813
BLAST score	275
E value	4.0e-24
Match length	145
% identity	39
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE >gi_2313265_gb_AAD07246.1_ (AE000538) fructose-bisphosphate aldolase (tsr) [Helicobacter pylori 26695]

Seq. No.	135251
Contig ID	118061_1.R1010
5'-most EST	jC-atXP25C125O4T7d1
Method	BLASTX
NCBI GI	g3047116
BLAST score	1082
E value	1.0e-142
Match length	288
% identity	94
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No. 135252
Contig ID 118072_1.R1010
5'-most EST g2759695

Seq. No. 135253
Contig ID 118089_1.R1010
5'-most EST jC-atXP26C128L1T7d1
Method BLASTN
NCBI GI g3241925
BLAST score 364
E value 0.0e+00
Match length 412
% identity 97
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK9, complete sequence [Arabidopsis thaliana]

Seq. No. 135254
Contig ID 118105_1.R1010
5'-most EST jC-atXP27C128O19T7d2
Method BLASTX
NCBI GI g4371280
BLAST score 367
E value 8.0e-35
Match length 83
% identity 87
NCBI Description (AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No. 135255
Contig ID 118121_1.R1010
5'-most EST jC-atXP27C132A15T7s2

Seq. No. 135256
Contig ID 118123_1.R1010
5'-most EST jC-atXP27C129O23T7d2
Method BLASTX
NCBI GI g3461838
BLAST score 408
E value 9.0e-40
Match length 82
% identity 96
NCBI Description (AC005315) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No. 135257
Contig ID 118150_1.R1010
5'-most EST jC-atXP27C131E22T7d2
Method BLASTX
NCBI GI g2244888
BLAST score 388
E value 3.0e-37
Match length 166
% identity 48
NCBI Description (Z97338) similarity to cytochrome P450 [Arabidopsis thaliana]

Seq. No. 135258

Contig ID	118159_1.R1010
5'-most EST	g2762500
Method	BLASTN
NCBI GI	g3242700
BLAST score	543
E value	0.0e+00
Match length	685
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F26B6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135259
Contig ID	118163_1.R1010
5'-most EST	g2762215
Method	BLASTX
NCBI GI	g4322940
BLAST score	164
E value	4.0e-11
Match length	90
% identity	26
NCBI Description	(AF096299) DNA-binding protein 2 [Nicotiana tabacum]

Seq. No.	135260
Contig ID	118167_1.R1010
5'-most EST	g2762474
Method	BLASTN
NCBI GI	g4159705
BLAST score	113
E value	1.0e-56
Match length	328
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGD8, complete sequence

Seq. No.	135261
Contig ID	118175_1.R1010
5'-most EST	jC-atXP27C131M21T7s2

Seq. No.	135262
Contig ID	118196_1.R1010
5'-most EST	jC-atXP27C132E19T7s2

Seq. No.	135263
Contig ID	118201_1.R1010
5'-most EST	g933999
Method	BLASTX
NCBI GI	g4220477
BLAST score	113
E value	1.0e-16
Match length	72
% identity	47
NCBI Description	(AC006069) unknown protein [Arabidopsis thaliana]

Seq. No.	135264
Contig ID	118254_1.R1010
5'-most EST	jC-atXP28C134M20T7d1
Method	BLASTX

NCBI GI	g2809262
BLAST score	539
E value	3.0e-55
Match length	126
% identity	87
NCBI Description	(AC002560) F21B7.31 [Arabidopsis thaliana]

Seq. No.	135265
Contig ID	118257_1.R1010
5'-most EST	g2763239

Seq. No.	135266
Contig ID	118258_1.R1010
5'-most EST	jC-atXP28C135E23T7s1

Seq. No.	135267
Contig ID	118261_1.R1010
5'-most EST	jC-atXP44C170I9T7005a1
Method	BLASTN
NCBI GI	g4490324
BLAST score	368
E value	0.0e+00
Match length	653
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14 (ESSA project)

Seq. No.	135268
Contig ID	118273_1.R1010
5'-most EST	g2047768
Method	BLASTN
NCBI GI	g3080430
BLAST score	205
E value	1.0e-111
Match length	288
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T19P19 (ESSAII project)

Seq. No.	135269
Contig ID	118281_1.R1010
5'-most EST	g473349

Seq. No.	135270
Contig ID	118282_1.R1010
5'-most EST	g2762328
Method	BLASTN
NCBI GI	g4337186
BLAST score	128
E value	1.0e-65
Match length	344
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T28I24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135271
Contig ID	118284_1.R1010

5'-most EST	g2762684
Method	BLASTN
NCBI GI	g3367500
BLAST score	97
E value	4.0e-47
Match length	297
% identity	83
NCBI Description	REVERSE-COMPLEMENT OF: F23J3.GCG.SEQ CHECK: 2754 FROM: 1 TO: 93489, complete sequence [Arabidopsis thaliana]

Seq. No.	135272
Contig ID	118312_1.R1010
5'-most EST	g2062776
Method	BLASTN
NCBI GI	g4056429
BLAST score	529
E value	0.0e+00
Match length	577
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F5O8 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135273
Contig ID	118314_1.R1010
5'-most EST	g2062799
Method	BLASTX
NCBI GI	g2262165
BLAST score	84
E value	3.0e-31
Match length	81
% identity	93
NCBI Description	(AC002329) predicted protein of unknown function [Arabidopsis thaliana]

Seq. No.	135274
Contig ID	118315_1.R1010
5'-most EST	g2445895
Method	BLASTN
NCBI GI	g3128166
BLAST score	346
E value	0.0e+00
Match length	358
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F4I1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135275
Contig ID	118324_1.R1010
5'-most EST	jC-atXP2C74B2T7d1

Seq. No.	135276
Contig ID	118325_1.R1010
5'-most EST	g2756992
Method	BLASTX
NCBI GI	g3894385
BLAST score	145
E value	6.0e-09

09594046.100000

Match length	113
% identity	4
NCBI Description	(AF053994) Hcr2-0A [Lycopersicon esculentum]

Seq. No.	135277
Contig ID	118330_1.R1010
5'-most EST	jC-atXP2C75F5T7d1

Seq. No.	135278
Contig ID	118331_1.R1010
5'-most EST	jC-atXP2C75H9T7d1
Method	BLASTX
NCBI GI	g4581143
BLAST score	243
E value	2.0e-20
Match length	154
% identity	35
NCBI Description	(AC006919) hypothetical protein [Arabidopsis thaliana]

Seq. No.	135279
Contig ID	118334_1.R1010
5'-most EST	g933548

Seq. No.	135280
Contig ID	118343_1.R1010
5'-most EST	jC-atXP2C78C9T7d1
Method	BLASTN
NCBI GI	g4753195
BLAST score	49
E value	2.0e-18
Match length	96
% identity	95
NCBI Description	Arabidopsis thaliana BAC F15A18 from chromosome V near 68.5 cM, complete sequence

Seq. No.	135281
Contig ID	118347_1.R1010
5'-most EST	g2047524
Method	BLASTN
NCBI GI	g2351070
BLAST score	78
E value	1.0e-35
Match length	147
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTH12, complete sequence [Arabidopsis thaliana]

Seq. No.	135282
Contig ID	118353_1.R1010
5'-most EST	g501852
Method	BLASTX
NCBI GI	g4185141
BLAST score	552
E value	7.0e-57
Match length	127
% identity	87
NCBI Description	(AC005724) putative calmodulin-binding protein [Arabidopsis

thaliana]

Seq. No.	135283
Contig ID	118354_1.R1010
5'-most EST	jC-atXP2C79A3T7d1

Seq. No.	135284
Contig ID	118357_1.R1010
5'-most EST	jC-atXP30C140L5T7d2
Method	BLASTX
NCBI GI	g4666287
BLAST score	333
E value	4.0e-31
Match length	105
% identity	59
NCBI Description	(D85764) cytosolic monodehydroascorbate reductase [Oryza sativa]

Seq. No.	135285
Contig ID	118372_1.R1010
5'-most EST	jC-atXP30C141I15T7d2

Seq. No.	135286
Contig ID	118374_1.R1010
5'-most EST	jC-atXP30C141N11T7d2

Seq. No.	135287
Contig ID	118378_1.R1010
5'-most EST	g2062849

Seq. No.	135288
Contig ID	118378_2.R1010
5'-most EST	jC-atXP30C142C14T7d2
Method	BLASTX
NCBI GI	g2392763
BLAST score	214
E value	4.0e-17
Match length	108
% identity	45
NCBI Description	(AC002534) hypothetical protein [Arabidopsis thaliana]

Seq. No.	135289
Contig ID	118394_1.R1010
5'-most EST	g3449711
Method	BLASTX
NCBI GI	g4455295
BLAST score	256
E value	6.0e-22
Match length	118
% identity	47
NCBI Description	(AL035528) isoflavone reductase-like protein [Arabidopsis thaliana]

Seq. No.	135290
Contig ID	118394_2.R1010
5'-most EST	jC-atXP30C143N21T7d2
Method	BLASTX

NCBI GI	g4455295
BLAST score	337
E value	6.0e-88
Match length	197
% identity	80
NCBI Description	(AL035528) isoflavone reductase-like protein [Arabidopsis thaliana]

Seq. No.	135291
Contig ID	118396_1.R1010
5'-most EST	jC-atXP30C142H16T7d2
Method	BLASTN
NCBI GI	g4757401
BLAST score	610
E value	0.0e+00
Match length	657
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGH6, complete sequence

Seq. No.	135292
Contig ID	118408_1.R1010
5'-most EST	jC-atXP30C142K24T7d2

Seq. No.	135293
Contig ID	118414_1.R1010
5'-most EST	g3449702

Seq. No.	135294
Contig ID	118418_1.R1010
5'-most EST	g934789
Method	BLASTX
NCBI GI	g1531758
BLAST score	410
E value	4.0e-40
Match length	95
% identity	80
NCBI Description	(X98772) AUX1 [Arabidopsis thaliana] >gi_3335360 (AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	135295
Contig ID	118422_2.R1010
5'-most EST	g2393547

Seq. No.	135296
Contig ID	118423_1.R1010
5'-most EST	g2393319

Seq. No.	135297
Contig ID	118428_1.R1010
5'-most EST	g2763089
Method	BLASTX
NCBI GI	g2465923
BLAST score	228
E value	8.0e-19
Match length	73
% identity	64

NCBI Description	(AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]
Seq. No.	135298
Contig ID	118444_1.R1010
5'-most EST	jC-atXP30C143N4T7s2
Method	BLASTX
NCBI GI	g2098575
BLAST score	312
E value	1.0e-28
Match length	91
% identity	64
NCBI Description	(AC002115) F25451_2 [Homo sapiens]
Seq. No.	135299
Contig ID	118445_1.R1010
5'-most EST	jC-atXP30C143N6T7d2
Method	BLASTN
NCBI GI	g3176693
BLAST score	331
E value	0.0e+00
Match length	375
% identity	97
NCBI Description	Arabidopsis thaliana chromosome I BAC T27I1 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	135300
Contig ID	118465_1.R1010
5'-most EST	g2062885
Seq. No.	135301
Contig ID	118469_1.R1010
5'-most EST	jC-atXP44C170K1T7093a1
Method	BLASTX
NCBI GI	g3941458
BLAST score	779
E value	4.0e-83
Match length	157
% identity	96
NCBI Description	(AF062883) putative transcription factor [Arabidopsis thaliana]
Seq. No.	135302
Contig ID	118482_1.R1010
5'-most EST	jC-atXP31C145E2T7d1
Seq. No.	135303
Contig ID	118493_1.R1010
5'-most EST	jC-atXP31C146H5T7d2
Method	BLASTX
NCBI GI	g2388956
BLAST score	207
E value	4.0e-16
Match length	76
% identity	57
NCBI Description	(Z98979) ribulose-phosphate 3-epimerase [Schizosaccharomyces pombe]

Seq. No.	135304
Contig ID	118495_1.R1010
5'-most EST	g2062915
Method	BLASTN
NCBI GI	g4585896
BLAST score	449
E value	0.0e+00
Match length	712
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F13I13 genomic sequence, complete sequence

Seq. No.	135305
Contig ID	118503_1.R1010
5'-most EST	g2062921
Method	BLASTN
NCBI GI	g4713943
BLAST score	588
E value	0.0e+00
Match length	636
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8K14 sequence, complete sequence

Seq. No.	135306
Contig ID	118511_1.R1010
5'-most EST	g2062937
Method	BLASTN
NCBI GI	g2582640
BLAST score	36
E value	2.0e-10
Match length	40
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	135307
Contig ID	118513_1.R1010
5'-most EST	jC-atXP32C146P15T7s1
Method	BLASTN
NCBI GI	g1072328
BLAST score	49
E value	2.0e-18
Match length	183
% identity	81
NCBI Description	B.campestris (ACP-SF1) gene for acyl carrier protein

Seq. No.	135308
Contig ID	118516_1.R1010
5'-most EST	jC-atXP32C146P6T7s1
Method	BLASTX
NCBI GI	g3445207
BLAST score	116
E value	6.0e-53
Match length	110
% identity	81

NCBI Description	(AC004786) unknown protein [Arabidopsis thaliana]
Seq. No.	135309
Contig ID	118517_1.R1010
5'-most EST	jC-atXP32C147D16T7s1
Seq. No.	135310
Contig ID	118519_1.R1010
5'-most EST	g1109722
Method	BLASTN
NCBI GI	g1946354
BLAST score	339
E value	0.0e+00
Match length	354
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T06B20 genomic sequence, complete sequence
Seq. No.	135311
Contig ID	118522_1.R1010
5'-most EST	g2062934
Seq. No.	135312
Contig ID	118529_1.R1010
5'-most EST	g3449758
Seq. No.	135313
Contig ID	118532_1.R1010
5'-most EST	g2062935
Method	BLASTX
NCBI GI	g3337348
BLAST score	205
E value	6.0e-16
Match length	62
% identity	69
NCBI Description	(AC004481) unknown protein, 5' partial [Arabidopsis thaliana]
Seq. No.	135314
Contig ID	118533_1.R1010
5'-most EST	g453715
Method	BLASTX
NCBI GI	g3367522
BLAST score	414
E value	2.0e-40
Match length	109
% identity	66
NCBI Description	(AC004392) EST gb_T04691 comes from this gene. [Arabidopsis thaliana]
Seq. No.	135315
Contig ID	118548_1.R1010
5'-most EST	g935320
Method	BLASTX
NCBI GI	g2462756
BLAST score	145
E value	1.0e-30

Match length	119
% identity	62
NCBI Description	(AC002292) putative receptor kinase [Arabidopsis thaliana]

Seq. No.	135316
Contig ID	118550_1.R1010
5'-most EST	g2763551

Seq. No.	135317
Contig ID	118552_1.R1010
5'-most EST	jC-atXP33C144023T7s2

Seq. No.	135318
Contig ID	118553_1.R1010
5'-most EST	g2062953
Method	BLASTN
NCBI GI	g4587582
BLAST score	292
E value	1.0e-163
Match length	477
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T16B14 genomic sequence, complete sequence

Seq. No.	135319
Contig ID	118553_2.R1010
5'-most EST	g935270
Method	BLASTX
NCBI GI	g4587587
BLAST score	423
E value	2.0e-41
Match length	147
% identity	63
NCBI Description	(AC007232) unknown protein [Arabidopsis thaliana]

Seq. No.	135320
Contig ID	118568_1.R1010
5'-most EST	jC-atXP33C148C14T7d2
Method	BLASTN
NCBI GI	g3108025
BLAST score	237
E value	1.0e-130
Match length	485
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T13D8, complete sequence [Arabidopsis thaliana]

Seq. No.	135321
Contig ID	118573_1.R1010
5'-most EST	jC-atXP33C148C6T7d2
Method	BLASTN
NCBI GI	g3510336
BLAST score	384
E value	0.0e+00
Match length	470
% identity	33
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K18J17, complete sequence [Arabidopsis thaliana]

Seq. No.	135322
Contig ID	118588_1.R1010
5'-most EST	g2763549
Method	BLASTN
NCBI GI	g3243214
BLAST score	199
E value	1.0e-108
Match length	321
% identity	98
NCBI Description	Arabidopsis thaliana BAC T19B17 from chromsome IV, near 19.3 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	135323
Contig ID	118594_1.R1010
5'-most EST	g2062945
Method	BLASTX
NCBI GI	g2500980
BLAST score	223
E value	5.0e-18
Match length	79
% identity	52
NCBI Description	GLUTAMYL-TRNA SYNTHETASE (GLUTAMATE--TRNA LIGASE) (GLURS) >gi_1076718_pir__S51684 glutamate--tRNA ligase (EC 6.1.1.17) precursor - barley >gi_603849_emb_CAA58505_ (X83523) glutamate--tRNA ligase [Hordeum vulgare]

Seq. No.	135324
Contig ID	118594_2.R1010
5'-most EST	g2580690
Method	BLASTX
NCBI GI	g2500981
BLAST score	418
E value	4.0e-44
Match length	140
% identity	67
NCBI Description	GLUTAMYL-TRNA SYNTHETASE (GLUTAMATE--TRNA LIGASE) (GLURS) >gi_1084418_pir__S51685 glutamate--tRNA ligase (EC 6.1.1.17) - common tobacco >gi_603867_emb_CAA58506_ (X83524) glutamate--tRNA ligase [Nicotiana tabacum]

Seq. No.	135325
Contig ID	118610_1.R1010
5'-most EST	jC-atXP33C148H10T7s2
Method	BLASTN
NCBI GI	g4589410
BLAST score	717
E value	0.0e+00
Match length	745
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F2O15, complete sequence

Seq. No.	135326
Contig ID	118617_1.R1010
5'-most EST	g2763625

Method	BLASTN
NCBI GI	g4376087
BLAST score	144
E value	3.0e-75
Match length	344
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	135327
Contig ID	118621_1.R1010
5'-most EST	g935268
Method	BLASTN
NCBI GI	g2244788
BLAST score	114
E value	5.0e-57
Match length	655
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	135328
Contig ID	118623_1.R1010
5'-most EST	jC-atXP33C148I21T7d2
Method	BLASTX
NCBI GI	g4371280
BLAST score	321
E value	1.0e-29
Match length	131
% identity	50
NCBI Description	(AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No.	135329
Contig ID	118624_1.R1010
5'-most EST	jC-atXP33C148I21T7s2

Seq. No.	135330
Contig ID	118638_1.R1010
5'-most EST	jC-atXP33C148K6T7d2

Seq. No.	135331
Contig ID	118649_1.R1010
5'-most EST	g693032
Method	BLASTX
NCBI GI	g4538948
BLAST score	268
E value	3.0e-23
Match length	86
% identity	56
NCBI Description	(AL049483) putative protein [Arabidopsis thaliana]

Seq. No.	135332
Contig ID	118660_1.R1010
5'-most EST	jC-atXP33C149F9T7d2
Method	BLASTX
NCBI GI	g2062171
BLAST score	419

E value	4.0e-41
Match length	165
% identity	75
NCBI Description	(AC001645) DNA binding protein (CDC27SH) isolog [Arabidopsis thaliana]

Seq. No.	135333
Contig ID	118662_1.R1010
5'-most EST	jC-atXP33C150A10T7d2
Method	BLASTX
NCBI GI	g4335773
BLAST score	220
E value	1.0e-17
Match length	110
% identity	49
NCBI Description	(AC006284) unknown protein [Arabidopsis thaliana]

Seq. No.	135334
Contig ID	118664_1.R1010
5'-most EST	g2763742

Seq. No.	135335
Contig ID	118667_1.R1010
5'-most EST	g3449789
Method	BLASTX
NCBI GI	g4587525
BLAST score	228
E value	1.0e-18
Match length	94
% identity	51
NCBI Description	(AC007060) Contains the PF_00650 CRAL/TRIO phosphatidyl-inositol-transfer protein domain. ESTs gb_T76582, gb_N06574 and gb_Z25700 come from this gene. [Arabidopsis thaliana]

Seq. No.	135336
Contig ID	118679_1.R1010
5'-most EST	g3449797
Method	BLASTX
NCBI GI	g1483222
BLAST score	170
E value	6.0e-12
Match length	64
% identity	70
NCBI Description	(X99097) peroxidase [Arabidopsis thaliana]

Seq. No.	135337
Contig ID	118680_1.R1010
5'-most EST	jC-atXP33C151A16T7d2
Method	BLASTX
NCBI GI	g1706740
BLAST score	263
E value	8.0e-23
Match length	107
% identity	47
NCBI Description	FLAVONOL 4'-SULFOTRANSFERASE (F4-ST) >gi_168169 (M84136) flavonol 4'-sulfotransferase [Flaveria chloraefolia]

Seq. No.	135338
Contig ID	118682_1.R1010
5'-most EST	jC-atXP33C151A17T7d2
Method	BLASTN
NCBI GI	g4580454
BLAST score	217
E value	1.0e-118
Match length	516
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T2G17 genomic sequence, complete sequence

Seq. No.	135339
Contig ID	118689_1.R1010
5'-most EST	jC-atXP33C151B20T7d2
Method	BLASTX
NCBI GI	g481815
BLAST score	328
E value	4.0e-30
Match length	240
% identity	35
NCBI Description	vegetative storage protein - western balsam poplar x cottonwood >gi_309839 (L20233) vegetative storage protein [Populus trichocarpa x Populus deltoides]

Seq. No.	135340
Contig ID	118694_1.R1010
5'-most EST	jC-atXP33C151C9T7s2
Method	BLASTX
NCBI GI	g2129575
BLAST score	167
E value	8.0e-26
Match length	80
% identity	79
NCBI Description	DNA repair protein homolog XPBara - Arabidopsis thaliana

Seq. No.	135341
Contig ID	118718_1.R1010
5'-most EST	jC-atXP34C149K12T7d1
Method	BLASTX
NCBI GI	g4185136
BLAST score	616
E value	2.0e-66
Match length	161
% identity	85
NCBI Description	(AC005724) putative trehalose-6-phosphate synthase [Arabidopsis thaliana]

Seq. No.	135342
Contig ID	118723_1.R1010
5'-most EST	g935683

Seq. No.	135343
Contig ID	118724_1.R1010
5'-most EST	jC-atXP34C149P15T7d1
Method	BLASTX

NCBI GI	g4263791
BLAST score	712
E value	3.0e-75
Match length	156
% identity	88
NCBI Description	(AC006068) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	135344
Contig ID	118726_1.R1010
5'-most EST	jC-atXP34C150D14T7d1

Seq. No.	135345
Contig ID	118727_1.R1010
5'-most EST	jC-atXP34C150E12T7d1

Seq. No.	135346
Contig ID	118729_1.R1010
5'-most EST	jC-atXP34C150E20T7d1
Method	BLASTN
NCBI GI	g3702732
BLAST score	233
E value	1.0e-128
Match length	448
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGF10, complete sequence [Arabidopsis thaliana]

Seq. No.	135347
Contig ID	118732_1.R1010
5'-most EST	jC-atXP34C150G20T7d1
Method	BLASTN
NCBI GI	g4726109
BLAST score	161
E value	3.0e-85
Match length	385
% identity	83
NCBI Description	Arabidopsis thaliana chromosome II BAC F13J11 genomic sequence, complete sequence

Seq. No.	135348
Contig ID	118735_1.R1010
5'-most EST	jC-atXP34C150I21T7d1
Method	BLASTN
NCBI GI	g2245031
BLAST score	355
E value	0.0e+00
Match length	433
% identity	49
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	135349
Contig ID	118749_1.R1010
5'-most EST	g2580787
Method	BLASTN
NCBI GI	g3985931

BLAST score	368
E value	0.0e+00
Match length	402
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21H1, complete sequence [Arabidopsis thaliana]

Seq. No.	135350
Contig ID	118749_2.R1010
5'-most EST	g935709
Method	BLASTN
NCBI GI	g3985931
BLAST score	184
E value	5.0e-99
Match length	316
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21H1, complete sequence [Arabidopsis thaliana]

Seq. No.	135351
Contig ID	118750_1.R1010
5'-most EST	jC-atXP34C150N9T7d1
Method	BLASTX
NCBI GI	g4335751
BLAST score	573
E value	4.0e-59
Match length	158
% identity	76
NCBI Description	(AC006284) putative methyltransferase [Arabidopsis thaliana]

Seq. No.	135352
Contig ID	118755_2.R1010
5'-most EST	g935414

Seq. No.	135353
Contig ID	118759_1.R1010
5'-most EST	jC-atXP34C151H10T7d1
Method	BLASTN
NCBI GI	g3241923
BLAST score	277
E value	1.0e-154
Match length	301
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMN10, complete sequence [Arabidopsis thaliana]

Seq. No.	135354
Contig ID	118780_1.R1010
5'-most EST	g2047812
Method	BLASTN
NCBI GI	g1946354
BLAST score	287
E value	1.0e-160
Match length	369
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T06B20 genomic

sequence, complete sequence

Seq. No.	135355
Contig ID	118811_1.R1010
5'-most EST	g935790
Method	BLASTX
NCBI GI	g2281085
BLAST score	562
E value	8.0e-58
Match length	126
% identity	90
NCBI Description	(AC002333) CTR1 protein kinase isolog [Arabidopsis thaliana]

Seq. No.	135356
Contig ID	118812_1.R1010
5'-most EST	jC-atXP35C153F18T7s2
Method	BLASTN
NCBI GI	g2281081
BLAST score	266
E value	1.0e-148
Match length	313
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F18O19 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135357
Contig ID	118813_1.R1010
5'-most EST	g935791
Method	BLASTX
NCBI GI	g3858935
BLAST score	249
E value	5.0e-24
Match length	77
% identity	75
NCBI Description	(AL021636) synaptobrevin-like protein [Arabidopsis thaliana] >gi_4103357 (AF025332) vesicle-associated membrane protein 7C; synaptobrevin 7C [Arabidopsis thaliana]

Seq. No.	135358
Contig ID	118818_1.R1010
5'-most EST	g935794

Seq. No.	135359
Contig ID	118820_1.R1010
5'-most EST	jC-atXP37C158B21T7d2
Method	BLASTN
NCBI GI	g2264311
BLAST score	523
E value	0.0e+00
Match length	531
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLN1, complete sequence [Arabidopsis thaliana]

Seq. No. 135360

Contig ID	118820_3.R1010
5'-most EST	jC-atXP35C153G13T7d1
Method	BLASTN
NCBI GI	g2264311
BLAST score	209
E value	1.0e-114
Match length	490
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLN1, complete sequence [Arabidopsis thaliana]

Seq. No.	135361
Contig ID	118822_1.R1010
5'-most EST	jC-atXP35C153G15T7d1
Method	BLASTN
NCBI GI	g3004543
BLAST score	290
E value	1.0e-162
Match length	511
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F19F24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135362
Contig ID	118822_2.R1010
5'-most EST	jC-atXP64C207B6T7d1
Method	BLASTN
NCBI GI	g3004543
BLAST score	332
E value	0.0e+00
Match length	340
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F19F24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135363
Contig ID	118831_1.R1010
5'-most EST	jC-atXP35C153K12T7d1
Method	BLASTN
NCBI GI	g4589421
BLAST score	35
E value	6.0e-10
Match length	158
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K5K13, complete sequence

Seq. No.	135364
Contig ID	118833_1.R1010
5'-most EST	g935467

Seq. No.	135365
Contig ID	118834_1.R1010
5'-most EST	jC-atXP35C153I12T7s2

Seq. No.	135366
Contig ID	118848_1.R1010

5'-most EST	g2763762
Method	BLASTN
NCBI GI	g3335331
BLAST score	41
E value	2.0e-13
Match length	99
% identity	97
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8F5 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135367
Contig ID	118852_1.R1010
5'-most EST	g935474

Seq. No.	135368
Contig ID	118854_1.R1010
5'-most EST	jC-atXP35C153M19T7d1
Method	BLASTX
NCBI GI	g627071
BLAST score	144
E value	1.0e-08
Match length	136
% identity	11
NCBI Description	histidine-rich protein - Plasmodium lophurae (fragment) >gi_552196 (M15317) histidine-rich protein [Plasmodium lophurae]

Seq. No.	135369
Contig ID	118854_3.R1010
5'-most EST	g2048322
Method	BLASTN
NCBI GI	g3335331
BLAST score	257
E value	1.0e-142
Match length	284
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8F5 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135370
Contig ID	118880_1.R1010
5'-most EST	g2047844

Seq. No.	135371
Contig ID	118884_1.R1010
5'-most EST	jC-atXP35C154F12T7d1
Method	BLASTX
NCBI GI	g4263820
BLAST score	177
E value	1.0e-14
Match length	92
% identity	40
NCBI Description	(AC006067) hypothetical protein [Arabidopsis thaliana]

Seq. No.	135372
Contig ID	118917_1.R1010
5'-most EST	g2763852

Seq. No.	135373
Contig ID	118921_1.R1010
5'-most EST	jC-atXP36C154N7T7d1
Method	BLASTX
NCBI GI	g1935909
BLAST score	174
E value	2.0e-12
Match length	89
% identity	38
NCBI Description	(U77345) lethal leaf-spot 1 [Zea mays]

Seq. No.	135374
Contig ID	118926_1.R1010
5'-most EST	jC-atXP36C154P1T7d1
Method	BLASTX
NCBI GI	g4389444
BLAST score	159
E value	1.0e-10
Match length	61
% identity	52
NCBI Description	(AE001574) hypothetical 23.1kd-like protein [Drosophila melanogaster]

Seq. No.	135375
Contig ID	118927_1.R1010
5'-most EST	g509459

Seq. No.	135376
Contig ID	118929_1.R1010
5'-most EST	jC-atXP80C232F19T7d1
Method	BLASTX
NCBI GI	g4587987
BLAST score	661
E value	1.0e-72
Match length	188
% identity	66
NCBI Description	(AF085279) hypothetical Ser-Thr protein kinase [Arabidopsis thaliana]

Seq. No.	135377
Contig ID	118935_1.R1010
5'-most EST	jC-atXP36C155B7T7d1
Method	BLASTN
NCBI GI	g3980374
BLAST score	275
E value	1.0e-153
Match length	475
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F16P2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135378
Contig ID	118939_1.R1010
5'-most EST	jC-atXP36C155C20T7d1
Method	BLASTN
NCBI GI	g2828185

BLAST score	437
E value	0.0e+00
Match length	530
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUD21, complete sequence [Arabidopsis thaliana]

Seq. No.	135379
Contig ID	118948_1.R1010
5'-most EST	g2047869
Method	BLASTN
NCBI GI	g4519187
BLAST score	275
E value	1.0e-153
Match length	358
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K1G2, complete sequence

Seq. No.	135380
Contig ID	118952_1.R1010
5'-most EST	jC-atXP36C156A11T7d1
Method	BLASTX
NCBI GI	g4467147
BLAST score	67
E value	3.0e-19
Match length	84
% identity	67
NCBI Description	(AL035540) putative protein [Arabidopsis thaliana]

Seq. No.	135381
Contig ID	118952_2.R1010
5'-most EST	g2722580
Method	BLASTN
NCBI GI	g4467131
BLAST score	286
E value	1.0e-160
Match length	429
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20M13 (ESSA project)

Seq. No.	135382
Contig ID	118965_1.R1010
5'-most EST	jC-atXP86CG9G6T7d2
Method	BLASTN
NCBI GI	g3873174
BLAST score	442
E value	0.0e+00
Match length	672
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14N23, complete sequence [Arabidopsis thaliana]

Seq. No.	135383
Contig ID	118967_1.R1010
5'-most EST	g3719095

Method	BLASTN
NCBI GI	g2564051
BLAST score	273
E value	1.0e-152
Match length	619
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD9, complete sequence [Arabidopsis thaliana]

Seq. No.	135384
Contig ID	118970_1.R1010
5'-most EST	jC-atXP22C114P4T7043a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	57
E value	5.0e-23
Match length	57
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	135385
Contig ID	118978_1.R1010
5'-most EST	jC-atXP36C156F18T7d1
Method	BLASTN
NCBI GI	g3297806
BLAST score	279
E value	1.0e-155
Match length	906
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17I5 (ESSA project)

Seq. No.	135386
Contig ID	118980_1.R1010
5'-most EST	g2763803
Method	BLASTX
NCBI GI	g2760830
BLAST score	341
E value	5.0e-32
Match length	63
% identity	100
NCBI Description	(AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	135387
Contig ID	118997_1.R1010
5'-most EST	g936012

Seq. No.	135388
Contig ID	119001_1.R1010
5'-most EST	g936016
Method	BLASTN
NCBI GI	g2570223
BLAST score	228
E value	1.0e-125
Match length	341
% identity	99

NCBI Description	Arabidopsis thaliana chromosome 1 BAC F20D22 sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	135389
Contig ID	119007_1.R1010
5'-most EST	jC-atXP36C157D13T7d1
Method	BLASTX
NCBI GI	g1246823
BLAST score	292
E value	1.0e-44
Match length	176
% identity	60
NCBI Description	(X89865) unknown [Phoenix dactylifera]
Seq. No.	135390
Contig ID	119008_1.R1010
5'-most EST	g2047896
Method	BLASTX
NCBI GI	g1246823
BLAST score	217
E value	2.0e-17
Match length	43
% identity	93
NCBI Description	(X89865) unknown [Phoenix dactylifera]
Seq. No.	135391
Contig ID	119021_1.R1010
5'-most EST	jC-atXP37C157G14T7d2
Method	BLASTN
NCBI GI	g2462264
BLAST score	48
E value	1.0e-17
Match length	56
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.	135392
Contig ID	119027_1.R1010
5'-most EST	jC-atXP37C157H10T7d2
Method	BLASTX
NCBI GI	g2252833
BLAST score	330
E value	2.0e-30
Match length	144
% identity	57
NCBI Description	(AF013293) A_IG005I10.12 gene product [Arabidopsis thaliana]
Seq. No.	135393
Contig ID	119028_1.R1010
5'-most EST	jC-atXP37C157H12T7d2
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	2.0e-19
Match length	51
% identity	100

NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.	135394
Contig ID	119034_1.R1010
5'-most EST	jC-atXP37C157I7T7d2
Method	BLASTX
NCBI GI	g1504008
BLAST score	177
E value	2.0e-12
Match length	120
% identity	38
NCBI Description	(D86967) Containing ATP/GTP-binding site motif A(P-loop): Similar to C.elegans protein(P1:CEC47E128);Similar to Mouse alpha-mannosidase(P1:B54407) [Homo sapiens]
Seq. No.	135395
Contig ID	119040_1.R1010
5'-most EST	jC-atXP37C157K20T7d2
Method	BLASTX
NCBI GI	g4406763
BLAST score	700
E value	8.0e-74
Match length	147
% identity	93
NCBI Description	(AC006836) unknown protein [Arabidopsis thaliana]
Seq. No.	135396
Contig ID	119058_1.R1010
5'-most EST	jC-atXP37C157P23T7d2
Method	BLASTN
NCBI GI	g2462264
BLAST score	59
E value	4.0e-24
Match length	59
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.	135397
Contig ID	119059_1.R1010
5'-most EST	jC-atXP37C157P3T7d2
Method	BLASTN
NCBI GI	g2462264
BLAST score	44
E value	3.0e-15
Match length	44
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.	135398
Contig ID	119064_1.R1010
5'-most EST	jC-atXP37C158A15T7d2
Method	BLASTX
NCBI GI	g4200165
BLAST score	285
E value	6.0e-64
Match length	189
% identity	64

DOCKET ALARM

NCBI Description	(Y16262) neutral invertase [Daucus carota]
Seq. No.	135399
Contig ID	119068_1.R1010
5'-most EST	jC-atXP37C158C8T7s2
Method	BLASTX
NCBI GI	g2829900
BLAST score	769
E value	5.0e-82
Match length	148
% identity	99
NCBI Description	(AC002311) similar to ripening-induced protein, gp_AJ001449_2465015 and major latex protein, gp_X91961_1107495 [Arabidopsis thaliana]
Seq. No.	135400
Contig ID	119069_1.R1010
5'-most EST	jC-atXP37C159A22T7d2
Method	BLASTN
NCBI GI	g3785968
BLAST score	182
E value	1.0e-97
Match length	434
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F2I9 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	135401
Contig ID	119071_1.R1010
5'-most EST	jC-atXP37C159B14T7d2
Method	BLASTX
NCBI GI	g2498731
BLAST score	598
E value	8.0e-62
Match length	173
% identity	66
NCBI Description	PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1 >gi_1362013_pir__S57611 zeta-crystallin homolog - Arabidopsis thaliana >gi_886428_emb_CAA89838_ (Z49768) zeta-crystallin homologue [Arabidopsis thaliana]
Seq. No.	135402
Contig ID	119080_1.R1010
5'-most EST	jC-atXP37C159D4T7d2
Method	BLASTX
NCBI GI	g4006886
BLAST score	361
E value	5.0e-34
Match length	160
% identity	49
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]
Seq. No.	135403
Contig ID	119091_1.R1010
5'-most EST	g2047708
Method	BLASTX
NCBI GI	g3603473

BLAST score	488
E value	6.0e-49
Match length	143
% identity	63
NCBI Description	(AF090698) elicitor-responsive gene-3 [Oryza sativa]

Seq. No.	135404
Contig ID	119092_1.R1010
5'-most EST	g937527
Method	BLASTX
NCBI GI	g3643602
BLAST score	407
E value	1.0e-39
Match length	134
% identity	69
NCBI Description	(AC005395) putative tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No.	135405
Contig ID	119099_1.R1010
5'-most EST	g2047925
Method	BLASTX
NCBI GI	g3702620
BLAST score	118
E value	2.0e-13
Match length	75
% identity	63
NCBI Description	(Y17329) calnexin [Pisum sativum]

Seq. No.	135406
Contig ID	119099_2.R1010
5'-most EST	g936089
Method	BLASTX
NCBI GI	g473878
BLAST score	383
E value	6.0e-37
Match length	119
% identity	72
NCBI Description	(U08315) calnexin homolog [Arabidopsis thaliana]

Seq. No.	135407
Contig ID	119121_1.R1010
5'-most EST	g930568
Method	BLASTN
NCBI GI	g3059018
BLAST score	328
E value	0.0e+00
Match length	385
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F1C12 (ESSAII project)

Seq. No.	135408
Contig ID	119122_1.R1010
5'-most EST	g2047929
Method	BLASTN
NCBI GI	g3059018

BLAST score	199
E value	1.0e-108
Match length	109
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F1C12 (ESSAII project)

Seq. No.	135409
Contig ID	119123_1.R1010
5'-most EST	jC-atXP38C158J17T7d1

Seq. No.	135410
Contig ID	119125_1.R1010
5'-most EST	g2047930
Method	BLASTN
NCBI GI	g3108024
BLAST score	364
E value	0.0e+00
Match length	434
% identity	96
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T1F15 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135411
Contig ID	119125_2.R1010
5'-most EST	jC-atXP38C158J19T7d1
Method	BLASTX
NCBI GI	g3176663
BLAST score	629
E value	6.0e-66
Match length	123
% identity	97
NCBI Description	(AC004393) Contains similarity to S-receptor kinase 8 precursor gb_D38563 from Brassica rapa. ESTs gb_T88253 and gb_AA394649 come from this gene. [Arabidopsis thaliana]

Seq. No.	135412
Contig ID	119136_1.R1010
5'-most EST	g2047933
Method	BLASTN
NCBI GI	g3046854
BLAST score	399
E value	0.0e+00
Match length	439
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRG7, complete sequence [Arabidopsis thaliana]

Seq. No.	135413
Contig ID	119143_1.R1010
5'-most EST	jC-atXP38C158K4T7d1
Method	BLASTX
NCBI GI	g3335363
BLAST score	162
E value	4.0e-11
Match length	131
% identity	19

NCBI Description (AC003028) hypothetical protein [Arabidopsis thaliana]

Seq. No. 135414
Contig ID 119152_1.R1010
5'-most EST jC-atXP38C159G21T7d1

Seq. No. 135415
Contig ID 119155_1.R1010
5'-most EST jC-atXP81C240M14T7s1

Seq. No. 135416
Contig ID 119155_2.R1010
5'-most EST jC-atXP38C159G2T7s2

Seq. No. 135417
Contig ID 119162_1.R1010
5'-most EST jC-atXP38C160E8T7s2
Method BLASTX
NCBI GI g2245014
BLAST score 442
E value 8.0e-44
Match length 84
% identity 100
NCBI Description (Z97341) glucosyltransferase homolog [Arabidopsis thaliana]

Seq. No. 135418
Contig ID 119166_1.R1010
5'-most EST g936117
Method BLASTN
NCBI GI g4585952
BLAST score 408
E value 0.0e+00
Match length 440
% identity 98
NCBI Description Genomic sequence for Arabidopsis thaliana BAC F26F24, complete sequence

Seq. No. 135419
Contig ID 119171_1.R1010
5'-most EST g2763832
Method BLASTX
NCBI GI g4584546
BLAST score 526
E value 1.0e-53
Match length 141
% identity 67
NCBI Description (AL049608) putative protein [Arabidopsis thaliana]

Seq. No. 135420
Contig ID 119184_1.R1010
5'-most EST g2749168
Method BLASTN
NCBI GI g4589445
BLAST score 311
E value 1.0e-175
Match length 439
% identity 95

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWL2, complete sequence
Seq. No.	135421
Contig ID	119185_1.R1010
5'-most EST	g936451
Seq. No.	135422
Contig ID	119190_1.R1010
5'-most EST	jC-atXP55C186O1T7s2
Method	BLASTN
NCBI GI	g3985954
BLAST score	405
E value	0.0e+00
Match length	445
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRG21, complete sequence [Arabidopsis thaliana]
Seq. No.	135423
Contig ID	119193_1.R1010
5'-most EST	jC-atXP38C160J23T7d1
Method	BLASTN
NCBI GI	g4490324
BLAST score	338
E value	0.0e+00
Match length	365
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14 (ESSA project)
Seq. No.	135424
Contig ID	119195_1.R1010
5'-most EST	jC-atXP38C160J3T7d1
Method	BLASTN
NCBI GI	g4589437
BLAST score	314
E value	1.0e-176
Match length	362
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPN9, complete sequence
Seq. No.	135425
Contig ID	119196_1.R1010
5'-most EST	g2749171
Method	BLASTN
NCBI GI	g4589437
BLAST score	344
E value	0.0e+00
Match length	421
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPN9, complete sequence
Seq. No.	135426
Contig ID	119203_1.R1010

5'-most EST	g2764258
Seq. No.	135427
Contig ID	119205_1.R1010
5'-most EST	g2749157
Method	BLASTN
NCBI GI	g3702735
BLAST score	313
E value	1.0e-176
Match length	354
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQL5, complete sequence [Arabidopsis thaliana]
Seq. No.	135428
Contig ID	119206_1.R1010
5'-most EST	jC-atXP39C161H6T7d1
Method	BLASTN
NCBI GI	g2924734
BLAST score	442
E value	0.0e+00
Match length	495
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXE10, complete sequence [Arabidopsis thaliana]
Seq. No.	135429
Contig ID	119216_1.R1010
5'-most EST	jC-atXP39C160L5T7s1
Method	BLASTX
NCBI GI	g4835244
BLAST score	396
E value	4.0e-38
Match length	180
% identity	48
NCBI Description	(AL049862) putative mitochondrial protein [Arabidopsis thaliana]
Seq. No.	135430
Contig ID	119225_1.R1010
5'-most EST	g936475
Method	BLASTX
NCBI GI	g4218120
BLAST score	286
E value	1.0e-25
Match length	112
% identity	54
NCBI Description	(AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]
Seq. No.	135431
Contig ID	119229_1.R1010
5'-most EST	g936477
Method	BLASTN
NCBI GI	g4220643
BLAST score	259
E value	1.0e-143

Match length	370
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD22, complete sequence [Arabidopsis thaliana]

Seq. No.	135432
Contig ID	119248_1.R1010
5'-most EST	g2749187
Method	BLASTN
NCBI GI	g4415905
BLAST score	276
E value	1.0e-154
Match length	395
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F13K3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135433
Contig ID	119248_2.R1010
5'-most EST	g936187
Method	BLASTN
NCBI GI	g4415905
BLAST score	256
E value	1.0e-142
Match length	395
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F13K3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135434
Contig ID	119259_1.R1010
5'-most EST	jC-atXP39C161D14T7d1
Method	BLASTN
NCBI GI	g4589439
BLAST score	319
E value	1.0e-179
Match length	879
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQM1, complete sequence

Seq. No.	135435
Contig ID	119263_1.R1010
5'-most EST	jC-atXP39C161D17T7d1
Method	BLASTX
NCBI GI	g3860262
BLAST score	347
E value	3.0e-53
Match length	158
% identity	70
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]

Seq. No.	135436
Contig ID	119265_1.R1010
5'-most EST	jC-atXP39C161D1T7s1

Seq. No. 135437

Contig ID	119284_1.R1010
5'-most EST	jC-atXP39C162G7T7d1
Method	BLASTX
NCBI GI	g2708331
BLAST score	703
E value	2.0e-74
Match length	164
% identity	82
NCBI Description	(AF038557) ligand gated channel-like protein [Arabidopsis thaliana]

Seq. No.	135438
Contig ID	119285_1.R1010
5'-most EST	jC-atXP39C161F12T7s1
Method	BLASTN
NCBI GI	g3080406
BLAST score	294
E value	1.0e-164
Match length	352
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F23E12 (ESSA project)

Seq. No.	135439
Contig ID	119288_1.R1010
5'-most EST	g936526
Method	BLASTN
NCBI GI	g4589439
BLAST score	419
E value	0.0e+00
Match length	455
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQM1, complete sequence

Seq. No.	135440
Contig ID	119292_1.R1010
5'-most EST	g936528

Seq. No.	135441
Contig ID	119298_1.R1010
5'-most EST	jC-atXP39C161G17T7s1
Method	BLASTN
NCBI GI	g2924730
BLAST score	137
E value	7.0e-71
Match length	361
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPI7, complete sequence [Arabidopsis thaliana]

Seq. No.	135442
Contig ID	119308_1.R1010
5'-most EST	g936546
Method	BLASTN
NCBI GI	g3983533
BLAST score	243

E value	1.0e-134
Match length	452
% identity	97
NCBI Description	Arabidopsis thaliana BAC T24G3 from chromosome V near 70 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	135443
Contig ID	119309_1.R1010
5'-most EST	g2749202
Method	BLASTX
NCBI GI	g4586245
BLAST score	248
E value	5.0e-21
Match length	109
% identity	43
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	135444
Contig ID	119334_1.R1010
5'-most EST	jC-atXP39C162H19T7s1

Seq. No.	135445
Contig ID	119353_1.R1010
5'-most EST	jC-atXP3C81E4T7d1
Method	BLASTX
NCBI GI	g2244964
BLAST score	456
E value	4.0e-55
Match length	150
% identity	77
NCBI Description	(Z97340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	135446
Contig ID	119354_1.R1010
5'-most EST	jC-atXP3C81E6T7d1
Method	BLASTX
NCBI GI	g2244866
BLAST score	226
E value	2.0e-18
Match length	146
% identity	38
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	135447
Contig ID	119357_1.R1010
5'-most EST	g501917
Method	BLASTX
NCBI GI	g2827715
BLAST score	313
E value	7.0e-29
Match length	103
% identity	60
NCBI Description	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	135448
Contig ID	119359_1.R1010

5'-most EST	g933622
Method	BLASTN
NCBI GI	g862320
BLAST score	125
E value	2.0e-63
Match length	145
% identity	97
NCBI Description	Arabidopsis thaliana tRNA-Met gene (clone pAtM-8)

Seq. No.	135449
Contig ID	119361_1.R1010
5'-most EST	g933625
Method	BLASTX
NCBI GI	g3980402
BLAST score	584
E value	3.0e-60
Match length	184
% identity	72
NCBI Description	(AC004561) putative tropinone reductase [Arabidopsis thaliana]

Seq. No.	135450
Contig ID	119362_1.R1010
5'-most EST	g933627
Method	BLASTX
NCBI GI	g4263791
BLAST score	486
E value	8.0e-49
Match length	176
% identity	44
NCBI Description	(AC006068) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	135451
Contig ID	119373_1.R1010
5'-most EST	g933664
Method	BLASTX
NCBI GI	g1173624
BLAST score	367
E value	6.0e-35
Match length	133
% identity	59
NCBI Description	(U34744) cytochrome P-450 [Phalaenopsis sp. 'hybrid SM9108']

Seq. No.	135452
Contig ID	119378_1.R1010
5'-most EST	g933681
Method	BLASTX
NCBI GI	g4522012
BLAST score	635
E value	4.0e-69
Match length	135
% identity	93
NCBI Description	(AC007069) hypothetical protein [Arabidopsis thaliana]

Seq. No.	135453

Contig ID	119379_1.R1010
5'-most EST	jC-atXP3C83G7T7d1
Method	BLASTX
NCBI GI	g2281085
BLAST score	468
E value	7.0e-47
Match length	149
% identity	55
NCBI Description	(AC002333) CTR1 protein kinase isolog [Arabidopsis thaliana]

Seq. No.	135454
Contig ID	119384_1.R1010
5'-most EST	g933692

Seq. No.	135455
Contig ID	119385_1.R1010
5'-most EST	g933695
Method	BLASTX
NCBI GI	g1524370
BLAST score	262
E value	1.0e-22
Match length	93
% identity	57
NCBI Description	(X92491) TOM20 [Solanum tuberosum]

Seq. No.	135456
Contig ID	119392_1.R1010
5'-most EST	jC-atXP108C170H10T7005d1
Method	BLASTN
NCBI GI	g4519186
BLAST score	129
E value	7.0e-66
Match length	749
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18B18, complete sequence

Seq. No.	135457
Contig ID	119392_3.R1010
5'-most EST	g958091
Method	BLASTN
NCBI GI	g4519186
BLAST score	77
E value	4.0e-35
Match length	170
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18B18, complete sequence

Seq. No.	135458
Contig ID	119393_1.R1010
5'-most EST	jC-atXP3C85A9T7d1
Method	BLASTX
NCBI GI	g2739389
BLAST score	806
E value	4.0e-86

Match length	265
% identity	32
NCBI Description	(AC002505) Cf-2.2 like protein [Arabidopsis thaliana]

Seq. No.	135459
Contig ID	119393_2.R1010
5'-most EST	g2393575
Method	BLASTX
NCBI GI	g2739389
BLAST score	266
E value	4.0e-23
Match length	121
% identity	49
NCBI Description	(AC002505) Cf-2.2 like protein [Arabidopsis thaliana]

Seq. No.	135460
Contig ID	119404_1.R1010
5'-most EST	g937048
Method	BLASTX
NCBI GI	g99772
BLAST score	417
E value	6.0e-41
Match length	107
% identity	79
NCBI Description	ubiquitin 81-aa extension protein 2 - Arabidopsis thaliana >gi_166936 (J05540) ubiquitin extension protein (UBQ6) [Arabidopsis thaliana] >gi_3522953 (AC004411) ubiquitin extension protein (UBQ6) [Arabidopsis thaliana]

Seq. No.	135461
Contig ID	119416_1.R1010
5'-most EST	g937078
Method	BLASTN
NCBI GI	g3297806
BLAST score	119
E value	3.0e-60
Match length	355
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17I5 (ESSA project)

Seq. No.	135462
Contig ID	119417_1.R1010
5'-most EST	jC-atXP40C161N2T7035a1
Method	BLASTX
NCBI GI	g3176726
BLAST score	506
E value	5.0e-51
Match length	108
% identity	94
NCBI Description	(AC002392) putative serine proteinase [Arabidopsis thaliana]

Seq. No.	135463
Contig ID	119417_2.R1010
5'-most EST	jC-atXP75C225N23T7d1
Method	BLASTX

NCBI GI	g3176726
BLAST score	772
E value	2.0e-82
Match length	149
% identity	100
NCBI Description	(AC002392) putative serine proteinase [Arabidopsis thaliana]

Seq. No.	135464
Contig ID	119423_1.R1010
5'-most EST	g2723035
Method	BLASTX
NCBI GI	g2146835
BLAST score	163
E value	6.0e-11
Match length	80
% identity	45
NCBI Description	hypothetical protein YCL039w - yeast (Saccharomyces cerevisiae) >gi_1907121_emb_CAA42377_ (X59720) YCL039w, len:745 [Saccharomyces cerevisiae]

Seq. No.	135465
Contig ID	119434_1.R1010
5'-most EST	g1520564
Method	BLASTN
NCBI GI	g3228389
BLAST score	265
E value	1.0e-147
Match length	486
% identity	95
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17L21, complete sequence [Arabidopsis thaliana]

Seq. No.	135466
Contig ID	119436_1.R1010
5'-most EST	g936620

Seq. No.	135467
Contig ID	119438_1.R1010
5'-most EST	jC-atXP40C162L8T7d1
Method	BLASTN
NCBI GI	g4371278
BLAST score	397
E value	0.0e+00
Match length	421
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T2N18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135468
Contig ID	119441_1.R1010
5'-most EST	jC-atXP40C162M4T7d1
Method	BLASTX
NCBI GI	g4539380
BLAST score	720
E value	8.0e-76
Match length	161

% identity	82
NCBI Description	(AL035526) putative protein [Arabidopsis thaliana]
Seq. No.	135469
Contig ID	119443_1.R1010
5'-most EST	g936637
Method	BLASTX
NCBI GI	g3522938
BLAST score	326
E value	3.0e-30
Match length	103
% identity	68
NCBI Description	(AC004411) unknown protein [Arabidopsis thaliana]
Seq. No.	135470
Contig ID	119462_1.R1010
5'-most EST	jC-atXP40C164E1T7d1
Seq. No.	135471
Contig ID	119463_1.R1010
5'-most EST	jC-atXP40C164E5T7d1
Method	BLASTN
NCBI GI	g3869065
BLAST score	283
E value	1.0e-158
Match length	473
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24M7, complete sequence [Arabidopsis thaliana]
Seq. No.	135472
Contig ID	119464_1.R1010
5'-most EST	g936638
Method	BLASTX
NCBI GI	g4587540
BLAST score	108
E value	4.0e-39
Match length	154
% identity	66
NCBI Description	(AC006577) Belongs to the PF_00657 Lipase/Acylhydrolase with GDSL-motif family. [Arabidopsis thaliana]
Seq. No.	135473
Contig ID	119468_1.R1010
5'-most EST	jC-atXP41C162O15T7d1
Seq. No.	135474
Contig ID	119469_1.R1010
5'-most EST	jC-atXP41C162O15T7s1
Seq. No.	135475
Contig ID	119471_1.R1010
5'-most EST	jC-atXP41C162O8T7d1
Method	BLASTX
NCBI GI	g4154352
BLAST score	75
E value	3.0e-20

Match length	114
% identity	51
NCBI Description	(AF110333) PrMC3 [Pinus radiata]

Seq. No.	135476
Contig ID	119479_1.R1010
5'-most EST	g936653
Method	BLASTX
NCBI GI	g4502897
BLAST score	282
E value	5.0e-25
Match length	96
% identity	54
NCBI Description	cleft lip and palate associated transmembrane protein 1 >gi_4039014 (AF037338) cleft lip and palate transmembrane protein 1 [Homo sapiens] >gi_4063033 (AF037339) cleft lip and palate transmembrane protein 1 [Homo sapiens]

Seq. No.	135477
Contig ID	119496_1.R1010
5'-most EST	jC-atXP41C163F3T7s1
Method	BLASTX
NCBI GI	g2498892
BLAST score	183
E value	1.0e-13
Match length	66
% identity	33
NCBI Description	SEC13-RELATED PROTEIN

Seq. No.	135478
Contig ID	119497_1.R1010
5'-most EST	g936696

Seq. No.	135479
Contig ID	119498_1.R1010
5'-most EST	g2047945

Seq. No.	135480
Contig ID	119501_1.R1010
5'-most EST	jC-atXP41C163G4T7d1
Method	BLASTX
NCBI GI	g4063743
BLAST score	276
E value	3.0e-24
Match length	93
% identity	63
NCBI Description	(AC005851) hypothetical protein [Arabidopsis thaliana]

Seq. No.	135481
Contig ID	119533_1.R1010
5'-most EST	jC-atXP41C164I22T7s1
Method	BLASTN
NCBI GI	g2618677
BLAST score	149
E value	4.0e-78
Match length	272
% identity	93

NCBI Description	Arabidopsis thaliana BAC F21B7 chromosome 1, complete sequence [Arabidopsis thaliana]
Seq. No.	135482
Contig ID	119539_1.R1010
5'-most EST	jC-atXP41C164J14T7s1
Method	BLASTX
NCBI GI	g2462754
BLAST score	49
E value	3.0e-24
Match length	117
% identity	66
NCBI Description	(AC002292) Unknown protein [Arabidopsis thaliana]
Seq. No.	135483
Contig ID	119549_1.R1010
5'-most EST	jC-atXP41C164L10T7s1
Method	BLASTN
NCBI GI	g2494106
BLAST score	203
E value	1.0e-110
Match length	314
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	135484
Contig ID	119561_1.R1010
5'-most EST	g936762
Method	BLASTX
NCBI GI	g1706189
BLAST score	155
E value	6.0e-10
Match length	51
% identity	51
NCBI Description	LOW-AFFINITY CATIONIC AMINO ACID TRANSPORTER-2 (CAT-2) (CAT2) (TEA PROTEIN) (T-CELL EARLY ACTIVATION PROTEIN) (20.5) >gi_627850_pir__A54011 CAT1/ecoR protein - mouse >gi_293315 (L11600) cationic amino acid transporter-2 [Mus musculus] >gi_517493 (L29006) membrane protein [Mus musculus]
Seq. No.	135485
Contig ID	119568_1.R1010
5'-most EST	g2047971
Method	BLASTX
NCBI GI	g4539004
BLAST score	142
E value	1.0e-08
Match length	48
% identity	50
NCBI Description	(AL049481) putative protein kinase [Arabidopsis thaliana]
Seq. No.	135486
Contig ID	119572_1.R1010
5'-most EST	g936772
Method	BLASTX

NCBI GI	g2047324
BLAST score	745
E value	4.0e-79
Match length	152
% identity	89
NCBI Description	(U80192) HAL3 homolog [Arabidopsis thaliana]

Seq. No.	135487
Contig ID	119594_1.R1010
5'-most EST	g695433
Method	BLASTN
NCBI GI	g3047074
BLAST score	517
E value	0.0e+00
Match length	643
% identity	100
NCBI Description	Arabidopsis thaliana BAC F21E10

Seq. No.	135488
Contig ID	119601_1.R1010
5'-most EST	g936797

Seq. No.	135489
Contig ID	119605_1.R1010
5'-most EST	jC-atXP41C166A2T7d1
Method	BLASTN
NCBI GI	g2477521
BLAST score	27
E value	3.0e-05
Match length	403
% identity	75
NCBI Description	Arabidopsis thaliana chromosome I BAC F22K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135490
Contig ID	119638_1.R1010
5'-most EST	g2749315
Method	BLASTX
NCBI GI	g4138265
BLAST score	248
E value	6.0e-52
Match length	221
% identity	49
NCBI Description	(AJ006228) Avr9 elicitor response protein [Nicotiana tabacum]

Seq. No.	135491
Contig ID	119645_1.R1010
5'-most EST	g2749298
Method	BLASTX
NCBI GI	g2464905
BLAST score	61
E value	8.0e-21
Match length	82
% identity	80
NCBI Description	(Z99708) minor allergen [Arabidopsis thaliana]

Seq. No.	135492
Contig ID	119652_1.R1010
5'-most EST	jC-atXP43C169D23T7s1
Method	BLASTN
NCBI GI	g4454004
BLAST score	647
E value	0.0e+00
Match length	709
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F24A6 (ESSAII project)

Seq. No.	135493
Contig ID	119655_1.R1010
5'-most EST	jC-atXP43C170D15T7s1
Method	BLASTN
NCBI GI	g2088638
BLAST score	113
E value	1.0e-56
Match length	342
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC T28M21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135494
Contig ID	119667_1.R1010
5'-most EST	g2749281

Seq. No.	135495
Contig ID	119677_1.R1010
5'-most EST	g2580700
Method	BLASTN
NCBI GI	g2815519
BLAST score	240
E value	1.0e-132
Match length	272
% identity	97
NCBI Description	Arabidopsis thaliana BAC T5J8 from chromosome IV, top arm, complete sequence [Arabidopsis thaliana]

Seq. No.	135496
Contig ID	119684_1.R1010
5'-most EST	jC-atXP43C171A2T7s1

Seq. No.	135497
Contig ID	119686_1.R1010
5'-most EST	g937423
Method	BLASTX
NCBI GI	g2828293
BLAST score	205
E value	4.0e-16
Match length	131
% identity	44
NCBI Description	(AL021687) putative protein [Arabidopsis thaliana]

Seq. No.	135498
Contig ID	119687_1.R1010

5'-most EST	g2764196
Method	BLASTX
NCBI GI	g3482910
BLAST score	480
E value	2.0e-48
Match length	110
% identity	79
NCBI Description	(AC003970) Similar to rice water stress induced protein gi_537404 [Arabidopsis thaliana]

Seq. No.	135499
Contig ID	119691_1.R1010
5'-most EST	g773548
Method	BLASTX
NCBI GI	g4454025
BLAST score	309
E value	3.0e-72
Match length	154
% identity	90
NCBI Description	(AL035394) putative cellulase [Arabidopsis thaliana]

Seq. No.	135500
Contig ID	119694_1.R1010
5'-most EST	g937545
Method	BLASTN
NCBI GI	g4519182
BLAST score	156
E value	3.0e-82
Match length	460
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K13H13, complete sequence

Seq. No.	135501
Contig ID	119695_1.R1010
5'-most EST	jC-atXP44C17OH19T7d1
Method	BLASTX
NCBI GI	g4586246
BLAST score	193
E value	4.0e-15
Match length	41
% identity	90
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	135502
Contig ID	119698_1.R1010
5'-most EST	g473340

Seq. No.	135503
Contig ID	119717_1.R1010
5'-most EST	g937878
Method	BLASTN
NCBI GI	g4756963
BLAST score	394
E value	0.0e+00
Match length	398
% identity	92

NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23 (ESSA project)
Seq. No.	135504
Contig ID	119719_2.R1010
5'-most EST	g2764237
Method	BLASTX
NCBI GI	g2262162
BLAST score	266
E value	5.0e-25
Match length	149
% identity	46
NCBI Description	(AC002329) hypothetical protein similar to A. thaliana protein F19K23.19 [Arabidopsis thaliana]
Seq. No.	135505
Contig ID	119722_1.R1010
5'-most EST	g1053458
Method	BLASTX
NCBI GI	g4006899
BLAST score	622
E value	5.0e-65
Match length	133
% identity	89
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]
Seq. No.	135506
Contig ID	119727_1.R1010
5'-most EST	g937904
Method	BLASTN
NCBI GI	g2760166
BLAST score	120
E value	8.0e-61
Match length	449
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK20, complete sequence [Arabidopsis thaliana]
Seq. No.	135507
Contig ID	119734_1.R1010
5'-most EST	g937978
Seq. No.	135508
Contig ID	119739_1.R1010
5'-most EST	g937600
Seq. No.	135509
Contig ID	119761_1.R1010
5'-most EST	g2749396
Method	BLASTN
NCBI GI	g4733984
BLAST score	184
E value	5.0e-99
Match length	271
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F14O4 genomic sequence, complete sequence

Seq. No.	135510
Contig ID	119764_1.R1010
5'-most EST	g905521
Method	BLASTX
NCBI GI	g2911067
BLAST score	499
E value	1.0e-50
Match length	138
% identity	70
NCBI Description	(AL021960) UV-damaged DNA-binding protein-like [Arabidopsis thaliana]

Seq. No.	135511
Contig ID	119770_1.R1010
5'-most EST	g2596241
Method	BLASTX
NCBI GI	g100225
BLAST score	393
E value	4.0e-38
Match length	96
% identity	73
NCBI Description	heat shock transcription factor 8 - tomato >gi_19260_emb_CAA47868_ (X67599) heat stress transcription factor 8 [Lycopersicon esculentum]

Seq. No.	135512
Contig ID	119771_1.R1010
5'-most EST	g905530
Method	BLASTX
NCBI GI	g3047125
BLAST score	155
E value	4.0e-55
Match length	120
% identity	100
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	135513
Contig ID	119773_1.R1010
5'-most EST	g905533
Method	BLASTX
NCBI GI	g3785995
BLAST score	665
E value	6.0e-70
Match length	136
% identity	95
NCBI Description	(AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	135514
Contig ID	119774_1.R1010
5'-most EST	g2749400
Method	BLASTN
NCBI GI	g3785992
BLAST score	284
E value	1.0e-158
Match length	386
% identity	93

NCBI Description	Arabidopsis thaliana chromosome II BAC T6A23 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	135515
Contig ID	119775_1.R1010
5'-most EST	g2749401
Seq. No.	135516
Contig ID	119779_1.R1010
5'-most EST	g905539
Method	BLASTX
NCBI GI	g434765
BLAST score	159
E value	2.0e-10
Match length	113
% identity	39
NCBI Description	(D21262) ORF [Homo sapiens]
Seq. No.	135517
Contig ID	119783_1.R1010
5'-most EST	g905961
Method	BLASTX
NCBI GI	g2708743
BLAST score	257
E value	4.0e-22
Match length	141
% identity	38
NCBI Description	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
Seq. No.	135518
Contig ID	119784_1.R1010
5'-most EST	g2749403
Seq. No.	135519
Contig ID	119790_1.R1010
5'-most EST	g2749405
Method	BLASTN
NCBI GI	g4220634
BLAST score	312
E value	1.0e-175
Match length	688
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9H21, complete sequence [Arabidopsis thaliana]
Seq. No.	135520
Contig ID	119791_1.R1010
5'-most EST	g2749366
Seq. No.	135521
Contig ID	119797_1.R1010
5'-most EST	g3449832
Seq. No.	135522
Contig ID	119801_1.R1010
5'-most EST	g905644

Method	BLASTX
NCBI GI	g627580
BLAST score	226
E value	3.0e-19
Match length	127
% identity	41
NCBI Description	prolyl oligopeptidase (EC 3.4.21.26) - human >gi_904214_dbj_BAA04661_ (D21102) prolyl endopeptidase [Homo sapiens]

Seq. No.	135523
Contig ID	119802_1.R1010
5'-most EST	g2749435
Method	BLASTX
NCBI GI	g4506043
BLAST score	74
E value	2.0e-23
Match length	106
% identity	53
NCBI Description	prolyl endopeptidase >gi_1346769_sp_P48147_PPCE_HUMAN PROLYL ENDOPEPTIDASE (POST-PROLINE CLEAVING ENZYME) (PE) >gi_558596_emb_CAA52605_ (X74496) prolyl oligopeptidase [Homo sapiens] >gi_1585155_prf__2124300A Pro oligopeptidase [Homo sapiens]

Seq. No.	135524
Contig ID	119815_1.R1010
5'-most EST	g906056

Seq. No.	135525
Contig ID	119819_1.R1010
5'-most EST	g906064
Method	BLASTN
NCBI GI	g2924733
BLAST score	168
E value	2.0e-89
Match length	191
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]

Seq. No.	135526
Contig ID	119820_1.R1010
5'-most EST	g2749442
Method	BLASTN
NCBI GI	g4220636
BLAST score	260
E value	1.0e-144
Match length	437
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFB16, complete sequence [Arabidopsis thaliana]

Seq. No.	135527
Contig ID	119833_1.R1010
5'-most EST	g2749446
Method	BLASTN

NCBI GI	g2182286
BLAST score	335
E value	0.0e+00
Match length	382
% identity	98
NCBI Description	Sequence of BAC F20P5 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	135528
Contig ID	119847_1.R1010
5'-most EST	jC-atXP47C176E11T7d2
Method	BLASTX
NCBI GI	g4835226
BLAST score	456
E value	3.0e-45
Match length	178
% identity	55
NCBI Description	(AL049862) putative protein [Arabidopsis thaliana]

Seq. No.	135529
Contig ID	119848_1.R1010
5'-most EST	jC-atXP47C176E11T7s2
Method	BLASTN
NCBI GI	g4835223
BLAST score	419
E value	0.0e+00
Match length	485
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F18B3 (ESSA project)

Seq. No.	135530
Contig ID	119856_1.R1010
5'-most EST	g905793

Seq. No.	135531
Contig ID	119860_1.R1010
5'-most EST	g2749469

Seq. No.	135532
Contig ID	119869_1.R1010
5'-most EST	jC-atXP44C171E11T7087a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	56
E value	2.0e-22
Match length	56
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	135533
Contig ID	119888_1.R1010
5'-most EST	g2733455
Method	BLASTX
NCBI GI	g4115386
BLAST score	589
E value	4.0e-61

Match length 122
% identity 98
NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]

Seq. No. 135534
Contig ID 119900_1.R1010
5'-most EST g905778
Method BLASTX
NCBI GI g2088661
BLAST score 192
E value 2.0e-14
Match length 129
% identity 33
NCBI Description (AF002109) hypothetical protein [Arabidopsis thaliana]

Seq. No. 135535
Contig ID 119903_1.R1010
5'-most EST g2597363
Method BLASTX
NCBI GI g3687833
BLAST score 561
E value 2.0e-57
Match length 172
% identity 19
NCBI Description (AF069737) notchless [Xenopus laevis]

Seq. No. 135536
Contig ID 119918_1.R1010
5'-most EST g2733511
Method BLASTX
NCBI GI g3915463
BLAST score 155
E value 4.0e-10
Match length 80
% identity 44
NCBI Description HYPOTHETICAL 33.1 KD PROTEIN SLR1592
>gi_1652063_dbj_BAA16988_ (D90902) hypothetical protein
[Synechocystis sp.]

Seq. No. 135537
Contig ID 119919_1.R1010
5'-most EST g2749484
Method BLASTX
NCBI GI g3915463
BLAST score 146
E value 4.0e-09
Match length 57
% identity 56
NCBI Description HYPOTHETICAL 33.1 KD PROTEIN SLR1592
>gi_1652063_dbj_BAA16988_ (D90902) hypothetical protein
[Synechocystis sp.]

Seq. No. 135538
Contig ID 119920_1.R1010
5'-most EST g906224
Method BLASTN
NCBI GI g2245031

BLAST score	258
E value	1.0e-143
Match length	341
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	135539
Contig ID	119921_1.R1010
5'-most EST	g905845
Method	BLASTN
NCBI GI	g3033373
BLAST score	367
E value	0.0e+00
Match length	400
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F19I3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135540
Contig ID	119922_1.R1010
5'-most EST	g2749488
Method	BLASTN
NCBI GI	g3033373
BLAST score	187
E value	1.0e-100
Match length	341
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F19I3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135541
Contig ID	119925_1.R1010
5'-most EST	g905852
Method	BLASTN
NCBI GI	g4580732
BLAST score	298
E value	1.0e-167
Match length	333
% identity	98
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F5J5, complete sequence

Seq. No.	135542
Contig ID	119935_1.R1010
5'-most EST	g2749491
Method	BLASTN
NCBI GI	g3402745
BLAST score	271
E value	1.0e-151
Match length	366
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F18E5 (ESSAII project)

Seq. No.	135543
Contig ID	119961_1.R1010

5'-most EST	jC-atXP49C17709T7d2
Method	BLASTX
NCBI GI	g3123712
BLAST score	190
E value	2.0e-32
Match length	171
% identity	44
NCBI Description	(D89051) ERD6 protein [Arabidopsis thaliana]

Seq. No.	135544
Contig ID	119973_1.R1010
5'-most EST	g2733463
Method	BLASTX
NCBI GI	g3928862
BLAST score	348
E value	3.0e-33
Match length	133
% identity	61
NCBI Description	(AF089710) disease resistance protein RPP8 [Arabidopsis thaliana]

Seq. No.	135545
Contig ID	119978_1.R1010
5'-most EST	g906286

Seq. No.	135546
Contig ID	119984_1.R1010
5'-most EST	jC-atXP49C178M11T7d2
Method	BLASTX
NCBI GI	g2119846
BLAST score	378
E value	2.0e-36
Match length	71
% identity	100
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	135547
Contig ID	119988_1.R1010
5'-most EST	g905880
Method	BLASTX
NCBI GI	g3212868
BLAST score	621
E value	1.0e-64
Match length	146
% identity	81
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	135548
Contig ID	120004_1.R1010
5'-most EST	g906839
Method	BLASTX

NCBI GI	g1698548
BLAST score	472
E value	7.0e-48
Match length	130
% identity	71
NCBI Description	(U58971) calmodulin-binding protein [Nicotiana tabacum]

Seq. No.	135549
Contig ID	120008_1.R1010
5'-most EST	jC-atXP4C85D7T7d1
Method	BLASTN
NCBI GI	g2351071
BLAST score	131
E value	5.0e-67
Match length	183
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MVA3, complete sequence [Arabidopsis thaliana]

Seq. No.	135550
Contig ID	120010_1.R1010
5'-most EST	jC-atXP4C85D9T7d1

Seq. No.	135551
Contig ID	120012_1.R1010
5'-most EST	g949358
Method	BLASTN
NCBI GI	g1632775
BLAST score	65
E value	7.0e-28
Match length	287
% identity	84
NCBI Description	A.thaliana t5r gene

Seq. No.	135552
Contig ID	120019_1.R1010
5'-most EST	g2393588
Method	BLASTN
NCBI GI	g4580365
BLAST score	310
E value	1.0e-174
Match length	341
% identity	72
NCBI Description	Arabidopsis thaliana chromosome I BAC F3F20 genomic sequence, complete sequence

Seq. No.	135553
Contig ID	120021_1.R1010
5'-most EST	g2393592
Method	BLASTX
NCBI GI	g4455349
BLAST score	308
E value	5.0e-28
Match length	68
% identity	87
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	135554
Contig ID	120022_1.R1010
5'-most EST	g501992
Method	BLASTX
NCBI GI	g2160185
BLAST score	411
E value	2.0e-40
Match length	120
% identity	61
NCBI Description	(AC000132) Similar to S. pombe ISP4 (gb_D83992). [Arabidopsis thaliana]

Seq. No.	135555
Contig ID	120034_1.R1010
5'-most EST	g2393599
Method	BLASTX
NCBI GI	g2213615
BLAST score	280
E value	2.0e-25
Match length	75
% identity	61
NCBI Description	(AC000103) F21J9.9 [Arabidopsis thaliana]

Seq. No.	135556
Contig ID	120043_1.R1010
5'-most EST	g502017
Method	BLASTN
NCBI GI	g2623294
BLAST score	168
E value	2.0e-89
Match length	382
% identity	71
NCBI Description	Arabidopsis thaliana chromosome II BAC T20B5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135557
Contig ID	120049_1.R1010
5'-most EST	g1565729

Seq. No.	135558
Contig ID	120051_1.R1010
5'-most EST	jC-atXP4C88I3T7d1
Method	BLASTN
NCBI GI	g3063438
BLAST score	213
E value	1.0e-116
Match length	542
% identity	99
NCBI Description	Complete sequence of Arabidopsis F22013, complete sequence [Arabidopsis thaliana]

Seq. No.	135559
Contig ID	120054_1.R1010
5'-most EST	g502045
Method	BLASTN
NCBI GI	g3695386
BLAST score	386

E value	0.0e+00
Match length	616
% identity	98
NCBI Description	Arabidopsis thaliana BAC T2L5

Seq. No.	135560
Contig ID	120069_1.R1010
5'-most EST	g2749522
Method	BLASTN
NCBI GI	g4756963
BLAST score	163
E value	2.0e-86
Match length	278
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23 (ESSA project)

Seq. No.	135561
Contig ID	120074_1.R1010
5'-most EST	g507076

Seq. No.	135562
Contig ID	120081_1.R1010
5'-most EST	g2749531
Method	BLASTN
NCBI GI	g3702722
BLAST score	262
E value	1.0e-145
Match length	383
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K12B20, complete sequence [Arabidopsis thaliana]

Seq. No.	135563
Contig ID	120090_1.R1010
5'-most EST	jC-atXP50C180F1T7s1
Method	BLASTN
NCBI GI	g4468103
BLAST score	144
E value	4.0e-75
Match length	380
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone M3E9 (ESSA project)

Seq. No.	135564
Contig ID	120093_1.R1010
5'-most EST	jC-atXP50C180F8T7s1

Seq. No.	135565
Contig ID	120100_1.R1010
5'-most EST	g2749558
Method	BLASTX
NCBI GI	g3063691
BLAST score	428
E value	4.0e-42
Match length	124

% identity	60
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]

Seq. No.	135566
Contig ID	120105_1.R1010
5'-most EST	g2749562
Method	BLASTN
NCBI GI	g3449320
BLAST score	304
E value	1.0e-170
Match length	312
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRB17, complete sequence [Arabidopsis thaliana]

Seq. No.	135567
Contig ID	120110_1.R1010
5'-most EST	jC-atXP50C181A7T7s1

Seq. No.	135568
Contig ID	120125_1.R1010
5'-most EST	g2749580

Seq. No.	135569
Contig ID	120135_1.R1010
5'-most EST	g2749587

Seq. No.	135570
Contig ID	120144_1.R1010
5'-most EST	jC-atXP76C226O24T7s1
Method	BLASTN
NCBI GI	g3004543
BLAST score	376
E value	0.0e+00
Match length	420
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F19F24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135571
Contig ID	120150_1.R1010
5'-most EST	g17063
Method	BLASTX
NCBI GI	g2529659
BLAST score	496
E value	7.0e-50
Match length	145
% identity	68
NCBI Description	(AC002535) putative pectinesterase [Arabidopsis thaliana] >gi_3738281 (AC005309) putative pectinesterase [Arabidopsis thaliana]

Seq. No.	135572
Contig ID	120154_1.R1010
5'-most EST	jC-atXP40C161K4T7081a1
Method	BLASTN
NCBI GI	g2264307

BLAST score	57
E value	7.0e-23
Match length	205
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MED24, complete sequence [Arabidopsis thaliana]

Seq. No.	135573
Contig ID	120154_2.R1010
5'-most EST	jC-atXP52C181K21T7d2
Method	BLASTN
NCBI GI	g2264307
BLAST score	63
E value	2.0e-26
Match length	115
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MED24, complete sequence [Arabidopsis thaliana]

Seq. No.	135574
Contig ID	120156_1.R1010
5'-most EST	jC-atXP52C181K22T7s2

Seq. No.	135575
Contig ID	120171_1.R1010
5'-most EST	jC-atXP52C181M6T7d2

Seq. No.	135576
Contig ID	120192_1.R1010
5'-most EST	jC-atXP52C181P11T7s2

Seq. No.	135577
Contig ID	120198_1.R1010
5'-most EST	jC-atXP52C182F18T7d2
Method	BLASTX
NCBI GI	g4337198
BLAST score	276
E value	3.0e-24
Match length	101
% identity	61
NCBI Description	(AC006403) putative auxin-induced protein [Arabidopsis thaliana]

Seq. No.	135578
Contig ID	120199_1.R1010
5'-most EST	jC-atXP52C182F18T7s2
Method	BLASTX
NCBI GI	g4337198
BLAST score	49
E value	3.0e-28
Match length	87
% identity	78
NCBI Description	(AC006403) putative auxin-induced protein [Arabidopsis thaliana]

Seq. No.	135579
Contig ID	120201_1.R1010

5'-most EST	jC-atXP52C182G15T7d2
Seq. No.	135580
Contig ID	120212_1.R1010
5'-most EST	jC-atXP52C182J18T7d2
Method	BLASTX
NCBI GI	g126201
BLAST score	52
E value	2.0e-19
Match length	76
% identity	67
NCBI Description	3-ISOPROPYLMALATE DEHYDROGENASE PRECURSOR (BETA-IPM DEHYDROGENASE) (IMDH) (3-IPM-DH) >gi_81676_pir__S20510 3-isopropylmalate dehydrogenase (EC 1.1.1.85) precursor - rape >gi_17827_emb_CAA42596_ (X59970) 3-isopropylmalate dehydrogenase [Brassica napus]
Seq. No.	135581
Contig ID	120215_1.R1010
5'-most EST	jC-atXP52C182J3T7s2
Seq. No.	135582
Contig ID	120218_1.R1010
5'-most EST	jC-atXP98CH2G10T7b1
Method	BLASTN
NCBI GI	g3097257
BLAST score	52
E value	4.0e-20
Match length	56
% identity	98
NCBI Description	Platichthys flesus Ki-ras gene (exons 1 to 4)
Seq. No.	135583
Contig ID	120218_3.R1010
5'-most EST	jC-atXP52C182K23T7d2
Method	BLASTX
NCBI GI	g1706319
BLAST score	397
E value	2.0e-38
Match length	150
% identity	52
NCBI Description	HISTIDINE DECARBOXYLASE (HDC) (TOM92) >gi_481829_pir__S39554 histidine decarboxylase (EC 4.1.1.22) - tomato >gi_416534_emb_CAA50719_ (X71900) histidine decarboxylase [Lycopersicon esculentum]
Seq. No.	135584
Contig ID	120224_1.R1010
5'-most EST	jC-atXP52C182L21T7d2
Seq. No.	135585
Contig ID	120226_1.R1010
5'-most EST	jC-atXP52C182L2T7d2
Method	BLASTX
NCBI GI	g2982444
BLAST score	633
E value	3.0e-66

Match length	148
% identity	86
NCBI Description	(AL022224) CLV1 receptor kinase like protein [Arabidopsis thaliana]
Seq. No.	135586
Contig ID	120227_1.R1010
5'-most EST	jC-atXP52C182M18T7d2
Seq. No.	135587
Contig ID	120234_1.R1010
5'-most EST	g2749636
Seq. No.	135588
Contig ID	120236_1.R1010
5'-most EST	g907039
Method	BLASTX
NCBI GI	g2129581
BLAST score	225
E value	2.0e-18
Match length	90
% identity	50
NCBI Description	envelope Ca2+-ATPase precursor - Arabidopsis thaliana >gi_471089_dbj_BAA03091_ (D13984) chloroplast envelope Ca2+-ATPase precursor [Arabidopsis thaliana] >gi_4165448_emb_CAA49558_ (X69940) envelope Ca2+-ATPase [Arabidopsis thaliana]
Seq. No.	135589
Contig ID	120237_1.R1010
5'-most EST	jC-atXP52C183B23T7d2
Method	BLASTX
NCBI GI	g4457221
BLAST score	172
E value	5.0e-12
Match length	50
% identity	62
NCBI Description	(AF127797) putative bZIP DNA-binding protein [Capsicum chinense]
Seq. No.	135590
Contig ID	120239_1.R1010
5'-most EST	jC-atXP52C183C13T7d2
Seq. No.	135591
Contig ID	120242_1.R1010
5'-most EST	g2749637
Method	BLASTX
NCBI GI	g3413710
BLAST score	164
E value	4.0e-11
Match length	77
% identity	48
NCBI Description	(AC004747) hypothetical protein [Arabidopsis thaliana]
Seq. No.	135592
Contig ID	120242_2.R1010

5'-most EST	jC-atXP52C183D14T7d2
Method	BLASTX
NCBI GI	g3834319
BLAST score	242
E value	3.0e-20
Match length	139
% identity	43
NCBI Description	(AC005679) Similar to gi_2244754 heat shock transcription factor HSF30 homolog from Arabidopsis thaliana chromosome 4 contig gb_Z97335. [Arabidopsis thaliana]

Seq. No.	135593
Contig ID	120244_1.R1010
5'-most EST	g2749638
Method	BLASTX
NCBI GI	g2244740
BLAST score	144
E value	8.0e-09
Match length	69
% identity	42
NCBI Description	(D88417) endo-1,4-beta-glucanase [Gossypium hirsutum]

Seq. No.	135594
Contig ID	120244_2.R1010
5'-most EST	jC-atXP52C183E12T7d2

Seq. No.	135595
Contig ID	120247_1.R1010
5'-most EST	g906582

Seq. No.	135596
Contig ID	120250_1.R1010
5'-most EST	jC-atXP52C183F22T7s2
Method	BLASTN
NCBI GI	g4325336
BLAST score	286
E value	1.0e-160
Match length	455
% identity	99
NCBI Description	Arabidopsis thaliana BAC F15P23

Seq. No.	135597
Contig ID	120256_1.R1010
5'-most EST	jC-atXP52C183G24T7s2

Seq. No.	135598
Contig ID	120276_1.R1010
5'-most EST	g957510
Method	BLASTN
NCBI GI	g2351063
BLAST score	357
E value	0.0e+00
Match length	400
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCL19, complete sequence [Arabidopsis thaliana]

Seq. No.	135599
Contig ID	120276_2.R1010
5'-most EST	jC-atXP55C186J7T7d2
Method	BLASTN
NCBI GI	g2351063
BLAST score	551
E value	0.0e+00
Match length	965
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCL19, complete sequence [Arabidopsis thaliana]

Seq. No.	135600
Contig ID	120278_1.R1010
5'-most EST	g957486
Method	BLASTX
NCBI GI	g4454051
BLAST score	265
E value	6.0e-24
Match length	133
% identity	46
NCBI Description	(AL035394) putative polygalacturonase [Arabidopsis thaliana]

Seq. No.	135601
Contig ID	120279_1.R1010
5'-most EST	g2445918
Method	BLASTN
NCBI GI	g3449313
BLAST score	42
E value	4.0e-14
Match length	118
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21P3, complete sequence [Arabidopsis thaliana]

Seq. No.	135602
Contig ID	120285_1.R1010
5'-most EST	jC-atXP55C186L2T7s2

Seq. No.	135603
Contig ID	120288_1.R1010
5'-most EST	g957499
Method	BLASTX
NCBI GI	g4218535
BLAST score	593
E value	2.0e-61
Match length	154
% identity	69
NCBI Description	(AJ010829) GRAB1 protein [Triticum sp.]

Seq. No.	135604
Contig ID	120290_1.R1010
5'-most EST	g587049

Seq. No.	135605
Contig ID	120302_1.R1010

5'-most EST	g2412870
Method	BLASTX
NCBI GI	g4115936
BLAST score	282
E value	4.0e-25
Match length	54
% identity	100
NCBI Description	(AF118223) No definition line found [Arabidopsis thaliana]

Seq. No.	135606
Contig ID	120311_1.R1010
5'-most EST	jC-atXP55C187E8T7d2
Method	BLASTN
NCBI GI	g4589427
BLAST score	392
E value	0.0e+00
Match length	459
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFG13, complete sequence

Seq. No.	135607
Contig ID	120327_1.R1010
5'-most EST	jC-atXP55C187I20T7d2
Method	BLASTN
NCBI GI	g3885325
BLAST score	609
E value	0.0e+00
Match length	776
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T20P8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135608
Contig ID	120333_1.R1010
5'-most EST	g2733294

Seq. No.	135609
Contig ID	120343_1.R1010
5'-most EST	jC-atXP55C187L17T7d2
Method	BLASTX
NCBI GI	g4753882
BLAST score	350
E value	5.0e-33
Match length	141
% identity	52
NCBI Description	(AL049754) putative aspartate aminotransferase [Streptomyces coelicolor]

Seq. No.	135610
Contig ID	120373_1.R1010
5'-most EST	g958166
Method	BLASTX
NCBI GI	g2781359
BLAST score	658
E value	4.0e-72
Match length	163

% identity	88
NCBI Description	(AC003113) F25O1.15 [Arabidopsis thaliana]

Seq. No.	135611
Contig ID	120378_1.R1010
5'-most EST	g2733952
Method	BLASTX
NCBI GI	g4218991
BLAST score	443
E value	8.0e-44
Match length	99
% identity	91
NCBI Description	(AF098632) subtilisin-like protease [Arabidopsis thaliana]

Seq. No.	135612
Contig ID	120380_1.R1010
5'-most EST	g957693

Seq. No.	135613
Contig ID	120391_1.R1010
5'-most EST	g958175

Seq. No.	135614
Contig ID	120393_1.R1010
5'-most EST	g957707

Seq. No.	135615
Contig ID	120395_1.R1010
5'-most EST	g870878
Method	BLASTX
NCBI GI	g2851455
BLAST score	86
E value	3.0e-12
Match length	106
% identity	43
NCBI Description	DYNAMIN-LIKE PROTEIN >gi_2267213 (L36939) dynamin-like GTP binding protein [Arabidopsis thaliana]

Seq. No.	135616
Contig ID	120396_1.R1010
5'-most EST	g958176
Method	BLASTX
NCBI GI	g3269287
BLAST score	509
E value	1.0e-51
Match length	141
% identity	76
NCBI Description	(AL030978) GH3 like protein [Arabidopsis thaliana]

Seq. No.	135617
Contig ID	120399_1.R1010
5'-most EST	g957716
Method	BLASTX
NCBI GI	g4508076
BLAST score	160
E value	1.0e-10
Match length	101

% identity	36
NCBI Description	(AC005882) 55659 [Arabidopsis thaliana]

Seq. No.	135618
Contig ID	120418_1.R1010
5'-most EST	g958228
Method	BLASTN
NCBI GI	g3449321
BLAST score	351
E value	0.0e+00
Match length	415
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTG10, complete sequence [Arabidopsis thaliana]

Seq. No.	135619
Contig ID	120433_1.R1010
5'-most EST	g957861
Method	BLASTN
NCBI GI	g3510343
BLAST score	362
E value	0.0e+00
Match length	421
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJC20, complete sequence [Arabidopsis thaliana]

Seq. No.	135620
Contig ID	120442_1.R1010
5'-most EST	g2047453
Method	BLASTN
NCBI GI	g4220643
BLAST score	248
E value	1.0e-137
Match length	501
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD22, complete sequence [Arabidopsis thaliana]

Seq. No.	135621
Contig ID	120443_1.R1010
5'-most EST	jC-atXP58C191M1T7s3

Seq. No.	135622
Contig ID	120445_1.R1010
5'-most EST	jC-atXP58C191L8T7s3

Seq. No.	135623
Contig ID	120470_1.R1010
5'-most EST	jC-atXP58C192F7T7s3
Method	BLASTX
NCBI GI	g1174470
BLAST score	176
E value	2.0e-12
Match length	53
% identity	60
NCBI Description	OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5)

(INTEGRAL MEMBRANE PROTEIN 1) >gi_508543 (L34260) integral membrane protein 1 [Mus musculus] >gi_1588285_prf__2208301A integral membrane protein [Mus musculus]

Seq. No.	135624
Contig ID	120481_1.R1010
5'-most EST	jC-atXP58C194E8T7s3
Method	BLASTN
NCBI GI	g2341023
BLAST score	302
E value	1.0e-169
Match length	362
% identity	96
NCBI Description	Sequence of BAC F19P19 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	135625
Contig ID	120482_1.R1010
5'-most EST	g2749702

Seq. No.	135626
Contig ID	120483_1.R1010
5'-most EST	jC-atXP117C141N21T7a1
Method	BLASTX
NCBI GI	g4512701
BLAST score	532
E value	4.0e-54
Match length	136
% identity	73
NCBI Description	(AC006569) putative tyrosine decarboxylase [Arabidopsis thaliana]

Seq. No.	135627
Contig ID	120492_1.R1010
5'-most EST	jC-atXP58C194A16T7s3
Method	BLASTX
NCBI GI	g4501901
BLAST score	146
E value	4.0e-09
Match length	63
% identity	44
NCBI Description	aminoacylase 1 >gi_461466_sp_Q03154_ACY1_HUMAN AMINOACYLASE-1 (N-ACYL-L-AMINO-ACID AMIDOHYDROLASE) (ACY-1) >gi_1082202_pir__A47488 aminoacylase (EC 3.5.1.14) - human >gi_178071 (L07548) aminoacylase-1 [Homo sapiens] >gi_285903_dbj_BAA03397_ (D14524) aminoacylase-1 [Homo sapiens] >gi_303595_dbj_BAA03814_ (D16307) 45kDa protein [Homo sapiens]

Seq. No.	135628
Contig ID	120501_1.R1010
5'-most EST	g2749724
Method	BLASTN
NCBI GI	g2760165
BLAST score	269
E value	1.0e-150
Match length	289

% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC9, complete sequence [Arabidopsis thaliana]
Seq. No.	135629
Contig ID	120510_1.R1010
5'-most EST	jC-atXP58C194K8T7s3
Seq. No.	135630
Contig ID	120513_1.R1010
5'-most EST	jC-atXP59C194N2T7d1
Method	BLASTX
NCBI GI	g3080426
BLAST score	294
E value	3.0e-26
Match length	170
% identity	38
NCBI Description	(AL022604) putative protein [Arabidopsis thaliana]
Seq. No.	135631
Contig ID	120603_1.R1010
5'-most EST	g2446231
Method	BLASTN
NCBI GI	g2462264
BLAST score	42
E value	5.0e-14
Match length	42
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.	135632
Contig ID	120615_1.R1010
5'-most EST	g2756855
Method	BLASTN
NCBI GI	g2182289
BLAST score	352
E value	0.0e+00
Match length	356
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC F11P17 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	135633
Contig ID	120617_1.R1010
5'-most EST	g2756837
Method	BLASTN
NCBI GI	g2275194
BLAST score	359
E value	0.0e+00
Match length	464
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T08I13 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	135634
Contig ID	120621_1.R1010
5'-most EST	g931440

Method	BLASTX
NCBI GI	g2959358
BLAST score	640
E value	1.0e-66
Match length	129
% identity	97
NCBI Description	(X96758) clathrin coat assembly protein AP17 [Zea mays]

Seq. No.	135635
Contig ID	120624_1.R1010
5'-most EST	g502091
Method	BLASTX
NCBI GI	g4584521
BLAST score	471
E value	5.0e-56
Match length	144
% identity	89
NCBI Description	(AL049607) putative protein [Arabidopsis thaliana]

Seq. No.	135636
Contig ID	120630_1.R1010
5'-most EST	g2756848
Method	BLASTX
NCBI GI	g2435514
BLAST score	607
E value	5.0e-63
Match length	147
% identity	83
NCBI Description	(AF024504) Similar to serine/threonine protein kinase; coded for by A. thaliana cDNA T20930; coded for by A. thaliana cDNA T43472 [Arabidopsis thaliana]

Seq. No.	135637
Contig ID	120632_1.R1010
5'-most EST	g2756852

Seq. No.	135638
Contig ID	120633_1.R1010
5'-most EST	g2756853
Method	BLASTX
NCBI GI	g4539335
BLAST score	131
E value	3.0e-49
Match length	208
% identity	54
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	135639
Contig ID	120635_1.R1010
5'-most EST	jC-atXP5C89I19T7039a1
Method	BLASTN
NCBI GI	g16397
BLAST score	470
E value	0.0e+00
Match length	634
% identity	99
NCBI Description	A.thaliana gene for nucleoside diphosphate kinase, exons

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Seq. No.	135640
Contig ID	120639_1.R1010
5'-most EST	jC-atXP5C90C12T7d1
Method	BLASTX
NCBI GI	g2811031
BLAST score	588
E value	5.0e-61
Match length	142
% identity	79
NCBI Description	BETAINE-ALDEHYDE DEHYDROGENASE PRECURSOR (BADH) >gi_2109299_gb_AAB58165.1_ (AF000132) betaine aldehyde dehydrogenase [Amaranthus hypochondriacus]

Seq. No.	135641
Contig ID	120644_1.R1010
5'-most EST	g958208

Seq. No.	135642
Contig ID	120650_1.R1010
5'-most EST	jC-atXP61C201E15T7d1

Seq. No.	135643
Contig ID	120658_1.R1010
5'-most EST	jC-atXP61C199P11T7d1
Method	BLASTX
NCBI GI	g3152614
BLAST score	614
E value	9.0e-64
Match length	163
% identity	80
NCBI Description	(AC004482) unknown protein [Arabidopsis thaliana]

Seq. No.	135644
Contig ID	120666_2.R1010
5'-most EST	g1053908
Method	BLASTN
NCBI GI	g3510343
BLAST score	333
E value	0.0e+00
Match length	333
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJC20, complete sequence [Arabidopsis thaliana]

Seq. No.	135645
Contig ID	120678_1.R1010
5'-most EST	jC-atXP61C200F5T7d1
Method	BLASTX
NCBI GI	g4539335
BLAST score	76
E value	1.0e-40
Match length	82
% identity	99
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	135646
Contig ID	120698_1.R1010
5'-most EST	jC-atXP61C200K24T7d1
Method	BLASTX
NCBI GI	g82231
BLAST score	435
E value	4.0e-43
Match length	82
% identity	100
NCBI Description	hypothetical protein 82 - common tobacco chloroplast >gi_225200_prf__1211235AE ORF 82 [Nicotiana tabacum]

Seq. No.	135647
Contig ID	120704_1.R1010
5'-most EST	g1053798
Method	BLASTX
NCBI GI	g4406818
BLAST score	378
E value	3.0e-36
Match length	114
% identity	61
NCBI Description	(AC006201) putative transcription factor-like protein [Arabidopsis thaliana]

Seq. No.	135648
Contig ID	120710_1.R1010
5'-most EST	jC-atXP61C200O24T7d1
Method	BLASTX
NCBI GI	g2909448
BLAST score	212
E value	9.0e-17
Match length	64
% identity	64
NCBI Description	(AL021929) fadE5 [Mycobacterium tuberculosis]

Seq. No.	135649
Contig ID	120712_1.R1010
5'-most EST	jC-atXP100C268G12T7b1
Method	BLASTX
NCBI GI	g2462834
BLAST score	185
E value	9.0e-25
Match length	179
% identity	39
NCBI Description	(AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No.	135650
Contig ID	120722_1.R1010
5'-most EST	g1053911

Seq. No.	135651
Contig ID	120725_1.R1010
5'-most EST	g2413820
Method	BLASTX
NCBI GI	g2194118
BLAST score	166
E value	2.0e-11

Match length	40
% identity	72
NCBI Description	(AC002062) F20P5.4 gene product [Arabidopsis thaliana]

Seq. No.	135652
Contig ID	120739_1.R1010
5'-most EST	jC-atXP61C201E2T7d1

Seq. No.	135653
Contig ID	120749_1.R1010
5'-most EST	jC-atXP61C201F7T7d1
Method	BLASTN
NCBI GI	g1871173
BLAST score	476
E value	0.0e+00
Match length	501
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T06D20 genomic sequence, complete sequence

Seq. No.	135654
Contig ID	120754_1.R1010
5'-most EST	jC-atXP61C201H9T7d1
Method	BLASTN
NCBI GI	g4510360
BLAST score	210
E value	1.0e-114
Match length	398
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F11F19 genomic sequence, complete sequence

Seq. No.	135655
Contig ID	120757_1.R1010
5'-most EST	jC-atXP61C201H24T7d1

Seq. No.	135656
Contig ID	120766_1.R1010
5'-most EST	jC-atXP2C77F12T7061a1
Method	BLASTX
NCBI GI	g4191788
BLAST score	836
E value	8.0e-90
Match length	157
% identity	100
NCBI Description	(AC005917) putative 1-aminocyclopropane-1-carboxylate oxidase [Arabidopsis thaliana]

Seq. No.	135657
Contig ID	120802_1.R1010
5'-most EST	jC-atXP62C201P3T7d2
Method	BLASTX
NCBI GI	g1817535
BLAST score	144
E value	1.0e-08
Match length	54
% identity	52

NCBI Description	(D78508) YfiK [Bacillus subtilis] >gi_2633154_emb_CAB12659_ (Z99108) similar to two-component response regulator [YfiJ] [Bacillus subtilis]
Seq. No.	135658
Contig ID	120817_1.R1010
5'-most EST	jC-atXP71CF1E2T7096d1
Method	BLASTX
NCBI GI	g2909583
BLAST score	340
E value	1.0e-31
Match length	146
% identity	50
NCBI Description	(AL021926) oxcA [Mycobacterium tuberculosis]
Seq. No.	135659
Contig ID	120821_1.R1010
5'-most EST	jC-atXP62C202M24T7d2
Method	BLASTX
NCBI GI	g4104561
BLAST score	289
E value	5.0e-47
Match length	242
% identity	41
NCBI Description	(AF036960) subtilisin-like protease [Glycine max]
Seq. No.	135660
Contig ID	120821_2.R1010
5'-most EST	g2758403
Method	BLASTX
NCBI GI	g4104561
BLAST score	363
E value	2.0e-34
Match length	130
% identity	55
NCBI Description	(AF036960) subtilisin-like protease [Glycine max]
Seq. No.	135661
Contig ID	120828_1.R1010
5'-most EST	jC-atXP62C202P6T7d2
Method	BLASTX
NCBI GI	g3193309
BLAST score	475
E value	2.0e-47
Match length	169
% identity	57
NCBI Description	(AF069300) No definition line found [Arabidopsis thaliana]
Seq. No.	135662
Contig ID	120851_1.R1010
5'-most EST	jC-atXP62C203F16T7d2
Method	BLASTX
NCBI GI	g4587607
BLAST score	521
E value	7.0e-53
Match length	212
% identity	81

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NCBI Description	(AC006951) putative antisense basic fibroblast growth factor [Arabidopsis thaliana]
Seq. No.	135663
Contig ID	120855_1.R1010
5'-most EST	g1054093
Method	BLASTX
NCBI GI	g2979551
BLAST score	219
E value	1.0e-17
Match length	102
% identity	50
NCBI Description	(AC003680) putative receptor protein kinase [Arabidopsis thaliana]
Seq. No.	135664
Contig ID	120858_1.R1010
5'-most EST	g1054395
Method	BLASTN
NCBI GI	g2760316
BLAST score	271
E value	1.0e-151
Match length	424
% identity	98
NCBI Description	The sequence of BAC F1N21 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]
Seq. No.	135665
Contig ID	120870_1.R1010
5'-most EST	g1054409
Method	BLASTN
NCBI GI	g3080352
BLAST score	285
E value	1.0e-159
Match length	343
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T5K18 (ESSAII project)
Seq. No.	135666
Contig ID	120876_1.R1010
5'-most EST	g1054039
Method	BLASTX
NCBI GI	g4415924
BLAST score	418
E value	4.0e-41
Match length	95
% identity	83
NCBI Description	(AC006282) putative glucosyl transferase [Arabidopsis thaliana]
Seq. No.	135667
Contig ID	120877_1.R1010
5'-most EST	g2446036
Method	BLASTN
NCBI GI	g4415905
BLAST score	45

E value	6.0e-16
Match length	547
% identity	52
NCBI Description	Arabidopsis thaliana chromosome II BAC F13K3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135668
Contig ID	120879_1.R1010
5'-most EST	jC-atXP63C203I13T7s2
Method	BLASTN
NCBI GI	g2058275
BLAST score	162
E value	3.0e-86
Match length	162
% identity	100
NCBI Description	A.thaliana atran2 gene

Seq. No.	135669
Contig ID	120882_1.R1010
5'-most EST	g2446038
Method	BLASTN
NCBI GI	g4079614
BLAST score	322
E value	0.0e+00
Match length	399
% identity	94
NCBI Description	Arabidopsis thaliana chromosome I BAC F21M11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135670
Contig ID	120898_1.R1010
5'-most EST	jC-atXP63C203N14T7d2
Method	BLASTX
NCBI GI	g2460200
BLAST score	124
E value	4.0e-15
Match length	137
% identity	38
NCBI Description	(AF020833) eukaryotic translation initiation factor 3 subunit [Homo sapiens]

Seq. No.	135671
Contig ID	120904_1.R1010
5'-most EST	jC-atXP63C203O6T7d2

Seq. No.	135672
Contig ID	120910_1.R1010
5'-most EST	g2446046

Seq. No.	135673
Contig ID	120915_2.R1010
5'-most EST	jC-atXP20C116B6T7088a1

Seq. No.	135674
Contig ID	120920_1.R1010
5'-most EST	jC-atXP63C204G7T7d2

Seq. No.	135675
Contig ID	120922_1.R1010
5'-most EST	g2446061
Method	BLASTX
NCBI GI	g3269297
BLAST score	61
E value	2.0e-16
Match length	77
% identity	58
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.	135676
Contig ID	120922_2.R1010
5'-most EST	g1054096
Method	BLASTN
NCBI GI	g3046855
BLAST score	354
E value	0.0e+00
Match length	515
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSL1, complete sequence [Arabidopsis thaliana]

Seq. No.	135677
Contig ID	120944_1.R1010
5'-most EST	jC-atXP63C204K18T7d2
Method	BLASTN
NCBI GI	g4468103
BLAST score	315
E value	1.0e-177
Match length	556
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone M3E9 (ESSA project)

Seq. No.	135678
Contig ID	120946_1.R1010
5'-most EST	jC-atXP63C204K1T7d2

Seq. No.	135679
Contig ID	120948_2.R1010
5'-most EST	jC-atXP63C204K9T7d2
Method	BLASTX
NCBI GI	g1617270
BLAST score	791
E value	2.0e-84
Match length	197
% identity	73
NCBI Description	(X94624) acyl-CoA synthetase [Brassica napus]

Seq. No.	135680
Contig ID	120953_1.R1010
5'-most EST	g906756

Seq. No.	135681
Contig ID	120956_1.R1010
5'-most EST	g2446068

Method	BLASTX
NCBI GI	g2880054
BLAST score	389
E value	1.0e-37
Match length	76
% identity	96
NCBI Description	(AC002340) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	135682
Contig ID	120961_1.R1010
5'-most EST	g2446070
Method	BLASTX
NCBI GI	g3892059
BLAST score	49
E value	3.0e-36
Match length	101
% identity	79
NCBI Description	(AC002330) predicted protein of unknown function [Arabidopsis thaliana]

Seq. No.	135683
Contig ID	120961_2.R1010
5'-most EST	jC-atXP63C205D17T7d2
Method	BLASTX
NCBI GI	g3892059
BLAST score	778
E value	4.0e-83
Match length	182
% identity	88
NCBI Description	(AC002330) predicted protein of unknown function [Arabidopsis thaliana]

Seq. No.	135684
Contig ID	120969_1.R1010
5'-most EST	g2446076
Method	BLASTN
NCBI GI	g3337347
BLAST score	202
E value	1.0e-109
Match length	406
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F13P17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135685
Contig ID	120974_1.R1010
5'-most EST	jC-atXP63C205A3T7s2
Method	BLASTX
NCBI GI	g2342736
BLAST score	343
E value	3.0e-32
Match length	65
% identity	100
NCBI Description	(AC002341) unknown protein [Arabidopsis thaliana]

Seq. No.	135686
Contig ID	120979_1.R1010

5'-most EST	g1054441
Method	BLASTN
NCBI GI	g2342717
BLAST score	272
E value	1.0e-151
Match length	329
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T14G11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135687
Contig ID	120986_1.R1010
5'-most EST	jC-atXP63C205C13T7s2
Method	BLASTN
NCBI GI	g2795802
BLAST score	339
E value	0.0e+00
Match length	423
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F17A14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135688
Contig ID	120997_1.R1010
5'-most EST	g2413482

Seq. No.	135689
Contig ID	121013_1.R1010
5'-most EST	jC-atXP65C206L10T7049d1
Method	BLASTX
NCBI GI	g4585877
BLAST score	399
E value	2.0e-38
Match length	277
% identity	38
NCBI Description	(AC005850) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	135690
Contig ID	121020_1.R1010
5'-most EST	jC-atXP64C205K1T7d1
Method	BLASTN
NCBI GI	g2264312
BLAST score	333
E value	0.0e+00
Match length	384
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK16, complete sequence [Arabidopsis thaliana]

Seq. No.	135691
Contig ID	121027_1.R1010
5'-most EST	jC-atXP64C205L7T7s1

Seq. No.	135692
Contig ID	121034_1.R1010
5'-most EST	jC-atXP64C205M23T7d1
Method	BLASTX

NCBI GI g3063691
BLAST score 515
E value 2.0e-52
Match length 145
% identity 67
NCBI Description (AL022537) putative protein [Arabidopsis thaliana]

Seq. No. 135693
Contig ID 121037_1.R1010
5'-most EST g1158685

Seq. No. 135694
Contig ID 121044_1.R1010
5'-most EST g1199979

Seq. No. 135695
Contig ID 121053_1.R1010
5'-most EST g1158300

Seq. No. 135696
Contig ID 121068_1.R1010
5'-most EST g906121
Method BLASTX
NCBI GI g4432854
BLAST score 158
E value 2.0e-10
Match length 106
% identity 36
NCBI Description (AC006300) hypothetical protein [Arabidopsis thaliana]

Seq. No. 135697
Contig ID 121070_1.R1010
5'-most EST g1565842
Method BLASTX
NCBI GI g2809246
BLAST score 294
E value 1.0e-26
Match length 163
% identity 41
NCBI Description (AC002560) F24O1.15 [Arabidopsis thaliana]

Seq. No. 135698
Contig ID 121073_1.R1010
5'-most EST g1158781
Method BLASTX
NCBI GI g3337361
BLAST score 1042
E value 1.0e-114
Match length 194
% identity 97
NCBI Description (AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No. 135699
Contig ID 121074_1.R1010
5'-most EST g2413829
Method BLASTX
NCBI GI g3337361

BLAST score	224
E value	3.0e-18
Match length	63
% identity	75
NCBI Description	(AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	135700
Contig ID	121096_1.R1010
5'-most EST	jC-atXP65C206016T7s1
Method	BLASTN
NCBI GI	g4757414
BLAST score	349
E value	0.0e+00
Match length	406
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYF24, complete sequence

Seq. No.	135701
Contig ID	121105_1.R1010
5'-most EST	g2047492

Seq. No.	135702
Contig ID	121114_1.R1010
5'-most EST	g2048687
Method	BLASTN
NCBI GI	g4757412
BLAST score	336
E value	0.0e+00
Match length	482
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK23, complete sequence

Seq. No.	135703
Contig ID	121119_1.R1010
5'-most EST	g2062775
Method	BLASTX
NCBI GI	g2983814
BLAST score	511
E value	1.0e-51
Match length	197
% identity	54
NCBI Description	(AE000739) tryptophan synthase beta subunit [Aquifex aeolicus]

Seq. No.	135704
Contig ID	121124_1.R1010
5'-most EST	g936461
Method	BLASTX
NCBI GI	g2832641
BLAST score	335
E value	2.0e-31
Match length	68
% identity	97
NCBI Description	(AL021710) glycolate oxidase - like protein [Arabidopsis thaliana]

Seq. No.	135705
Contig ID	121125_1.R1010
5'-most EST	jC-atXP65C208J23T7071d1
Method	BLASTX
NCBI GI	g4741197
BLAST score	281
E value	8.0e-25
Match length	145
% identity	43
NCBI Description	(AL049746) aldose 1-epimerase-like protein [Arabidopsis thaliana]

Seq. No.	135706
Contig ID	121141_1.R1010
5'-most EST	jC-atXP66C208N17T7d1
Method	BLASTN
NCBI GI	g2564045
BLAST score	277
E value	1.0e-154
Match length	415
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K8K14, complete sequence [Arabidopsis thaliana]

Seq. No.	135707
Contig ID	121144_1.R1010
5'-most EST	g1158479
Method	BLASTX
NCBI GI	g136125
BLAST score	150
E value	1.0e-09
Match length	92
% identity	35
NCBI Description	PUTATIVE AC TRANSPOSASE (ORFA) >gi_22113_emb_CAA29005_ (X05424) ORFa [Zea mays]

Seq. No.	135708
Contig ID	121145_1.R1010
5'-most EST	g1158846
Method	BLASTX
NCBI GI	g3367537
BLAST score	147
E value	4.0e-16
Match length	106
% identity	48
NCBI Description	(AC004392) Contains similarity to ANK repeat region of Fowlpox virus BamHI-orf7 protein homolog C18F10.7 gi_485107 from Caenorhabditis elegans cosmid gb_U00049. This gene is continued from unannotated gene on BAC F19K23 gb_AC000375. [Arabid

Seq. No.	135709
Contig ID	121149_1.R1010
5'-most EST	jC-atXP66C209H10T7d1
Method	BLASTN
NCBI GI	g2828184

BLAST score	83
E value	9.0e-39
Match length	383
% identity	55
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSN9, complete sequence [Arabidopsis thaliana]

Seq. No.	135710
Contig ID	121161_1.R1010
5'-most EST	jC-atXP66C210F5T7d1

Seq. No.	135711
Contig ID	121163_1.R1010
5'-most EST	jC-atXP66C210G15T7d1

Seq. No.	135712
Contig ID	121168_1.R1010
5'-most EST	g1158526
Method	BLASTX
NCBI GI	g4455158
BLAST score	551
E value	2.0e-56
Match length	169
% identity	70
NCBI Description	(AL021687) kinase-like protein [Arabidopsis thaliana]

Seq. No.	135713
Contig ID	121173_1.R1010
5'-most EST	jC-atXP66C211F3T7d1

Seq. No.	135714
Contig ID	121181_1.R1010
5'-most EST	g1159030
Method	BLASTX
NCBI GI	g2829899
BLAST score	194
E value	1.0e-14
Match length	64
% identity	59
NCBI Description	(AC002311) similar to ripening-induced protein, gp_AJ001449_2465015 and major#latex protein, gp_X91961_1107495 [Arabidopsis thaliana]

Seq. No.	135715
Contig ID	121185_1.R1010
5'-most EST	g1159007

Seq. No.	135716
Contig ID	121191_1.R1010
5'-most EST	g1159011
Method	BLASTX
NCBI GI	g266922
BLAST score	148
E value	2.0e-09
Match length	92
% identity	35
NCBI Description	50S RIBOSOMAL PROTEIN L13 >gi_97861_pir__S23063 ribosomal

protein L13 - Staphylococcus carnosus
>gi_46912_emb_CAA45367_ (X63912) ribosomal protein L13
[Staphylococcus carnosus] >gi_383760_prf__1904196A
ribosomal protein L13 [Staphylococcus carnosus]

Seq. No.	135717
Contig ID	121192_1.R1010
5'-most EST	g1159012

Seq. No.	135718
Contig ID	121194_1.R1010
5'-most EST	g1158591
Method	BLASTX
NCBI GI	g2864615
BLAST score	367
E value	1.0e-40
Match length	138
% identity	70
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana]

Seq. No.	135719
Contig ID	121213_1.R1010
5'-most EST	g1158626
Method	BLASTN
NCBI GI	g2182285
BLAST score	116
E value	2.0e-58
Match length	384
% identity	96
NCBI Description	Sequence of BAC F5I14 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	135720
Contig ID	121221_1.R1010
5'-most EST	g1158640
Method	BLASTX
NCBI GI	g3249096
BLAST score	453
E value	4.0e-45
Match length	110
% identity	27
NCBI Description	(AC003114) Match to mRNA for importin alpha-like protein 4 (impa4) gb_Y14616 from A. thaliana. ESTs gb_N96440, gb_N37503, gb_N37498 and gb_T42198 come from this gene. [Arabidopsis thaliana]

Seq. No.	135721
Contig ID	121224_1.R1010
5'-most EST	g1159062
Method	BLASTX
NCBI GI	g1931652
BLAST score	514
E value	3.0e-52
Match length	114
% identity	87
NCBI Description	(U95973) phosphatidylinositol-4-phosphate 5-kinase isolog [Arabidopsis thaliana]

Seq. No.	135722
Contig ID	121228_1.R1010
5'-most EST	g1159067

Seq. No.	135723
Contig ID	121231_1.R1010
5'-most EST	g1159073
Method	BLASTN
NCBI GI	g3063690
BLAST score	316
E value	1.0e-178
Match length	463
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11 (ESSAII project)

Seq. No.	135724
Contig ID	121255_1.R1010
5'-most EST	g1158665

Seq. No.	135725
Contig ID	121258_1.R1010
5'-most EST	jC-atXP68C214F17T7s1
Method	BLASTN
NCBI GI	g4159705
BLAST score	520
E value	0.0e+00
Match length	610
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGD8, complete sequence

Seq. No.	135726
Contig ID	121290_1.R1010
5'-most EST	g1159161
Method	BLASTN
NCBI GI	g4757388
BLAST score	361
E value	0.0e+00
Match length	462
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F15L12, complete sequence

Seq. No.	135727
Contig ID	121294_1.R1010
5'-most EST	g3449412
Method	BLASTN
NCBI GI	g4159706
BLAST score	184
E value	5.0e-99
Match length	309
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGL6, complete sequence

Seq. No.	135728
Contig ID	121299_1.R1010
5'-most EST	g1159549

Seq. No.	135729
Contig ID	121307_1.R1010
5'-most EST	g550267
Method	BLASTN
NCBI GI	g2564046
BLAST score	309
E value	1.0e-173
Match length	349
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MGI19, complete sequence [Arabidopsis thaliana]

Seq. No.	135730
Contig ID	121338_1.R1010
5'-most EST	g1159231

Seq. No.	135731
Contig ID	121347_1.R1010
5'-most EST	g1159610
Method	BLASTX
NCBI GI	g1730107
BLAST score	174
E value	2.0e-12
Match length	108
% identity	36
NCBI Description	LEUCOANTHOCYANIDIN DIOXYGENASE (LDOX) (LEUCOANTHOCYANIDIN HYDROXYLASE) >gi_421870_pir__S33144 anthocyanidin hydroxylase - apple tree >gi_296844_emb_CAA50498_ (X71360) anthocyanidin hydroxylase [Malus sp.] >gi_4588783_gb_AAD26205.1_AF117269_1 (AF117269) anthocyanidin synthase [Malus domestica]

Seq. No.	135732
Contig ID	121359_1.R1010
5'-most EST	g2596253
Method	BLASTX
NCBI GI	g4128197
BLAST score	142
E value	1.0e-08
Match length	49
% identity	61
NCBI Description	(U75273) acyl-CoA binding protein [Arabidopsis thaliana]

Seq. No.	135733
Contig ID	121360_1.R1010
5'-most EST	jC-atXP6C90H3T7s1

Seq. No.	135734
Contig ID	121371_1.R1010
5'-most EST	g2393647
Method	BLASTN
NCBI GI	g4678705
BLAST score	238

E value	1.0e-131
Match length	322
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7 (ESSA project)

Seq. No.	135735
Contig ID	121383_1.R1010
5'-most EST	jC-atXP6C90L24T7d1
Method	BLASTN
NCBI GI	g3702737
BLAST score	283
E value	1.0e-158
Match length	327
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSN2, complete sequence [Arabidopsis thaliana]

Seq. No.	135736
Contig ID	121385_1.R1010
5'-most EST	g773541
Method	BLASTX
NCBI GI	g2213601
BLAST score	840
E value	2.0e-90
Match length	196
% identity	81
NCBI Description	(AC000348) T7N9.21 [Arabidopsis thaliana]

Seq. No.	135737
Contig ID	121391_1.R1010
5'-most EST	g2393651
Method	BLASTN
NCBI GI	g3702737
BLAST score	171
E value	3.0e-91
Match length	345
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSN2, complete sequence [Arabidopsis thaliana]

Seq. No.	135738
Contig ID	121396_1.R1010
5'-most EST	jC-atXP6C90M3T7d1

Seq. No.	135739
Contig ID	121422_1.R1010
5'-most EST	g2756858

Seq. No.	135740
Contig ID	121432_1.R1010
5'-most EST	g2393657
Method	BLASTN
NCBI GI	g4584387
BLAST score	324
E value	0.0e+00
Match length	446

% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7 (ESSA project)

Seq. No.	135741
Contig ID	121445_1.R1010
5'-most EST	jC-atXP6C91C2T7d1
Method	BLASTN
NCBI GI	g2696018
BLAST score	405
E value	0.0e+00
Match length	506
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC9, complete sequence [Arabidopsis thaliana]

Seq. No.	135742
Contig ID	121451_1.R1010
5'-most EST	jC-atXP6C91C4T7d1

Seq. No.	135743
Contig ID	121459_1.R1010
5'-most EST	jC-atXP44C170H13T7036a1
Method	BLASTX
NCBI GI	g2565436
BLAST score	218
E value	3.0e-17
Match length	115
% identity	42
NCBI Description	(AF028842) DegP protease precursor [Arabidopsis thaliana]

Seq. No.	135744
Contig ID	121484_1.R1010
5'-most EST	jC-atXP6C91E5T7d2
Method	BLASTX
NCBI GI	g4056500
BLAST score	477
E value	1.0e-53
Match length	127
% identity	94
NCBI Description	(AC005896) putative acetyltransferase [Arabidopsis thaliana]

Seq. No.	135745
Contig ID	121487_1.R1010
5'-most EST	g1565782
Method	BLASTX
NCBI GI	g1723376
BLAST score	77
E value	4.0e-18
Match length	125
% identity	44
NCBI Description	HYPOTHETICAL 20.1 KD PROTEIN IN YCF37-PSAF INTERGENIC REGION (ORF174) >gi_2147509_pir__S73113 hypothetical protein 174 - Porphyra purpurea chloroplast >gi_1276658 (U38804) ORF174 [Porphyra purpurea]

Seq. No.	135746
Contig ID	121497_1.R1010
5'-most EST	g2747887
Method	BLASTX
NCBI GI	g2827541
BLAST score	495
E value	6.0e-50
Match length	106
% identity	92
NCBI Description	(AL021635) putative protein [Arabidopsis thaliana]

Seq. No.	135747
Contig ID	121528_1.R1010
5'-most EST	jC-atXP70C221C16T7d1
Method	BLASTN
NCBI GI	g2914688
BLAST score	463
E value	0.0e+00
Match length	499
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F24L7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135748
Contig ID	121547_1.R1010
5'-most EST	jC-atXP71C221H24T7s2
Method	BLASTX
NCBI GI	g4249403
BLAST score	617
E value	3.0e-64
Match length	140
% identity	89
NCBI Description	(AC006072) unknown protein [Arabidopsis thaliana]

Seq. No.	135749
Contig ID	121565_1.R1010
5'-most EST	jC-atXP71C222J18T7089d1

Seq. No.	135750
Contig ID	121571_1.R1010
5'-most EST	jC-atXP71C222M14T7s2
Method	BLASTN
NCBI GI	g3449313
BLAST score	153
E value	4.0e-80
Match length	539
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21P3, complete sequence [Arabidopsis thaliana]

Seq. No.	135751
Contig ID	121574_1.R1010
5'-most EST	jC-atXP71C222M6T7s2
Method	BLASTN
NCBI GI	g2924651
BLAST score	274
E value	1.0e-153

Match length	349
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana]

Seq. No.	135752
Contig ID	121584_1.R1010
5'-most EST	jC-atXP71C22209T7s2

Seq. No.	135753
Contig ID	121589_1.R1010
5'-most EST	g1159394

Seq. No.	135754
Contig ID	121591_1.R1010
5'-most EST	jC-atXP72C221M23T7d1
Method	BLASTX
NCBI GI	g2078350
BLAST score	612
E value	1.0e-63
Match length	160
% identity	77
NCBI Description	(U95923) transaldolase [Solanum tuberosum]

Seq. No.	135755
Contig ID	121604_1.R1010
5'-most EST	g1216552
Method	BLASTX
NCBI GI	g2492519
BLAST score	613
E value	1.0e-72
Match length	152
% identity	93
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT 7) >gi_1395191_dbj_BAA13021_ (D86121) 26S proteasome ATPase subunit [Spinacia oleracea]

Seq. No.	135756
Contig ID	121618_1.R1010
5'-most EST	jC-atXP72C22106T7d1
Method	BLASTN
NCBI GI	g2264305
BLAST score	306
E value	1.0e-172
Match length	409
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK23, complete sequence [Arabidopsis thaliana]

Seq. No.	135757
Contig ID	121645_1.R1010
5'-most EST	jC-atXP121C95J22T7068d1
Method	BLASTX
NCBI GI	g4454032
BLAST score	189
E value	5.0e-14
Match length	131

% identity	31
NCBI Description	(AL035394) putative protein [Arabidopsis thaliana]

Seq. No.	135758
Contig ID	121722_1.R1010
5'-most EST	g2393388

Seq. No.	135759
Contig ID	121727_1.R1010
5'-most EST	jC-atXP75C226L2T7d1
Method	BLASTN
NCBI GI	g2570223
BLAST score	556
E value	0.0e+00
Match length	614
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F20D22 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135760
Contig ID	121745_1.R1010
5'-most EST	jC-atXP75C228D21T7d1
Method	BLASTX
NCBI GI	g2982464
BLAST score	225
E value	3.0e-18
Match length	112
% identity	40
NCBI Description	(AL022223) putative protein [Arabidopsis thaliana]

Seq. No.	135761
Contig ID	121756_1.R1010
5'-most EST	jC-atXP75C228F20T7d1
Method	BLASTN
NCBI GI	g3241927
BLAST score	676
E value	0.0e+00
Match length	684
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTE17, complete sequence [Arabidopsis thaliana]

Seq. No.	135762
Contig ID	121803_1.R1010
5'-most EST	jC-atXP76C226O21T7s1
Method	BLASTN
NCBI GI	g4586098
BLAST score	333
E value	0.0e+00
Match length	389
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F16J13 (ESSA project)

Seq. No.	135763
Contig ID	121809_1.R1010
5'-most EST	g2412862

Method	BLASTX
NCBI GI	g2618691
BLAST score	406
E value	1.0e-39
Match length	111
% identity	75
NCBI Description	(AC002510) putative chloroplast envelope Ca2+-ATPase [Arabidopsis thaliana]

Seq. No.	135764
Contig ID	121899_1.R1010
5'-most EST	jC-atXP76C227L17T7d1
Method	BLASTX
NCBI GI	g3776567
BLAST score	336
E value	9.0e-84
Match length	183
% identity	86
NCBI Description	(AC005388) Strong similarity to F21B7.33 gi_2809264 from A. thaliana BAC gb_AC002560. EST gb_N65119 comes from this gene. [Arabidopsis thaliana]

Seq. No.	135765
Contig ID	121903_1.R1010
5'-most EST	g1216747
Method	BLASTN
NCBI GI	g3869067
BLAST score	372
E value	0.0e+00
Match length	459
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCK7, complete sequence [Arabidopsis thaliana]

Seq. No.	135766
Contig ID	121905_1.R1010
5'-most EST	g1216749
Method	BLASTX
NCBI GI	g3912919
BLAST score	597
E value	9.0e-70
Match length	142
% identity	97
NCBI Description	(AF001308) hypothetical protein [Arabidopsis thaliana]

Seq. No.	135767
Contig ID	121926_1.R1010
5'-most EST	g2749655
Method	BLASTX
NCBI GI	g3738296
BLAST score	247
E value	7.0e-21
Match length	112
% identity	46
NCBI Description	(AC005309) hypothetical protein [Arabidopsis thaliana]

Seq. No. 135768

Contig ID	121926_2.R1010
5'-most EST	g958238
Method	BLASTN
NCBI GI	g2656026
BLAST score	458
E value	0.0e+00
Match length	526
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDF20

Seq. No.	135769
Contig ID	121944_1.R1010
5'-most EST	g1217339
Method	BLASTN
NCBI GI	g3608126
BLAST score	211
E value	1.0e-115
Match length	430
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T32F12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135770
Contig ID	121948_1.R1010
5'-most EST	g1217334
Method	BLASTX
NCBI GI	g2832618
BLAST score	512
E value	5.0e-52
Match length	138
% identity	43
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	135771
Contig ID	121955_1.R1010
5'-most EST	g2749507
Method	BLASTX
NCBI GI	g2117725
BLAST score	371
E value	2.0e-35
Match length	87
% identity	80
NCBI Description	1,4-alpha-glucan branching enzyme (EC 2.4.1.18) isoform SBE2.2 precursor - Arabidopsis thaliana (fragment) >gi_726490 (U22428) starch branching enzyme class II [Arabidopsis thaliana]

Seq. No.	135772
Contig ID	121978_1.R1010
5'-most EST	g1217107

Seq. No.	135773
Contig ID	121979_1.R1010
5'-most EST	g2749283

Seq. No. 135774

Contig ID	122004_1.R1010
5'-most EST	jC-atXP77C230H20T7d1
Method	BLASTN
NCBI GI	g2656032
BLAST score	152
E value	6.0e-80
Match length	425
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZF18

Seq. No.	135775
Contig ID	122019_1.R1010
5'-most EST	jC-atXP77C230K17T7d1

Seq. No.	135776
Contig ID	122045_1.R1010
5'-most EST	jC-atXP7C91I21T7d1

Seq. No.	135777
Contig ID	122065_1.R1010
5'-most EST	jC-atXP7C91K17T7d1
Method	BLASTX
NCBI GI	g3337352
BLAST score	250
E value	2.0e-29
Match length	138
% identity	59
NCBI Description	(AC004481) putative chromatin structural protein Supt5hp [Arabidopsis thaliana]

Seq. No.	135778
Contig ID	122067_1.R1010
5'-most EST	g3450510
Method	BLASTN
NCBI GI	g4581103
BLAST score	150
E value	1.0e-78
Match length	393
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC T24I21 genomic sequence, complete sequence

Seq. No.	135779
Contig ID	122072_1.R1010
5'-most EST	jC-atXP7C91L10T7s1
Method	BLASTX
NCBI GI	g2194119
BLAST score	445
E value	2.0e-44
Match length	86
% identity	94
NCBI Description	(AC002062) No definition line found [Arabidopsis thaliana]

Seq. No.	135780
Contig ID	122073_1.R1010
5'-most EST	jC-atXP7C91L2T7d1

Method	BLASTX
NCBI GI	g2252851
BLAST score	689
E value	1.0e-72
Match length	171
% identity	87
NCBI Description	(AF013294) No definition line found [Arabidopsis thaliana]

Seq. No.	135781
Contig ID	122076_1.R1010
5'-most EST	jC-atXP7C91M17T7d1
Method	BLASTX
NCBI GI	g4056462
BLAST score	662
E value	9.0e-70
Match length	128
% identity	96
NCBI Description	(AC005990) Strong similarity to gb_Y09876 aldehyde dehydrogenase (NAD+) from Nicotiana tabacum and a member of the aldehyde dehydrogenase family PF_00171. ESTs gb_F15117, gb_R83958 and gb_586262 come from this gene. [Arabidopsis thaliana]

Seq. No.	135782
Contig ID	122077_1.R1010
5'-most EST	g2393671
Method	BLASTX
NCBI GI	g3337352
BLAST score	59
E value	8.0e-15
Match length	70
% identity	64
NCBI Description	(AC004481) putative chromatin structural protein Supt5hp [Arabidopsis thaliana]

Seq. No.	135783
Contig ID	122083_1.R1010
5'-most EST	g2393673
Method	BLASTN
NCBI GI	g2252848
BLAST score	354
E value	0.0e+00
Match length	390
% identity	98
NCBI Description	Arabidopsis thaliana BAC TM018A10

Seq. No.	135784
Contig ID	122087_1.R1010
5'-most EST	g2393679
Method	BLASTX
NCBI GI	g2495120
BLAST score	207
E value	3.0e-16
Match length	102
% identity	40
NCBI Description	POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF >gi_1652979_dbj_BAA17896_ (D90910) thiophen and furan

oxidation protein [Synechocystis sp.]

Seq. No.	135785
Contig ID	122089_1.R1010
5'-most EST	g2393677

Seq. No.	135786
Contig ID	122094_1.R1010
5'-most EST	g2757021

Seq. No.	135787
Contig ID	122095_1.R1010
5'-most EST	jC-atXP7C91P20T7d1
Method	BLASTX
NCBI GI	g1524359
BLAST score	408
E value	7.0e-40
Match length	135
% identity	60
NCBI Description	(X98090) GTPase [Synechocystis PCC6803]

Seq. No.	135788
Contig ID	122098_1.R1010
5'-most EST	g2047552
Method	BLASTX
NCBI GI	g4581117
BLAST score	554
E value	2.0e-58
Match length	121
% identity	93
NCBI Description	(AC005825) putative ubiquitin-conjugating enzyme E2;GB:T21483 appears to be a partially-spliced transcript from this gene [Arabidopsis thaliana]

Seq. No.	135789
Contig ID	122109_1.R1010
5'-most EST	g1565823
Method	BLASTX
NCBI GI	g1709358
BLAST score	176
E value	1.0e-12
Match length	98
% identity	38
NCBI Description	NUCLEOSIDE-TRIPHOSPHATASE (NUCLEOSIDE TRIPHOSPHATE PHOSPHOHYDROLASE) (NTPASE) >gi_629638_pir__S48859 nucleoside triphosphatase - garden pea >gi_2129890_pir__S65147 nucleoside triphosphatase precursor, chromatin-associated - garden pea >gi_563612_emb_CAA83655_ (Z32743) nucleoside triphosphatase [Pisum sativum] >gi_4519173_dbj_BAA75506.1_ (AB022319) nucleoside triphosphatase (NTPase) [Pisum sativum]

Seq. No.	135790
Contig ID	122126_1.R1010
5'-most EST	g3450482
Method	BLASTN
NCBI GI	g2980787

BLAST score	282
E value	1.0e-157
Match length	459
% identity	62
NCBI Description	Arabidopsis thaliana DNA chromosome 4, P1 clone M7J2 (ESSAII project)

Seq. No.	135791
Contig ID	122131_1.R1010
5'-most EST	g2747550
Method	BLASTX
NCBI GI	g3335374
BLAST score	605
E value	6.0e-63
Match length	123
% identity	95
NCBI Description	(AC003028) glutaredoxin-like protein [Arabidopsis thaliana]

Seq. No.	135792
Contig ID	122144_1.R1010
5'-most EST	jC-atXP7C92D2T7s1
Method	BLASTX
NCBI GI	g3386565
BLAST score	218
E value	1.0e-17
Match length	69
% identity	64
NCBI Description	(AF079588) 1-aminocyclopropane-1-carboxylate oxidase [Sorghum bicolor]

Seq. No.	135793
Contig ID	122150_1.R1010
5'-most EST	g2748394
Method	BLASTX
NCBI GI	g3080441
BLAST score	185
E value	9.0e-14
Match length	96
% identity	50
NCBI Description	(AL022605) putative protein [Arabidopsis thaliana]

Seq. No.	135794
Contig ID	122152_1.R1010
5'-most EST	jC-atXP80C231L1T7d1
Method	BLASTN
NCBI GI	g4220644
BLAST score	404
E value	0.0e+00
Match length	453
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXL8, complete sequence [Arabidopsis thaliana]

Seq. No.	135795
Contig ID	122184_1.R1010
5'-most EST	g1217470
Method	BLASTN

NCBI GI	g3510344
BLAST score	203
E value	1.0e-110
Match length	495
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJG14, complete sequence [Arabidopsis thaliana]

Seq. No.	135796
Contig ID	122213_1.R1010
5'-most EST	g2047786
Method	BLASTX
NCBI GI	g2244898
BLAST score	127
E value	8.0e-07
Match length	81
% identity	50
NCBI Description	(Z97338) strong similarity to protein phosphatase 2A regulatory chain, 74K [Arabidopsis thaliana]

Seq. No.	135797
Contig ID	122274_1.R1010
5'-most EST	jC-atXP80C240I16T7d1
Method	BLASTN
NCBI GI	g2244870
BLAST score	447
E value	0.0e+00
Match length	506
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	135798
Contig ID	122298_1.R1010
5'-most EST	g396863
Method	BLASTN
NCBI GI	g4589409
BLAST score	317
E value	1.0e-178
Match length	325
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F17P19, complete sequence

Seq. No.	135799
Contig ID	122303_1.R1010
5'-most EST	jC-atXP29C138K22T7095d1
Method	BLASTX
NCBI GI	g3128184
BLAST score	151
E value	2.0e-99
Match length	204
% identity	90
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	135800
Contig ID	122303_2.R1010

5'-most EST	g1217247
Method	BLASTX
NCBI GI	g3128184
BLAST score	501
E value	1.0e-50
Match length	141
% identity	74
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	135801
Contig ID	122312_1.R1010
5'-most EST	jC-atXP12C103A10T7042a1
Method	BLASTN
NCBI GI	g3766106
BLAST score	371
E value	0.0e+00
Match length	564
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F9K20 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135802
Contig ID	122322_1.R1010
5'-most EST	g2048559

Seq. No.	135803
Contig ID	122323_1.R1010
5'-most EST	jC-atXP81C240J5T7d1
Method	BLASTX
NCBI GI	g4191791
BLAST score	368
E value	4.0e-66
Match length	129
% identity	99
NCBI Description	(AC005917) putative sf21 {Helianthus annuus} protein [Arabidopsis thaliana]

Seq. No.	135804
Contig ID	122328_1.R1010
5'-most EST	jC-atXP81C240K17T7d1
Method	BLASTX
NCBI GI	g4589123
BLAST score	293
E value	3.0e-26
Match length	125
% identity	52
NCBI Description	(AF126374) At14a protein [Arabidopsis thaliana]

Seq. No.	135805
Contig ID	122337_1.R1010
5'-most EST	g493432
Method	BLASTX
NCBI GI	g4539416
BLAST score	741
E value	2.0e-80
Match length	196
% identity	85

NCBI Description	(AL049171) 1-aminocyclopropane-1-carboxylate synthase-like protein [Arabidopsis thaliana]
Seq. No.	135806
Contig ID	122338_1.R1010
5'-most EST	g507023
Method	BLASTX
NCBI GI	g4539416
BLAST score	149
E value	9.0e-12
Match length	39
% identity	97
NCBI Description	(AL049171) 1-aminocyclopropane-1-carboxylate synthase-like protein [Arabidopsis thaliana]
Seq. No.	135807
Contig ID	122348_1.R1010
5'-most EST	jC-atXP81C240L8T7d1
Method	BLASTN
NCBI GI	g4510360
BLAST score	453
E value	0.0e+00
Match length	509
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F11F19 genomic sequence, complete sequence
Seq. No.	135808
Contig ID	122352_1.R1010
5'-most EST	jC-atXP81C240M10T7s1
Method	BLASTN
NCBI GI	g2827538
BLAST score	283
E value	1.0e-158
Match length	363
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T12H17 (ESSAII project)
Seq. No.	135809
Contig ID	122457_1.R1010
5'-most EST	g1269287
Method	BLASTN
NCBI GI	g4165340
BLAST score	276
E value	1.0e-154
Match length	463
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC F11M15 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	135810
Contig ID	122460_1.R1010
5'-most EST	jC-atXP88C241P11T7s1
Method	BLASTN
NCBI GI	g4581084
BLAST score	354

E value	0.0e+00
Match length	409
% identity	96
NCBI Description	Arabidopsis thaliana chromosome I BAC T30F21 genomic sequence, complete sequence

Seq. No.	135811
Contig ID	122482_1.R1010
5'-most EST	g1269300
Method	BLASTX
NCBI GI	g2288985
BLAST score	330
E value	1.0e-30
Match length	119
% identity	54
NCBI Description	(AC002335) hypothetical protein [Arabidopsis thaliana]

Seq. No.	135812
Contig ID	122486_1.R1010
5'-most EST	g496838
Method	BLASTX
NCBI GI	g3618316
BLAST score	224
E value	3.0e-24
Match length	99
% identity	46
NCBI Description	(AB001886) zinc finger protein [Oryza sativa]

Seq. No.	135813
Contig ID	122501_1.R1010
5'-most EST	g1269312
Method	BLASTN
NCBI GI	g4589439
BLAST score	262
E value	1.0e-145
Match length	416
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQM1, complete sequence

Seq. No.	135814
Contig ID	122555_1.R1010
5'-most EST	jC-atXP88C242G7T7d1
Method	BLASTN
NCBI GI	g4732167
BLAST score	178
E value	2.0e-95
Match length	392
% identity	92
NCBI Description	Arabidopsis thaliana BAC F28D6

Seq. No.	135815
Contig ID	122572_1.R1010
5'-most EST	g1269355
Method	BLASTX
NCBI GI	g4581143
BLAST score	234

E value	2.0e-19
Match length	109
% identity	39
NCBI Description	(AC006919) hypothetical protein [Arabidopsis thaliana]

Seq. No.	135816
Contig ID	122580_1.R1010
5'-most EST	jC-atXP123C162F21T7081d1
Method	BLASTN
NCBI GI	g3047060
BLAST score	195
E value	1.0e-105
Match length	478
% identity	95
NCBI Description	Arabidopsis thaliana BAC F7N22

Seq. No.	135817
Contig ID	122587_1.R1010
5'-most EST	g1269365
Method	BLASTN
NCBI GI	g1313929
BLAST score	268
E value	1.0e-149
Match length	624
% identity	86
NCBI Description	B.oleracea mRNA for IFA binding protein

Seq. No.	135818
Contig ID	122591_1.R1010
5'-most EST	g1269434
Method	BLASTX
NCBI GI	g3080446
BLAST score	439
E value	2.0e-43
Match length	153
% identity	63
NCBI Description	(AL022605) puative protein [Arabidopsis thaliana]

Seq. No.	135819
Contig ID	122602_1.R1010
5'-most EST	g16700
Method	BLASTX
NCBI GI	g2505874
BLAST score	639
E value	7.0e-67
Match length	123
% identity	99
NCBI Description	(Y12776) putative kinase [Arabidopsis thaliana]

Seq. No.	135820
Contig ID	122604_1.R1010
5'-most EST	g1269443
Method	BLASTN
NCBI GI	g4519195
BLAST score	147
E value	7.0e-77
Match length	417

% identity	76
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MQC12, complete sequence
Seq. No.	135821
Contig ID	122611_1.R1010
5'-most EST	jC-atXP89C242J19T7d1
Seq. No.	135822
Contig ID	122618_1.R1010
5'-most EST	jC-atXP122C159G13T7008a1
Method	BLASTX
NCBI GI	g3269285
BLAST score	394
E value	7.0e-38
Match length	215
% identity	44
NCBI Description	(AL030978) hypothetical protein [Arabidopsis thaliana]
Seq. No.	135823
Contig ID	122714_1.R1010
5'-most EST	jC-atXP89C245E18T7d1
Seq. No.	135824
Contig ID	122723_1.R1010
5'-most EST	jC-atXP8C92D17T7d1
Method	BLASTN
NCBI GI	g1707006
BLAST score	336
E value	0.0e+00
Match length	375
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T1B8 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	135825
Contig ID	122734_1.R1010
5'-most EST	g2393682
Method	BLASTX
NCBI GI	g3135277
BLAST score	157
E value	3.0e-10
Match length	119
% identity	38
NCBI Description	(AC003058) hypothetical protein [Arabidopsis thaliana] >gi_4191776 (AC005917) hypothetical protein [Arabidopsis thaliana]
Seq. No.	135826
Contig ID	122736_1.R1010
5'-most EST	g3450543
Method	BLASTN
NCBI GI	g3928074
BLAST score	317
E value	1.0e-178
Match length	366
% identity	98

DOCID: WO 0144450A1

NCBI Description	Arabidopsis thaliana chromosome II BAC T7F6 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	135827
Contig ID	122755_1.R1010
5'-most EST	jC-atXP8C92H10T7d1
Seq. No.	135828
Contig ID	122762_1.R1010
5'-most EST	jC-atXP8C92H24T7s1
Method	BLASTX
NCBI GI	g3355480
BLAST score	91
E value	1.0e-12
Match length	137
% identity	44
NCBI Description	(AC004218) Medicago nodulin N21-like protein [Arabidopsis thaliana]
Seq. No.	135829
Contig ID	122775_1.R1010
5'-most EST	jC-atXP8C92J13T7d1
Seq. No.	135830
Contig ID	122779_1.R1010
5'-most EST	jC-atXP8C92J24T7d1
Method	BLASTN
NCBI GI	g4220468
BLAST score	404
E value	0.0e+00
Match length	506
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T8O11 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	135831
Contig ID	122783_1.R1010
5'-most EST	jC-atXP8C92K11T7d1
Method	BLASTX
NCBI GI	g4056432
BLAST score	865
E value	3.0e-93
Match length	167
% identity	100
NCBI Description	(AC005990) Similar to gi_2245014 glucosyltransferase homolog from Arabidopsis thaliana chromosome 4 contig gb_Z97341. ESTs gb_T20778 and gb_AA586281 come from this gene. [Arabidopsis thaliana]
Seq. No.	135832
Contig ID	122787_1.R1010
5'-most EST	jC-atXP8C92K15T7s1
Method	BLASTN
NCBI GI	g4678340
BLAST score	400
E value	0.0e+00
Match length	468

% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone T29H11 (ESSA project)
Seq. No.	135833
Contig ID	122791_1.R1010
5'-most EST	jC-atXP8C92K1T7s1
Seq. No.	135834
Contig ID	122792_1.R1010
5'-most EST	g2393697
Method	BLASTN
NCBI GI	g2833627
BLAST score	415
E value	0.0e+00
Match length	519
% identity	96
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F17O7 complete sequence [Arabidopsis thaliana]
Seq. No.	135835
Contig ID	122797_1.R1010
5'-most EST	jC-atXP8C92L10T7s1
Method	BLASTN
NCBI GI	g2351069
BLAST score	163
E value	2.0e-86
Match length	412
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSH12, complete sequence [Arabidopsis thaliana]
Seq. No.	135836
Contig ID	122802_1.R1010
5'-most EST	g2393700
Method	BLASTN
NCBI GI	g4220632
BLAST score	383
E value	0.0e+00
Match length	513
% identity	82
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K6M13, complete sequence [Arabidopsis thaliana]
Seq. No.	135837
Contig ID	122802_2.R1010
5'-most EST	jC-atXP8C92L5T7s1
Method	BLASTX
NCBI GI	g4835236
BLAST score	387
E value	2.0e-37
Match length	133
% identity	62
NCBI Description	(AL049862) putative protein [Arabidopsis thaliana]
Seq. No.	135838
Contig ID	122804_1.R1010

5'-most EST	jC-atXP8C92L7T7s1
Method	BLASTN
NCBI GI	g3873174
BLAST score	341
E value	0.0e+00
Match length	453
% identity	96
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14N23, complete sequence [Arabidopsis thaliana]

Seq. No.	135839
Contig ID	122810_1.R1010
5'-most EST	jC-atXP8C92M22T7d1
Method	BLASTX
NCBI GI	g3892714
BLAST score	83
E value	2.0e-30
Match length	99
% identity	81
NCBI Description	(AL033545) trehalose-6-phosphate phosphatase-like protein [Arabidopsis thaliana]

Seq. No.	135840
Contig ID	122819_1.R1010
5'-most EST	g1216024
Method	BLASTN
NCBI GI	g4757678
BLAST score	35
E value	4.0e-10
Match length	123
% identity	82
NCBI Description	Arabidopsis thaliana chromosome I BAC F9H16 genomic sequence, complete sequence

Seq. No.	135841
Contig ID	122822_1.R1010
5'-most EST	jC-atXP8C92N21T7s1

Seq. No.	135842
Contig ID	122823_1.R1010
5'-most EST	g3450557
Method	BLASTX
NCBI GI	g872116
BLAST score	57
E value	7.0e-18
Match length	82
% identity	58
NCBI Description	(X79770) sti (stress inducible protein) [Glycine max]

Seq. No.	135843
Contig ID	122824_1.R1010
5'-most EST	jC-atXP104CE10D11T7b1
Method	BLASTX
NCBI GI	g872116
BLAST score	687
E value	3.0e-72
Match length	158

% identity	31
NCBI Description	(X79770) sti (stress inducible protein) [Glycine max]

Seq. No.	135844
Contig ID	122830_1.R1010
5'-most EST	jC-atXP8C92O18T7d1

Seq. No.	135845
Contig ID	122834_1.R1010
5'-most EST	jC-atXP8C92O4T7d1
Method	BLASTN
NCBI GI	g3869065
BLAST score	448
E value	0.0e+00
Match length	517
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24M7, complete sequence [Arabidopsis thaliana]

Seq. No.	135846
Contig ID	122838_1.R1010
5'-most EST	g2393712
Method	BLASTX
NCBI GI	g4388834
BLAST score	351
E value	5.0e-33
Match length	107
% identity	60
NCBI Description	(AC006528) putative disease resistance protein RPP1, 3' partial [Arabidopsis thaliana]

Seq. No.	135847
Contig ID	122838_2.R1010
5'-most EST	g2748854
Method	BLASTX
NCBI GI	g3757516
BLAST score	439
E value	2.0e-43
Match length	144
% identity	58
NCBI Description	(AC005167) putative TMV resistance protein [Arabidopsis thaliana]

Seq. No.	135848
Contig ID	122859_1.R1010
5'-most EST	g1269391
Method	BLASTN
NCBI GI	g3337347
BLAST score	446
E value	0.0e+00
Match length	462
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F13P17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135849
Contig ID	122887_1.R1010

5'-most EST	g1269399
Seq. No.	135850
Contig ID	122889_1.R1010
5'-most EST	jC-atXP90C245F10T7d2
Seq. No.	135851
Contig ID	122893_1.R1010
5'-most EST	g1269500
Method	BLASTX
NCBI GI	g2344900
BLAST score	509
E value	9.0e-52
Match length	107
% identity	91
NCBI Description	(AC002388) EREBP isolog [Arabidopsis thaliana]
Seq. No.	135852
Contig ID	122919_1.R1010
5'-most EST	g1269517
Method	BLASTX
NCBI GI	g2104951
BLAST score	307
E value	6.0e-28
Match length	88
% identity	66
NCBI Description	(U96717) MAP kinase-like protein [Selaginella lepidophylla]
Seq. No.	135853
Contig ID	122919_3.R1010
5'-most EST	jC-atXP90C245J15T7s2
Seq. No.	135854
Contig ID	122931_1.R1010
5'-most EST	g2576644
Method	BLASTX
NCBI GI	g4559366
BLAST score	508
E value	2.0e-51
Match length	99
% identity	99
NCBI Description	(AC006585) putative tyrosine transaminase [Arabidopsis thaliana]
Seq. No.	135855
Contig ID	122931_3.R1010
5'-most EST	g1054021
Method	BLASTX
NCBI GI	g4559366
BLAST score	432
E value	1.0e-42
Match length	87
% identity	99
NCBI Description	(AC006585) putative tyrosine transaminase [Arabidopsis thaliana]
Seq. No.	135856

Contig ID	122963_1.R1010
5'-most EST	jC-atXP90C246C11T7d2
Method	BLASTN
NCBI GI	g3293582
BLAST score	125
E value	7.0e-64
Match length	342
% identity	99
NCBI Description	Arabidopsis thaliana BAC T15F16

Seq. No.	135857
Contig ID	122964_1.R1010
5'-most EST	jC-atXP90C246C16T7d2

Seq. No.	135858
Contig ID	122973_1.R1010
5'-most EST	g2748419
Method	BLASTX
NCBI GI	g3068714
BLAST score	419
E value	4.0e-41
Match length	157
% identity	60
NCBI Description	(AF049236) unknown [Arabidopsis thaliana]

Seq. No.	135859
Contig ID	122992_1.R1010
5'-most EST	jC-atXP90C246G18T7d2
Method	BLASTX
NCBI GI	g2344894
BLAST score	186
E value	7.0e-36
Match length	144
% identity	65
NCBI Description	(AC002388) hypothetical protein [Arabidopsis thaliana]

Seq. No.	135860
Contig ID	123008_1.R1010
5'-most EST	g1269596
Method	BLASTX
NCBI GI	g3688188
BLAST score	726
E value	5.0e-77
Match length	141
% identity	97
NCBI Description	(AL031804) pyruvate decarboxylase-1 (Pdc1) [Arabidopsis thaliana]

Seq. No.	135861
Contig ID	123009_1.R1010
5'-most EST	g510754
Method	BLASTX
NCBI GI	g3688188
BLAST score	125
E value	1.0e-44
Match length	90
% identity	100

NCBI Description	(AL031804) pyruvate decarboxylase-1 (Pdc1) [Arabidopsis thaliana]
Seq. No.	135862
Contig ID	123020_1.R1010
5'-most EST	g2047935
Method	BLASTX
NCBI GI	g2190547
BLAST score	253
E value	1.0e-21
Match length	128
% identity	49
NCBI Description	(AC001229) ESTs gb_T43256,gb_46316,gb_N64930,gb_AA395255,gb_AA404382 come from this gene. [Arabidopsis thaliana]
Seq. No.	135863
Contig ID	123024_1.R1010
5'-most EST	g1269609
Method	BLASTN
NCBI GI	g3241925
BLAST score	309
E value	1.0e-173
Match length	342
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK9, complete sequence [Arabidopsis thaliana]
Seq. No.	135864
Contig ID	123034_1.R1010
5'-most EST	jC-atXP91C247G10T7d1
Method	BLASTN
NCBI GI	g3335331
BLAST score	372
E value	0.0e+00
Match length	404
% identity	70
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8F5 sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	135865
Contig ID	123042_1.R1010
5'-most EST	jC-atXP91C247H16T7d1
Seq. No.	135866
Contig ID	123052_1.R1010
5'-most EST	g2722056
Method	BLASTX
NCBI GI	g4835234
BLAST score	429
E value	3.0e-42
Match length	89
% identity	93
NCBI Description	(AL049862) putative cold acclimation protein [Arabidopsis thaliana]
Seq. No.	135867

Contig ID	123071_1.R1010
5'-most EST	jC-atXP92C247N12T7074d1
Method	BLASTN
NCBI GI	g3941523
BLAST score	40
E value	7.0e-13
Match length	40
% identity	100
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	135868
Contig ID	123072_1.R1010
5'-most EST	jC-atXP92C247N23T7082d1
Method	BLASTX
NCBI GI	g3426051
BLAST score	428
E value	7.0e-42
Match length	185
% identity	49
NCBI Description	(AC005168) hypothetical protein [Arabidopsis thaliana]

Seq. No.	135869
Contig ID	123073_1.R1010
5'-most EST	jC-atXP92C246O22T7052d1
Method	BLASTX
NCBI GI	g3980385
BLAST score	605
E value	3.0e-66
Match length	145
% identity	92
NCBI Description	(AC004561) putative 18 kDa class I heat shock protein [Arabidopsis thaliana]

Seq. No.	135870
Contig ID	123094_1.R1010
5'-most EST	jC-atXP92C249C14T7053d1
Method	BLASTX
NCBI GI	g2244817
BLAST score	635
E value	3.0e-66
Match length	207
% identity	69
NCBI Description	(Z97336) disease resistance protein RPS2 homolog [Arabidopsis thaliana]

Seq. No.	135871
Contig ID	123095_1.R1010
5'-most EST	jC-atXP94CG11A10T7b1
Method	BLASTN
NCBI GI	g4589440
BLAST score	159
E value	7.0e-84
Match length	582
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSD21, complete sequence

Seq. No.	135872
Contig ID	123098_1.R1010
5'-most EST	jC-atXP92C249D16T7077d1
Method	BLASTX
NCBI GI	g2129641
BLAST score	609
E value	3.0e-63
Match length	152
% identity	71
NCBI Description	major latex protein type 1 - Arabidopsis thaliana >gi_1107493_emb_CAA63026_ (X91960) major latex protein type1 [Arabidopsis thaliana]

Seq. No.	135873
Contig ID	123102_1.R1010
5'-most EST	jC-atXP92C246O18T7028d1
Method	BLASTN
NCBI GI	g4589446
BLAST score	415
E value	0.0e+00
Match length	487
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: T12B11, complete sequence

Seq. No.	135874
Contig ID	123109_1.R1010
5'-most EST	jC-atXP96C248A15T7b1
Method	BLASTN
NCBI GI	g3941523
BLAST score	52
E value	4.0e-20
Match length	52
% identity	100
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	135875
Contig ID	123111_1.R1010
5'-most EST	jC-atXP96C248C23T7b1
Method	BLASTN
NCBI GI	g3941523
BLAST score	51
E value	2.0e-19
Match length	51
% identity	100
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	135876
Contig ID	123113_1.R1010
5'-most EST	jC-atXP96C248B22T7b1
Method	BLASTX
NCBI GI	g2264368
BLAST score	457
E value	2.0e-45

Match length	91
% identity	100
NCBI Description	(AC002354) putative tetracycline transporter-like protein [Arabidopsis thaliana]

Seq. No.	135877
Contig ID	123118_1.R1010
5'-most EST	jC-atXP96C248D13T7b1
Method	BLASTN
NCBI GI	g3800746
BLAST score	50
E value	7.0e-19
Match length	50
% identity	100
NCBI Description	Cuphea pulcherrima 3-ketoacyl-ACP synthase (Kas4) mRNA, complete cds

Seq. No.	135878
Contig ID	123126_1.R1010
5'-most EST	jC-atXP96C248I16T7b1
Method	BLASTX
NCBI GI	g2072720
BLAST score	368
E value	6.0e-35
Match length	181
% identity	46
NCBI Description	(Z95121) hypothetical protein Rv3253c [Mycobacterium tuberculosis]

Seq. No.	135879
Contig ID	123128_1.R1010
5'-most EST	jC-atXP96C248J10T7b1
Method	BLASTX
NCBI GI	g2660673
BLAST score	545
E value	1.0e-55
Match length	184
% identity	26
NCBI Description	(AC002342) unknown protein [Arabidopsis thaliana]

Seq. No.	135880
Contig ID	123137_1.R1010
5'-most EST	jC-atXP96C248E9T7b1
Method	BLASTN
NCBI GI	g3461810
BLAST score	197
E value	1.0e-106
Match length	376
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T17M13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135881
Contig ID	123150_1.R1010
5'-most EST	jC-atXP96C250A3T7b1
Method	BLASTN
NCBI GI	g2656028

BLAST score	124
E value	5.0e-63
Match length	574
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNF13

Seq. No.	135882
Contig ID	123161_1.R1010
5'-most EST	jC-atXP96C250F9T7d1
Method	BLASTN
NCBI GI	g1707006
BLAST score	210
E value	1.0e-114
Match length	254
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T1B8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135883
Contig ID	123162_1.R1010
5'-most EST	jC-atXP97C249M14T7d1
Method	BLASTN
NCBI GI	g4519188
BLAST score	670
E value	0.0e+00
Match length	713
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L19, complete sequence

Seq. No.	135884
Contig ID	123163_1.R1010
5'-most EST	jC-atXP13C104C2T7042a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	57
E value	5.0e-23
Match length	61
% identity	98
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	135885
Contig ID	123165_1.R1010
5'-most EST	g1327783
Method	BLASTX
NCBI GI	g1628622
BLAST score	317
E value	3.0e-29
Match length	95
% identity	61
NCBI Description	(U72631) flavonol synthase [Arabidopsis thaliana] >gi_1805305 (U84258) flavonol synthase [Arabidopsis thaliana] >gi_1805307 (U84259) flavonol synthase [Arabidopsis thaliana] >gi_1805309 (U84260) flavonol synthase [Arabidopsis thaliana]

Seq. No.	135886
Contig ID	123173_1.R1010
5'-most EST	g1520687
Method	BLASTX
NCBI GI	g4490718
BLAST score	1123
E value	1.0e-123
Match length	261
% identity	84
NCBI Description	(AL035709) bZIP transcription factor-like protein [Arabidopsis thaliana]

Seq. No.	135887
Contig ID	123177_1.R1010
5'-most EST	g1520694
Method	BLASTX
NCBI GI	g2723477
BLAST score	499
E value	2.0e-50
Match length	167
% identity	63
NCBI Description	(D89824) GTP-binding protein [Arabidopsis thaliana]

Seq. No.	135888
Contig ID	123183_1.R1010
5'-most EST	jC-atXP97C251F20T7d1
Method	BLASTN
NCBI GI	g4589440
BLAST score	331
E value	0.0e+00
Match length	767
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSD21, complete sequence

Seq. No.	135889
Contig ID	123191_1.R1010
5'-most EST	g2393715
Method	BLASTX
NCBI GI	g4056480
BLAST score	197
E value	3.0e-19
Match length	103
% identity	54
NCBI Description	(AC005896) putative adenylate kinase [Arabidopsis thaliana]

Seq. No.	135890
Contig ID	123195_1.R1010
5'-most EST	g2596342
Method	BLASTX
NCBI GI	g3249077
BLAST score	509
E value	1.0e-51
Match length	95
% identity	100
NCBI Description	(AC004473) Similar to prunasin hydrolase precursor

gb_U50201 from Prunus serotina. ESTs gb_T21225 and gb_AA586305 come from this gene. [Arabidopsis thaliana]

Seq. No.	135891
Contig ID	123200_1.R1010
5'-most EST	jC-atXP9C93E19T7s1

Seq. No.	135892
Contig ID	123212_1.R1010
5'-most EST	g2596378
Method	BLASTN
NCBI GI	g3510343
BLAST score	144
E value	3.0e-75
Match length	341
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJC20, complete sequence [Arabidopsis thaliana]

Seq. No.	135893
Contig ID	123213_1.R1010
5'-most EST	jC-atXP9C93I10T7s1
Method	BLASTN
NCBI GI	g3510343
BLAST score	114
E value	4.0e-57
Match length	475
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJC20, complete sequence [Arabidopsis thaliana]

Seq. No.	135894
Contig ID	123217_1.R1010
5'-most EST	jC-atXP9C93I15T7d1

Seq. No.	135895
Contig ID	123229_1.R1010
5'-most EST	g2757051
Method	BLASTN
NCBI GI	g3241925
BLAST score	502
E value	0.0e+00
Match length	518
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK9, complete sequence [Arabidopsis thaliana]

Seq. No.	135896
Contig ID	123236_1.R1010
5'-most EST	g2048822
Method	BLASTN
NCBI GI	g4263373
BLAST score	231
E value	1.0e-127
Match length	479
% identity	97
NCBI Description	Arabidopsis thaliana BAC T15G18 from chromosome IV, near 25

cM, complete sequence [Arabidopsis thaliana]

Seq. No.	135897
Contig ID	123253_1.R1010
5'-most EST	jC-atXP74C223N13T7004d1
Method	BLASTX
NCBI GI	g4507229
BLAST score	517
E value	3.0e-52
Match length	160
% identity	62
NCBI Description	Succinic semialdehyde dehydrogenase >gi_3766467_emb_CAA72076_ (Y11192) NAD+ dependent succinic semialdehyde dehydrogenase [Homo sapiens] >gi_4164365_emb_CAA20248_ (AL031230) dJ73M23.2 (NAD+-dependent succinic semialdehyde dehydrogenase (SSADH, EC 1.2.1.24)) [Homo sapiens]

Seq. No.	135898
Contig ID	123253_2.R1010
5'-most EST	g2048825
Method	BLASTX
NCBI GI	g1800047
BLAST score	264
E value	6.0e-23
Match length	69
% identity	68
NCBI Description	(D90890) SUCCINATE-SEMIALDEHYDE DEHYDROGENASE (NADP+) (EC 1.2.1.16) (SSDH). [Escherichia coli]

Seq. No.	135899
Contig ID	123255_1.R1010
5'-most EST	jC-atXP9C93P6T7s1
Method	BLASTN
NCBI GI	g4589425
BLAST score	436
E value	0.0e+00
Match length	616
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBA10, complete sequence

Seq. No.	135900
Contig ID	123256_1.R1010
5'-most EST	g2756934
Method	BLASTX
NCBI GI	g1172498
BLAST score	375
E value	6.0e-45
Match length	132
% identity	81
NCBI Description	PHYTOCHROME E >gi_1076376_pir__S46313 phytochrome E - Arabidopsis thaliana >gi_452817_emb_CAA54075_ (X76610) phytochrome E [Arabidopsis thaliana]

Seq. No.	135901
Contig ID	123265_1.R1010

5'-most EST	jC-atXP122C152I4T7007a1
Method	BLASTX
NCBI GI	g4490737
BLAST score	340
E value	1.0e-31
Match length	148
% identity	55
NCBI Description	(AL035708) putative protein [Arabidopsis thaliana]

Seq. No.	135902
Contig ID	123267_1.R1010
5'-most EST	g2047780
Method	BLASTN
NCBI GI	g2341023
BLAST score	290
E value	1.0e-162
Match length	481
% identity	98
NCBI Description	Sequence of BAC F19P19 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	135903
Contig ID	123271_1.R1010
5'-most EST	jC-atXP9C94C4T7d1
Method	BLASTX
NCBI GI	g133356
BLAST score	170
E value	6.0e-12
Match length	108
% identity	35
NCBI Description	DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT (C160) >gi_66978_pir__RNBY3L DNA-directed RNA polymerase (EC 2.7.7.6) III 160K chain - yeast (Saccharomyces cerevisiae) >gi_4400_emb_CAA26905_ (X03129) RNA polymerase III largest subunit [Saccharomyces cerevisiae] >gi_1050828_emb_CAA62123_ (X90518) ORF O3254 [Saccharomyces cerevisiae] >gi_1164961_emb_CAA64036_ (X94335) YOR3254c [Saccharomyces cerevisiae] >gi_1420309_emb_CAA99314_ (Z75024) ORF YOR116c [Saccharomyces cerevisiae]

Seq. No.	135904
Contig ID	123274_1.R1010
5'-most EST	g2048831
Method	BLASTN
NCBI GI	g3869070
BLAST score	327
E value	0.0e+00
Match length	395
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MGO3, complete sequence [Arabidopsis thaliana]

Seq. No.	135905
Contig ID	123277_1.R1010
5'-most EST	jC-atXP9C94E17T7d1
Method	BLASTX
NCBI GI	g2618729

BLAST score	217
E value	4.0e-17
Match length	84
% identity	56
NCBI Description	(U49076) IAA20 [Arabidopsis thaliana]

Seq. No.	135906
Contig ID	123280_1.R1010
5'-most EST	jC-atXP9C94F11T7d1
Method	BLASTX
NCBI GI	g4263779
BLAST score	139
E value	3.0e-37
Match length	96
% identity	92
NCBI Description	(AC006068) hypothetical protein [Arabidopsis thaliana]

Seq. No.	135907
Contig ID	123282_1.R1010
5'-most EST	jC-atXP9C94F4T7d1
Method	BLASTX
NCBI GI	g2129562
BLAST score	114
E value	8.0e-13
Match length	64
% identity	58
NCBI Description	class III ADH, glutathione-dependent formaldehyde dehydrogenase. - Arabidopsis thaliana >gi_1143388_emb_CAA57973_ (X82647) class III ADH, glutathione-dependent formaldehyde dehydrogenase. [Arabidopsis thaliana]

Seq. No.	135908
Contig ID	123287_1.R1010
5'-most EST	g2048840

Seq. No.	135909
Contig ID	123290_1.R1010
5'-most EST	jC-atXP9C94I21T7s1
Method	BLASTN
NCBI GI	g3461834
BLAST score	206
E value	1.0e-112
Match length	326
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC T9I4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135910
Contig ID	123292_1.R1010
5'-most EST	g2048843
Method	BLASTN
NCBI GI	g4589122
BLAST score	261
E value	1.0e-145
Match length	300
% identity	96

NCBI Description	Arabidopsis thaliana At14a protein mRNA, complete cds
Seq. No.	135911
Contig ID	123293_1.R1010
5'-most EST	g1158838
Method	BLASTX
NCBI GI	g2244762
BLAST score	419
E value	3.0e-41
Match length	100
% identity	78
NCBI Description	(Z97335) major latex protein [Arabidopsis thaliana]
Seq. No.	135912
Contig ID	123297_1.R1010
5'-most EST	jC-atXP9C94J10T7s1
Method	BLASTX
NCBI GI	g3819697
BLAST score	365
E value	7.0e-35
Match length	83
% identity	88
NCBI Description	(AJ009608) BnMAP4K alpha1 [Brassica napus]
Seq. No.	135913
Contig ID	123302_1.R1010
5'-most EST	jC-atXP9C94L4T7d1
Method	BLASTX
NCBI GI	g3461847
BLAST score	98
E value	3.0e-32
Match length	75
% identity	99
NCBI Description	(AC005315) putative ubiquitin [Arabidopsis thaliana]
Seq. No.	135914
Contig ID	123371_1.R1010
5'-most EST	jC-atXmonuni10Ah04a1
Method	BLASTN
NCBI GI	g4159707
BLAST score	339
E value	0.0e+00
Match length	451
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJK13, complete sequence
Seq. No.	135915
Contig ID	123393_1.R1010
5'-most EST	g2062928
Method	BLASTN
NCBI GI	g3449329
BLAST score	216
E value	1.0e-118
Match length	437
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MDH9, complete sequence [Arabidopsis thaliana]

Seq. No.	135916
Contig ID	123536_1.R1010
5'-most EST	jC-atXmonuni10Da06a1
Method	BLASTN
NCBI GI	g3128142
BLAST score	341
E value	0.0e+00
Match length	431
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQN23, complete sequence [Arabidopsis thaliana]

Seq. No.	135917
Contig ID	124090_1.R1010
5'-most EST	jC-atXmonuni25Da05b1
Method	BLASTN
NCBI GI	g3327388
BLAST score	258
E value	1.0e-143
Match length	451
% identity	6
NCBI Description	Arabidopsis thaliana chromosome II BAC T12J2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135918
Contig ID	124156_1.R1010
5'-most EST	jC-atXP22C122C14T7055a1
Method	BLASTN
NCBI GI	g4589950
BLAST score	393
E value	0.0e+00
Match length	421
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T28P16 genomic sequence, complete sequence

Seq. No.	135919
Contig ID	124212_1.R1010
5'-most EST	jC-atXP24C123M15T7063d1
Method	BLASTN
NCBI GI	g4580454
BLAST score	48
E value	1.0e-17
Match length	141
% identity	49
NCBI Description	Arabidopsis thaliana chromosome II BAC T2G17 genomic sequence, complete sequence

Seq. No.	135920
Contig ID	124276_1.R1010
5'-most EST	jC-atXmonuni26Ad04a1
Method	BLASTN
NCBI GI	g4263694
BLAST score	210
E value	1.0e-114

Match length	418
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F22D22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135921
Contig ID	124317_1.R1010
5'-most EST	jC-atXmonuni26Af06a1
Method	BLASTX
NCBI GI	g4262180
BLAST score	301
E value	2.0e-27
Match length	63
% identity	90
NCBI Description	(AC005508) 29621 [Arabidopsis thaliana]

Seq. No.	135922
Contig ID	124330_1.R1010
5'-most EST	jC-atXP5C90E1T7088a1
Method	BLASTN
NCBI GI	g3869065
BLAST score	360
E value	0.0e+00
Match length	693
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24M7, complete sequence [Arabidopsis thaliana]

Seq. No.	135923
Contig ID	124367_1.R1010
5'-most EST	jC-atXmonuni26Ba05a1
Method	BLASTX
NCBI GI	g4646203
BLAST score	389
E value	2.0e-37
Match length	153
% identity	48
NCBI Description	(AC007230) Belongs to PF_00026 Eukaryotic aspartyl protease family. [Arabidopsis thaliana]

Seq. No.	135924
Contig ID	124381_1.R1010
5'-most EST	jC-atXmonuni26Cc05a1
Method	BLASTN
NCBI GI	g3869071
BLAST score	449
E value	0.0e+00
Match length	453
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MIL23, complete sequence [Arabidopsis thaliana]

Seq. No.	135925
Contig ID	124396_1.R1010
5'-most EST	g3449566
Method	BLASTN
NCBI GI	g4678315

BLAST score	323
E value	0.0e+00
Match length	435
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone T17F15 (ESSA project)

Seq. No.	135926
Contig ID	124429_1.R1010
5'-most EST	g2749477

Seq. No.	135927
Contig ID	124442_1.R1010
5'-most EST	jC-atXmonuni26Be02a1
Method	BLASTN
NCBI GI	g4096078
BLAST score	40
E value	4.0e-13
Match length	64
% identity	91
NCBI Description	Arabidopsis thaliana chromosome I BAC T5A14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135928
Contig ID	124948_1.R1010
5'-most EST	jC-atXmonuni27Ag06a1
Method	BLASTX
NCBI GI	g2341032
BLAST score	561
E value	1.0e-57
Match length	116
% identity	94
NCBI Description	(AC000104) EST gb_ATTS0956 comes from this gene. [Arabidopsis thaliana]

Seq. No.	135929
Contig ID	125229_1.R1010
5'-most EST	g496411
Method	BLASTN
NCBI GI	g2264303
BLAST score	317
E value	1.0e-178
Match length	365
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBB18, complete sequence [Arabidopsis thaliana]

Seq. No.	135930
Contig ID	125409_1.R1010
5'-most EST	jC-atXP20728r2
Method	BLASTX
NCBI GI	g4581109
BLAST score	499
E value	3.0e-50
Match length	147
% identity	65
NCBI Description	(AC005825) unknown protein [Arabidopsis thaliana]

Seq. No.	135931
Contig ID	125410_1.R1010
5'-most EST	jC-atXP20725r2
Method	BLASTX
NCBI GI	g4416307
BLAST score	429
E value	2.0e-46
Match length	131
% identity	78
NCBI Description	(AF105716) hypothetical protein [Zea mays]

Seq. No.	135932
Contig ID	125411_1.R1010
5'-most EST	jC-atXP20608r2
Method	BLASTN
NCBI GI	g413796
BLAST score	46
E value	2.0e-16
Match length	46
% identity	100
NCBI Description	Cloning vector pMAMneoBlue, complete sequence

Seq. No.	135933
Contig ID	125412_1.R1010
5'-most EST	jC-atXP20581r2
Method	BLASTN
NCBI GI	g2147
BLAST score	42
E value	5.0e-14
Match length	42
% identity	100
NCBI Description	S.scrofa UABP-2 gene exon

Seq. No.	135934
Contig ID	125413_1.R1010
5'-most EST	jC-atXP20075r2
Method	BLASTX
NCBI GI	g2982285
BLAST score	327
E value	9.0e-30
Match length	63
% identity	78
NCBI Description	(AF051227) GASA5-like protein [Picea mariana]

Seq. No.	135935
Contig ID	125430_1.R1010
5'-most EST	jC-atXP117C141024T7a1
Method	BLASTX
NCBI GI	g3445210
BLAST score	307
E value	1.0e-34
Match length	166
% identity	55
NCBI Description	(AC004786) putative flavonol 3-o-glucosyltransferase [Arabidopsis thaliana]

Seq. No.	135936
Contig ID	125488_1.R1010
5'-most EST	jC-atXP117C140C21T7a1

Seq. No.	135937
Contig ID	125507_1.R1010
5'-most EST	jC-atXP112C130P5T7d2
Method	BLASTX
NCBI GI	g3834323
BLAST score	324
E value	1.0e-29
Match length	243
% identity	34
NCBI Description	(AC005679) F9K20.25 [Arabidopsis thaliana]

Seq. No.	135938
Contig ID	125508_1.R1010
5'-most EST	jC-atXP112C130O23T7d2
Method	BLASTN
NCBI GI	g2582640
BLAST score	39
E value	3.0e-12
Match length	39
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	135939
Contig ID	125509_1.R1010
5'-most EST	jC-atXP112C130O14T7d2
Method	BLASTX
NCBI GI	g2244765
BLAST score	192
E value	3.0e-14
Match length	110
% identity	39
NCBI Description	(Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No.	135940
Contig ID	125520_1.R1010
5'-most EST	jC-atXP71C222P11T7030d1
Method	BLASTN
NCBI GI	g1785673
BLAST score	319
E value	1.0e-179
Match length	395
% identity	95
NCBI Description	A.thaliana mitochondrial genome, part A

Seq. No.	135941
Contig ID	125530_1.R1010
5'-most EST	jC-atXP112C129F3T7d2
Method	BLASTX
NCBI GI	g4587587
BLAST score	286
E value	3.0e-25
Match length	186

% identity	38
NCBI Description	(AC007232) unknown protein [Arabidopsis thaliana]

Seq. No.	135942
Contig ID	125541_1.R1010
5'-most EST	jC-atXP112C129A21T7d2
Method	BLASTX
NCBI GI	g2702365
BLAST score	178
E value	1.0e-12
Match length	116
% identity	40
NCBI Description	(AF036706) similar to S. cerevisiae Lpg15p (GB:U43281) [Caenorhabditis elegans]

Seq. No.	135943
Contig ID	125542_1.R1010
5'-most EST	jC-atXP112C128I19T7d2
Method	BLASTX
NCBI GI	g133321
BLAST score	184
E value	3.0e-13
Match length	93
% identity	31
NCBI Description	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1) >gi_279534_pir__JDMU1 DNA-directed RNA polymerase (EC 2.7.7.6) II largest chain (version 1) - Arabidopsis thaliana >gi_16505_emb_CAA37130_ (X52954) RNA polymerase II [Arabidopsis thaliana]

Seq. No.	135944
Contig ID	125548_1.R1010
5'-most EST	jC-atXP112C127P7T7d2
Method	BLASTX
NCBI GI	g3201628
BLAST score	833
E value	1.0e-103
Match length	245
% identity	76
NCBI Description	(AC004669) unknown protein [Arabidopsis thaliana]

Seq. No.	135945
Contig ID	125564_1.R1010
5'-most EST	jC-atXP112C127A21T7d2
Method	BLASTN
NCBI GI	g4263762
BLAST score	81
E value	3.0e-37
Match length	164
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC F17L24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	135946
Contig ID	125567_1.R1010
5'-most EST	jC-atXP112C126O20T7d2
Method	BLASTX

NCBI GI	g3021274
BLAST score	1089
E value	1.0e-119
Match length	216
% identity	73
NCBI Description	(AL022347) serine/threonine kinase - like protein [Arabidopsis thaliana]

Seq. No.	135947
Contig ID	125569_1.R1010
5'-most EST	jC-atXP112C125P3T7a1
Method	BLASTN
NCBI GI	g2832639
BLAST score	479
E value	0.0e+00
Match length	543
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28J12 (ESSAII project)

Seq. No.	135948
Contig ID	125576_1.R1010
5'-most EST	jC-atXN611170r2
Method	BLASTX
NCBI GI	g4455155
BLAST score	166
E value	4.0e-11
Match length	43
% identity	74
NCBI Description	(AL022023) EF-1 alpha-like protein (fragment) [Arabidopsis thaliana]

Seq. No.	135949
Contig ID	125578_1.R1010
5'-most EST	jC-atXN606176r2
Method	BLASTN
NCBI GI	g1944204
BLAST score	44
E value	3.0e-15
Match length	96
% identity	94
NCBI Description	Oryza sativa mRNA for RicMT, complete cds

Seq. No.	135950
Contig ID	125579_2.R1010
5'-most EST	jC-atXN605212r2
Method	BLASTX
NCBI GI	g3551954
BLAST score	237
E value	3.0e-19
Match length	132
% identity	39
NCBI Description	(AF082030) senescence-associated protein 5 [Hemerocallis hybrid cultivar]

Seq. No.	135951
Contig ID	125580_1.R1010

5'-most EST	jC-atXN594206r2
Method	BLASTN
NCBI GI	g902585
BLAST score	45
E value	1.0e-15
Match length	77
% identity	90
NCBI Description	Zea mays clone MubG9 ubiquitin gene, complete cds

Seq. No.	135952
Contig ID	125581_1.R1010
5'-most EST	jC-atXN585214r2

Seq. No.	135953
Contig ID	125582_1.R1010
5'-most EST	jC-atXN579208r2

Seq. No.	135954
Contig ID	125583_2.R1010
5'-most EST	jC-atXN563193d2
Method	BLASTX
NCBI GI	g3941500
BLAST score	184
E value	3.0e-13
Match length	64
% identity	61
NCBI Description	(AF062904) putative transcription factor [Arabidopsis thaliana]

Seq. No.	135955
Contig ID	125584_2.R1010
5'-most EST	jC-atXN560189r2
Method	BLASTN
NCBI GI	g209241
BLAST score	34
E value	4.0e-09
Match length	53
% identity	100
NCBI Description	R6K synthetic cosmid vector

Seq. No.	135956
Contig ID	125585_1.R1010
5'-most EST	jC-atXN458168d2
Method	BLASTX
NCBI GI	g2160144
BLAST score	299
E value	1.0e-26
Match length	236
% identity	42
NCBI Description	(AC000375) Strong similarity to Arabidopsis oligopeptide transporter (gb_X77503). [Arabidopsis thaliana]

Seq. No.	135957
Contig ID	125586_1.R1010
5'-most EST	jC-atXN457160r2
Method	BLASTN
NCBI GI	g58124

BLAST score	35
E value	1.0e-09
Match length	55
% identity	100
NCBI Description	Cloning vector pGEM3 (pJMSP-0) polylinker sequence (SP6 polymerase transcription vector)

Seq. No.	135958
Contig ID	125587_1.R1010
5'-most EST	jC-atXN455156r2

Seq. No.	135959
Contig ID	125588_1.R1010
5'-most EST	jC-atXN451155a2
Method	BLASTN
NCBI GI	g22246
BLAST score	367
E value	0.0e+00
Match length	373
% identity	99
NCBI Description	Z. mays, cultivar COTX amplified 451 region DNA

Seq. No.	135960
Contig ID	125589_1.R1010
5'-most EST	jC-atXN449157a2
Method	BLASTN
NCBI GI	g209392
BLAST score	44
E value	3.0e-15
Match length	148
% identity	89
NCBI Description	Cloning vector PSU2719 DNA

Seq. No.	135961
Contig ID	125590_1.R1010
5'-most EST	jC-atXN447163r2

Seq. No.	135962
Contig ID	125591_1.R1010
5'-most EST	jC-atXN445148d2

Seq. No.	135963
Contig ID	125592_1.R1010
5'-most EST	jC-atXN444151r2

Seq. No.	135964
Contig ID	125593_1.R1010
5'-most EST	jC-atXN443152r2

Seq. No.	135965
Contig ID	125594_2.R1010
5'-most EST	jC-atXN442143r1

Seq. No.	135966
Contig ID	125595_1.R1010
5'-most EST	jC-atXN439146d2

Seq. No.	135967
Contig ID	125596_1.R1010
5'-most EST	jC-atXN438161r2

Seq. No.	135968
Contig ID	125597_1.R1010
5'-most EST	jC-atXN414104d2
Method	BLASTX
NCBI GI	g3420052
BLAST score	420
E value	7.0e-41
Match length	143
% identity	61
NCBI Description	(AC004680) putative ubiqinone reductase [Arabidopsis thaliana]

Seq. No.	135969
Contig ID	125598_1.R1010
5'-most EST	jC-atXN40990a2
Method	BLASTN
NCBI GI	g493617
BLAST score	41
E value	2.0e-13
Match length	80
% identity	99
NCBI Description	Synthetic plasimd pHSG399 DNA

Seq. No.	135970
Contig ID	125599_1.R1010
5'-most EST	jC-atXN29949r1
Method	BLASTN
NCBI GI	g209101
BLAST score	34
E value	3.0e-09
Match length	34
% identity	100
NCBI Description	Shuttle vector consisting of DNA from E.coli and yeast. >gi_345214_emb_A01519.1_A01519 Nucleotide sequence of multilinker (modified from pUC18) >gi_1250059_gb_I15151_I15151 Sequence 22 from patent US 5460941 >gi_3409283_gb_I89343_I89343 Sequence 4 from patent US

Seq. No.	135971
Contig ID	125600_1.R1010
5'-most EST	jC-atXN29084d1
Method	BLASTN
NCBI GI	g3819625
BLAST score	60
E value	9.0e-25
Match length	99
% identity	96
NCBI Description	Hordeum vulgare genomic DNA fragment; clone MWG2217

Seq. No.	135972
Contig ID	125601_1.R1010
5'-most EST	jC-atXN25759a1

Seq. No.	135973
Contig ID	125602_1.R1010
5'-most EST	jC-atXN32830d1

Seq. No.	135974
Contig ID	125604_1.R1010
5'-most EST	jC-atXN303164r1
Method	BLASTX
NCBI GI	g2956717
BLAST score	90
E value	5.4e-02
Match length	95
% identity	75
NCBI Description	(Y09722) beta-carotene hydroxylase 2 [Capsicum annuum]

Seq. No.	135975
Contig ID	125606_1.R1010
5'-most EST	jC-atXN29582r1
Method	BLASTN
NCBI GI	g4538840
BLAST score	36
E value	3.0e-10
Match length	56
% identity	100
NCBI Description	Sus scrofa V-ATPase gene, exon

Seq. No.	135976
Contig ID	125607_1.R1010
5'-most EST	jC-atXN29241a1
Method	BLASTN
NCBI GI	g1333680
BLAST score	49
E value	4.0e-18
Match length	61
% identity	95
NCBI Description	Cloning vector pKF19k DNA, complete sequence

Seq. No.	135977
Contig ID	125608_1.R1010
5'-most EST	jC-atXN288113r1

Seq. No.	135978
Contig ID	125609_2.R1010
5'-most EST	jC-atXN28761r1

Seq. No.	135979
Contig ID	125610_2.R1010
5'-most EST	jC-atXN28680f1
Method	BLASTN
NCBI GI	g209392
BLAST score	38
E value	1.0e-11
Match length	129
% identity	95
NCBI Description	Cloning vector PSU2719 DNA

Seq. No.	135980
Contig ID	125611_1.R1010
5'-most EST	jC-atXN28593r1
Method	BLASTN
NCBI GI	g58124
BLAST score	36
E value	3.0e-10
Match length	55
% identity	100
NCBI Description	Cloning vector pGEM3 (pJMSP-0) polylinker sequence (SP6 polymerase transcription vector)

Seq. No.	135981
Contig ID	125612_1.R1010
5'-most EST	jC-atXN27742r1
Method	BLASTX
NCBI GI	g2130082
BLAST score	230
E value	1.0e-18
Match length	212
% identity	6
NCBI Description	protein kinase Xa21 (EC 2.7.1.-) - rice >gi_1122443 (U37133) receptor kinase-like protein [Oryza sativa] >gi_2586085 (U72723) receptor kinase-like protein [Oryza longistaminata] >gi_1586408_prf__2203451A receptor kinase-like protein [Oryza sativa]

Seq. No.	135982
Contig ID	125613_1.R1010
5'-most EST	jC-atXN26870a1

Seq. No.	135983
Contig ID	125615_1.R1010
5'-most EST	jC-atXN264100r2

Seq. No.	135984
Contig ID	125617_1.R1010
5'-most EST	jC-atXN25277a1

Seq. No.	135985
Contig ID	125618_1.R1010
5'-most EST	jC-atXN24756f2

Seq. No.	135986
Contig ID	125619_1.R1010
5'-most EST	jC-atXN23948r2
Method	BLASTX
NCBI GI	g3056586
BLAST score	270
E value	3.0e-23
Match length	130
% identity	42
NCBI Description	(AC004255) T1F9.7 [Arabidopsis thaliana]

Seq. No.	135987
Contig ID	125620_2.R1010
5'-most EST	jC-atXN23846r2

Seq. No. 135988
Contig ID 125621_1.R1010
5'-most EST jC-atXN23744r2

Seq. No. 135989
Contig ID 125622_1.R1010
5'-most EST jC-atXN23439r2

Seq. No. 135990
Contig ID 125623_1.R1010
5'-most EST jC-atXN223219d2

Seq. No. 135991
Contig ID 125624_1.R1010
5'-most EST jC-atXN21233d1

Seq. No. 135992
Contig ID 125625_2.R1010
5'-most EST jC-atXN211218d2

Seq. No. 135993
Contig ID 125626_1.R1010
5'-most EST jC-atXN120232r2

Seq. No. 135994
Contig ID 125627_1.R1010
5'-most EST jC-atXN114228r2

Seq. No. 135995
Contig ID 125628_1.R1010
5'-most EST jC-atXN110229d2

Seq. No. 135996
Contig ID 125629_1.R1010
5'-most EST jC-atXN107234r1

Seq. No. 135997
Contig ID 125631_1.R1010
5'-most EST jC-atXN10134d1

Seq. No. 135998
Contig ID 125632_1.R1010
5'-most EST jC-atXB944r2

Seq. No. 135999
Contig ID 125634_1.R1010
5'-most EST jC-atXB833r2

Seq. No. 136000
Contig ID 125635_1.R1010
5'-most EST jC-atXB823r2

Seq. No. 136001
Contig ID 125636_1.R1010
5'-most EST jC-atXB815d2

Seq. No.	136002
Contig ID	125637_1.R1010
5'-most EST	jC-atXB810r2
Seq. No.	136003
Contig ID	125638_1.R1010
5'-most EST	jC-atXB805r2
Seq. No.	136004
Contig ID	125640_1.R1010
5'-most EST	jC-atXB761r2
Seq. No.	136005
Contig ID	125641_1.R1010
5'-most EST	jC-atXB743d2
Seq. No.	136006
Contig ID	125642_1.R1010
5'-most EST	jC-atXB708d2
Seq. No.	136007
Contig ID	125643_1.R1010
5'-most EST	jC-atXB632r2
Method	BLASTN
NCBI GI	g22103
BLAST score	42
E value	5.0e-14
Match length	214
% identity	83
NCBI Description	Zea mays A2 gene
Seq. No.	136008
Contig ID	125645_1.R1010
5'-most EST	jC-atXB304r2
Seq. No.	136009
Contig ID	125646_1.R1010
5'-most EST	jC-atXA34r2
Method	BLASTX
NCBI GI	g2895866
BLAST score	137
E value	1.0e-07
Match length	95
% identity	83
NCBI Description	(AF045770) methylmalonate semi-aldehyde dehydrogenase [Oryza sativa]
Seq. No.	136010
Contig ID	125647_1.R1010
5'-most EST	jC-atXA12f2
Method	BLASTN
NCBI GI	g58275
BLAST score	54
E value	3.0e-21
Match length	128
% identity	95
NCBI Description	Plasmid vector pSU

Seq. No.	136011
Contig ID	125652_1.R1010
5'-most EST	jC-atXP86CG9H6T7d2
Method	BLASTX
NCBI GI	g4512715
BLAST score	744
E value	6.0e-79
Match length	191
% identity	77
NCBI Description	(AC006569) unknown protein [Arabidopsis thaliana]

Seq. No.	136012
Contig ID	125656_2.R1010
5'-most EST	jC-atXP86CG9H4T7d2
Method	BLASTN
NCBI GI	g4220641
BLAST score	672
E value	0.0e+00
Match length	924
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUL3, complete sequence [Arabidopsis thaliana]

Seq. No.	136013
Contig ID	125682_1.R1010
5'-most EST	jC-atXP86CG9F8T7d2
Method	BLASTX
NCBI GI	g3643604
BLAST score	203
E value	1.0e-135
Match length	267
% identity	14
NCBI Description	(AC005395) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	136014
Contig ID	125761_1.R1010
5'-most EST	jC-atXP86CG4H3T7d2
Method	BLASTX
NCBI GI	g584794
BLAST score	363
E value	2.0e-90
Match length	235
% identity	78
NCBI Description	PLASMA MEMBRANE ATPASE 1 (PROTON PUMP) >gi_282953_pir__A41779 H+-transporting ATPase (EC 3.6.1.35) - curled-leaved tobacco >gi_170289 (M80489) plasma membrane H+ ATPase [Nicotiana plumbaginifolia]

Seq. No.	136015
Contig ID	125771_1.R1010
5'-most EST	jC-atXP86CG4G1T7d2
Method	BLASTX
NCBI GI	g2827630
BLAST score	68
E value	7.0e-86

Match length	219
% identity	79
NCBI Description	(AL021636) putative protein [Arabidopsis thaliana]

Seq. No.	136016
Contig ID	125784_1.R1010
5'-most EST	jC-atXP86CG10D4T7d2
Method	BLASTN
NCBI GI	g4467358
BLAST score	44
E value	3.0e-15
Match length	44
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for Phosphatidylinositol 4-Kinase

Seq. No.	136017
Contig ID	125840_1.R1010
5'-most EST	jC-atXP34C153A23T7a1
Method	BLASTN
NCBI GI	g3941523
BLAST score	45
E value	8.0e-16
Match length	49
% identity	98
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	136018
Contig ID	125848_1.R1010
5'-most EST	jC-atXP34C150P21T7a1
Method	BLASTX
NCBI GI	g2462834
BLAST score	145
E value	4.0e-12
Match length	92
% identity	47
NCBI Description	(AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No.	136019
Contig ID	125929_1.R1010
5'-most EST	jC-atXP71C222O9T7061d1
Method	BLASTX
NCBI GI	g2077943
BLAST score	393
E value	9.0e-38
Match length	158
% identity	49
NCBI Description	(D88672) phospholipase D [Rattus norvegicus]

Seq. No.	136020
Contig ID	125937_1.R1010
5'-most EST	jC-atXP32C147L2T7d2
Method	BLASTX
NCBI GI	g4432857
BLAST score	317
E value	7.0e-29
Match length	151

% identity	41
NCBI Description	(AC006300) hypothetical protein [Arabidopsis thaliana]
Seq. No.	136021
Contig ID	125943_1.R1010
5'-most EST	jC-atXP32C147K8T7d2
Seq. No.	136022
Contig ID	125944_1.R1010
5'-most EST	jC-atXP32C147H10T7d2
Method	BLASTN
NCBI GI	g2342717
BLAST score	66
E value	2.0e-28
Match length	78
% identity	10
NCBI Description	Arabidopsis thaliana chromosome II BAC T14G11 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	136023
Contig ID	125951_1.R1010
5'-most EST	jC-atXP32C147J9T7d2
Method	BLASTN
NCBI GI	g1946354
BLAST score	288
E value	1.0e-161
Match length	654
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T06B20 genomic sequence, complete sequence
Seq. No.	136024
Contig ID	125966_1.R1010
5'-most EST	jC-atXP32C147F21T7d2
Method	BLASTN
NCBI GI	g4589421
BLAST score	167
E value	1.0e-88
Match length	606
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K5K13, complete sequence
Seq. No.	136025
Contig ID	126017_1.R1010
5'-most EST	jC-atXP31C146J10T7d2
Method	BLASTN
NCBI GI	g2656032
BLAST score	33
E value	9.0e-09
Match length	104
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZF18
Seq. No.	136026
Contig ID	126040_1.R1010

5'-most EST	jC-atXP31C145O4T7d2
Method	BLASTN
NCBI GI	g3510347
BLAST score	332
E value	0.0e+00
Match length	533
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]

Seq. No.	136027
Contig ID	126078_1.R1010
5'-most EST	jC-atXP31C144G24T7d2
Method	BLASTX
NCBI GI	g3912921
BLAST score	187
E value	9.0e-14
Match length	154
% identity	37
NCBI Description	(AF001308) G/T DNA mismatch repair enzyme [Arabidopsis thaliana]

Seq. No.	136028
Contig ID	126158_1.R1010
5'-most EST	jC-atXP29C135M10T7005d1
Method	BLASTX
NCBI GI	g4455363
BLAST score	468
E value	2.0e-68
Match length	188
% identity	78
NCBI Description	(AL035524) Medicago nodulin N21-like protein [Arabidopsis thaliana]

Seq. No.	136029
Contig ID	126168_1.R1010
5'-most EST	jC-atXP29C135J16T7065d1
Method	BLASTX
NCBI GI	g2443883
BLAST score	625
E value	5.0e-65
Match length	184
% identity	73
NCBI Description	(AC002294) Similar to RPS-2 disease resistance protein [Arabidopsis thaliana]

Seq. No.	136030
Contig ID	126250_2.R1010
5'-most EST	g2597732
Method	BLASTN
NCBI GI	g2656031
BLAST score	239
E value	1.0e-132
Match length	382
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC20

Seq. No.	136031
Contig ID	126268_1.R1010
5'-most EST	jC-atXP112C130O23T7a1
Method	BLASTX
NCBI GI	g3150404
BLAST score	97
E value	5.0e-03
Match length	95
% identity	12
NCBI Description	(AC004165) putative mitochondrial carrier protein [Arabidopsis thaliana]

Seq. No.	136032
Contig ID	126278_1.R1010
5'-most EST	jC-atXP112C129O22T7a1

Seq. No.	136033
Contig ID	126288_1.R1010
5'-most EST	jC-atXP112C129G21T7a1
Method	BLASTN
NCBI GI	g2689438
BLAST score	569
E value	0.0e+00
Match length	593
% identity	94
NCBI Description	Arabidopsis thaliana BAC F24O1 chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	136034
Contig ID	126342_1.R1010
5'-most EST	jC-atXP98CH8D1T7b1
Method	BLASTX
NCBI GI	g2244973
BLAST score	543
E value	2.0e-55
Match length	169
% identity	72
NCBI Description	(Z97340) similarity to extensin class 1 protein [Arabidopsis thaliana]

Seq. No.	136035
Contig ID	126438_1.R1010
5'-most EST	jC-atXP46C174G2T7032a1
Method	BLASTX
NCBI GI	g3047096
BLAST score	842
E value	2.0e-90
Match length	187
% identity	89
NCBI Description	(AF058826) similar to eukaryotic protein kinase domains (Pfam: pkinase.hmm, score: 189.74) [Arabidopsis thaliana]

Seq. No.	136036
Contig ID	126552_1.R1010
5'-most EST	jC-atXP18C115D23T7029a1
Method	BLASTN

NCBI GI	g2760316
BLAST score	305
E value	1.0e-171
Match length	404
% identity	97
NCBI Description	The sequence of BAC F1N21 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	136037
Contig ID	126554_1.R1010
5'-most EST	g2739541

Seq. No.	136038
Contig ID	126561_1.R1010
5'-most EST	jC-atXP18C113P14T7004a1
Method	BLASTN
NCBI GI	g2583106
BLAST score	288
E value	1.0e-161
Match length	347
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F4L23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136039
Contig ID	126565_1.R1010
5'-most EST	jC-atXP18C113M5T7026a1
Method	BLASTX
NCBI GI	g3114901
BLAST score	135
E value	3.0e-19
Match length	91
% identity	55
NCBI Description	(AJ005804) pcbere [Populus balsamifera subsp. trichocarpa] >gi_3114905_emb_CAA06709.1_ (AJ005806) pceberh [Populus balsamifera subsp. trichocarpa]

Seq. No.	136040
Contig ID	126576_1.R1010
5'-most EST	jC-atXP18C111E10T7064a1
Method	BLASTN
NCBI GI	g598848
BLAST score	40
E value	5.0e-13
Match length	44
% identity	98
NCBI Description	Human HepG2 3' region MboI cDNA, clone hmd4h12m3

Seq. No.	136041
Contig ID	126591_1.R1010
5'-most EST	jC-atXP18C108O17T7022a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	1.0e-19
Match length	51
% identity	100

NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.	136042
Contig ID	126595_1.R1010
5'-most EST	jC-atXP18C108N14T7077a1
Method	BLASTN
NCBI GI	g2264317
BLAST score	213
E value	1.0e-116
Match length	288
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUG13, complete sequence [Arabidopsis thaliana]
Seq. No.	136043
Contig ID	126602_1.R1010
5'-most EST	jC-atXP104CE8A3T7b1
Method	BLASTN
NCBI GI	g4680765
BLAST score	407
E value	0.0e+00
Match length	446
% identity	98
NCBI Description	Arabidopsis thaliana BAC F14I23 from chromosome V near 69 cM, complete sequence
Seq. No.	136044
Contig ID	126613_1.R1010
5'-most EST	jC-atXP104CE7B7T7b1
Method	BLASTX
NCBI GI	g4678920
BLAST score	767
E value	1.0e-81
Match length	158
% identity	98
NCBI Description	(AL049711) putative heat shock transcription factor [Arabidopsis thaliana]
Seq. No.	136045
Contig ID	126653_1.R1010
5'-most EST	jC-atXP104CE10C2T7b1
Method	BLASTN
NCBI GI	g4165340
BLAST score	536
E value	0.0e+00
Match length	626
% identity	96
NCBI Description	Arabidopsis thaliana chromosome I BAC F11M15 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	136046
Contig ID	126676_1.R1010
5'-most EST	jC-atXP102CE6A2T7035d1
Method	BLASTX
NCBI GI	g4572681
BLAST score	235
E value	4.0e-19

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Match length	67
% identity	66
NCBI Description	(AC006954) putative ubiquitin carboxyl terminal hydrolase [Arabidopsis thaliana]

Seq. No.	136047
Contig ID	126683_1.R1010
5'-most EST	jC-atXP102CE5F3T7b1
Method	BLASTX
NCBI GI	g3650032
BLAST score	497
E value	4.0e-50
Match length	85
% identity	100
NCBI Description	(AC005396) gibberellin-regulated protein GAST1-like [Arabidopsis thaliana]

Seq. No.	136048
Contig ID	126684_1.R1010
5'-most EST	jC-atXP102CE5F2T7016d1
Method	BLASTX
NCBI GI	g2702376
BLAST score	201
E value	3.0e-15
Match length	49
% identity	80
NCBI Description	(AF038605) Similar to acyl-CoA dehydrogenase; coded for by C. elegans cDNA yk58h2.3; coded for by C. elegans cDNA yk466c12.3; coded for by C. elegans cDNA yk258d6.3; coded for by C. elegans cDNA yk158e10.3; coded for by C. elegans cDNA yk427... >gi_4455127_gb_AAD21088_ (AF127558) isovaleryl-CoA dehydrogenase precursor [Caenorhabditis elegans]

Seq. No.	136049
Contig ID	126690_1.R1010
5'-most EST	jC-atXP102CE5E3T7055d1
Method	BLASTX
NCBI GI	g3047123
BLAST score	407
E value	2.0e-39
Match length	116
% identity	63
NCBI Description	(AF058919) similar to the family of glycosyl hydrolases [Arabidopsis thaliana]

Seq. No.	136050
Contig ID	126693_1.R1010
5'-most EST	jC-atXP102CE5D5T7b1
Method	BLASTX
NCBI GI	g1651965
BLAST score	189
E value	6.0e-14
Match length	107
% identity	39
NCBI Description	(D90901) hypothetical protein [Synechocystis sp.]

Seq. No.	136051
Contig ID	126698_1.R1010
5'-most EST	jC-atXP102CE5C7T7054d1
Method	BLASTX
NCBI GI	g82200
BLAST score	319
E value	3.0e-29
Match length	96
% identity	60
NCBI Description	hypothetical protein 1244 - common tobacco chloroplast

Seq. No.	136052
Contig ID	126718_1.R1010
5'-most EST	jC-atXP102CE3H4T7091d1
Method	BLASTN
NCBI GI	g4589950
BLAST score	238
E value	1.0e-131
Match length	273
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T28P16 genomic sequence, complete sequence

Seq. No.	136053
Contig ID	126876_1.R1010
5'-most EST	jC-atXP96C249K4T7b1
Method	BLASTX
NCBI GI	g1619962
BLAST score	287
E value	6.0e-69
Match length	192
% identity	67
NCBI Description	(U72068) catalase isozyme [Pseudomonas fluorescens]

Seq. No.	136054
Contig ID	126940_1.R1010
5'-most EST	jC-atXP92C249E2T7006d1

Seq. No.	136055
Contig ID	126958_1.R1010
5'-most EST	jC-atXP92C247P6T7035d1
Method	BLASTX
NCBI GI	g4006829
BLAST score	448
E value	2.0e-44
Match length	212
% identity	56
NCBI Description	(AC005970) putative protein kinase [Arabidopsis thaliana]

Seq. No.	136056
Contig ID	126967_1.R1010
5'-most EST	jC-atXP92C247N11T7066d1
Method	BLASTX
NCBI GI	g2347199
BLAST score	423
E value	1.0e-46
Match length	176

% identity	58
NCBI Description	(AC002338) protein kinase isolog [Arabidopsis thaliana]

Seq. No.	136057
Contig ID	126982_1.R1010
5'-most EST	jC-atXP92C246N12T7026d1
Method	BLASTN
NCBI GI	g2462264
BLAST score	51
E value	2.0e-19
Match length	59
% identity	97
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	136058
Contig ID	126986_3.R1010
5'-most EST	g958192
Method	BLASTX
NCBI GI	g3928099
BLAST score	284
E value	1.0e-28
Match length	149
% identity	24
NCBI Description	(AC005770) unknown protein [Arabidopsis thaliana]

Seq. No.	136059
Contig ID	127023_1.R1010
5'-most EST	jC-atXP4C88F5T7052a1
Method	BLASTX
NCBI GI	g407938
BLAST score	229
E value	4.0e-38
Match length	154
% identity	53
NCBI Description	(U02494) epoxide hydrolase [Solanum tuberosum]

Seq. No.	136060
Contig ID	127026_1.R1010
5'-most EST	jC-atXP123C117E8T7052a1

Seq. No.	136061
Contig ID	127035_1.R1010
5'-most EST	jC-atXP4C88D9T7044a1
Method	BLASTX
NCBI GI	g421924
BLAST score	237
E value	8.0e-25
Match length	145
% identity	48
NCBI Description	peroxidase (EC 1.11.1.7) - tomato >gi_296910_emb_CAA50597_ (X71593) peroxidase [Lycopersicon esculentum]

Seq. No.	136062
Contig ID	127139_1.R1010
5'-most EST	jC-atXP46C172I6T7029a1
Method	BLASTX
NCBI GI	g4510388

BLAST score	871
E value	8.0e-94
Match length	165
% identity	100
NCBI Description	(AC007017) unknown protein [Arabidopsis thaliana]

Seq. No.	136063
Contig ID	127150_1.R1010
5'-most EST	jC-atXP46C172G2T7028a1
Method	BLASTX
NCBI GI	g282430
BLAST score	435
E value	2.0e-42
Match length	234
% identity	40
NCBI Description	leucine--tRNA ligase (EC 6.1.1.4) - Bacillus subtilis >gi_143148 (M88581) transfer RNA-Leu synthetase [Bacillus subtilis]

Seq. No.	136064
Contig ID	127156_1.R1010
5'-most EST	jC-atXP46C172F20T7020a1

Seq. No.	136065
Contig ID	127190_1.R1010
5'-most EST	jC-atXP44C170K19T7046a1
Method	BLASTX
NCBI GI	g3548808
BLAST score	242
E value	5.0e-30
Match length	158
% identity	48
NCBI Description	(AC005313) unknown protein [Arabidopsis thaliana]

Seq. No.	136066
Contig ID	127210_1.R1010
5'-most EST	jC-atXP44C170H11T7028a1
Method	BLASTN
NCBI GI	g3860242
BLAST score	589
E value	0.0e+00
Match length	673
% identity	97
NCBI Description	Arabidopsis thaliana chromosome I BAC T13M11 genomic sequence, complete sequence

Seq. No.	136067
Contig ID	127213_1.R1010
5'-most EST	jC-atXP44C169M4T7089a1
Method	BLASTN
NCBI GI	g4580732
BLAST score	195
E value	1.0e-105
Match length	331
% identity	96
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F5J5, complete sequence

Seq. No.	136068
Contig ID	127219_1.R1010
5'-most EST	jC-atXP44C169L24T7081a1
Method	BLASTX
NCBI GI	g4314391
BLAST score	597
E value	2.0e-76
Match length	179
% identity	88
NCBI Description	(AC006232) unknown protein [Arabidopsis thaliana]

Seq. No.	136069
Contig ID	127237_1.R1010
5'-most EST	jC-atXP44C168J10T7082a1
Method	BLASTX
NCBI GI	g3142300
BLAST score	43
E value	2.0e-47
Match length	144
% identity	67
NCBI Description	(AC002411) Contains similarity to pre-mRNA processing protein PRP39 gb_L29224 from S. cerevisiae. ESTs gb_R64908 and gb_T88158, gb_N38703 and gb_AA651043 come from this gene. [Arabidopsis thaliana]

Seq. No.	136070
Contig ID	127250_1.R1010
5'-most EST	jC-atXP37C159B1T7d2
Method	BLASTX
NCBI GI	g3738309
BLAST score	593
E value	7.0e-87
Match length	283
% identity	65
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	136071
Contig ID	127300_1.R1010
5'-most EST	jC-atXP37C157I19T7d2
Method	BLASTN
NCBI GI	g2462264
BLAST score	47
E value	5.0e-17
Match length	51
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	136072
Contig ID	127331_1.R1010
5'-most EST	jC-atXP2C79D5T7092a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	3.0e-21
Match length	54
% identity	100

NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.	136073
Contig ID	127336_1.R1010
5'-most EST	jC-atXP2C78H8T7087a1
Method	BLASTN
NCBI GI	g2864607
BLAST score	519
E value	0.0e+00
Match length	547
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6 (ESSAII project)
Seq. No.	136074
Contig ID	127358_1.R1010
5'-most EST	jC-atXP2C77G12T7067a1
Method	BLASTX
NCBI GI	g2827143
BLAST score	712
E value	3.0e-75
Match length	167
% identity	79
NCBI Description	(AF027174) cellulose synthase catalytic subunit [Arabidopsis thaliana]
Seq. No.	136075
Contig ID	127383_1.R1010
5'-most EST	jC-atXP2C75H9T7035a1
Method	BLASTX
NCBI GI	g4651204
BLAST score	165
E value	4.0e-11
Match length	58
% identity	50
NCBI Description	(AB026262) ring finger protein [Cicer arietinum]
Seq. No.	136076
Contig ID	127385_2.R1010
5'-most EST	g2413857
Method	BLASTN
NCBI GI	g4185128
BLAST score	384
E value	0.0e+00
Match length	414
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II P1 MSF3 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	136077
Contig ID	127408_1.R1010
5'-most EST	jC-atXP2C73H10T7012a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	42
E value	6.0e-14
Match length	42

% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	136078
Contig ID	127417_1.R1010
5'-most EST	jC-atXP26C128L4T7071a1
Method	BLASTN
NCBI GI	g2980787
BLAST score	551
E value	0.0e+00
Match length	669
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, P1 clone M7J2 (ESSAII project)

Seq. No.	136079
Contig ID	127421_1.R1010
5'-most EST	jC-atXP26C128L1T7055a1
Method	BLASTN
NCBI GI	g3241925
BLAST score	249
E value	1.0e-137
Match length	635
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK9, complete sequence [Arabidopsis thaliana]

Seq. No.	136080
Contig ID	127517_1.R1010
5'-most EST	jC-atXP24C123N7T7008a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	3.0e-21
Match length	54
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	136081
Contig ID	127535_1.R1010
5'-most EST	jC-atXP24C123M22T7087a1

Seq. No.	136082
Contig ID	127565_1.R1010
5'-most EST	jC-atXP24C123J23T7038a1
Method	BLASTN
NCBI GI	g4757414
BLAST score	489
E value	0.0e+00
Match length	588
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYF24, complete sequence

Seq. No.	136083
Contig ID	127566_1.R1010
5'-most EST	jC-atXP24C123J17T7030d1

Method	BLASTN
NCBI GI	g2656028
BLAST score	273
E value	1.0e-152
Match length	690
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNF13

Seq. No.	136084
Contig ID	127573_1.R1010
5'-most EST	jC-atXP24C123I21T7066d1
Method	BLASTN
NCBI GI	g2564051
BLAST score	247
E value	1.0e-136
Match length	689
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD9, complete sequence [Arabidopsis thaliana]

Seq. No.	136085
Contig ID	127575_1.R1010
5'-most EST	jC-atXP24C123I19T7058a1
Method	BLASTX
NCBI GI	g3924596
BLAST score	410
E value	7.0e-40
Match length	102
% identity	80
NCBI Description	(AF069442) putative phospho-ser/thr phosphatase [Arabidopsis thaliana]

Seq. No.	136086
Contig ID	127577_1.R1010
5'-most EST	jC-atXP24C123I18T7050a1
Method	BLASTX
NCBI GI	g1532175
BLAST score	411
E value	8.0e-40
Match length	124
% identity	76
NCBI Description	(U63815) similar to protein disulfide isomerase [Arabidopsis thaliana]

Seq. No.	136087
Contig ID	127585_1.R1010
5'-most EST	jC-atXP24C123F9T7060a1
Method	BLASTX
NCBI GI	g2335101
BLAST score	562
E value	3.0e-89
Match length	166
% identity	95
NCBI Description	(AC002339) unknown protein [Arabidopsis thaliana]

Seq. No.	136088

Contig ID	127590_1.R1010
5'-most EST	jC-atXP24C123E1T7020d1
Method	BLASTX
NCBI GI	g3738310
BLAST score	428
E value	4.0e-96
Match length	207
% identity	89
NCBI Description	(AC005309) putative nuclear protein [Arabidopsis thaliana]

Seq. No.	136089
Contig ID	127591_1.R1010
5'-most EST	jC-atXP24C123E1T7020a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	57
E value	6.0e-23
Match length	57
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	136090
Contig ID	127595_1.R1010
5'-most EST	jC-atXP24C123D13T7083a1
Method	BLASTN
NCBI GI	g4757395
BLAST score	538
E value	0.0e+00
Match length	566
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L13, complete sequence

Seq. No.	136091
Contig ID	127604_1.R1010
5'-most EST	jC-atXP24C123D15T7091a1
Method	BLASTX
NCBI GI	g3559805
BLAST score	150
E value	4.0e-29
Match length	123
% identity	56
NCBI Description	(AJ006787) putative phytochelatin synthetase [Arabidopsis thaliana]

Seq. No.	136092
Contig ID	127607_1.R1010
5'-most EST	jC-atXP24C123D12T7075d1
Method	BLASTX
NCBI GI	g4646199
BLAST score	536
E value	1.0e-114
Match length	224
% identity	32
NCBI Description	(AC007230) EST gb_T22166 comes from this gene. [Arabidopsis thaliana]

Seq. No.	136093
Contig ID	127616_1.R1010
5'-most EST	jC-atXP24C123C19T7035a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	44
E value	3.0e-15
Match length	52
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	136094
Contig ID	127619_1.R1010
5'-most EST	jC-atXP24C123C10T7019a1
Method	BLASTN
NCBI GI	g3449327
BLAST score	328
E value	0.0e+00
Match length	600
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCA23, complete sequence [Arabidopsis thaliana]

Seq. No.	136095
Contig ID	127629_1.R1010
5'-most EST	jC-atXP24C122L18T7093a1
Method	BLASTN
NCBI GI	g2244788
BLAST score	372
E value	0.0e+00
Match length	792
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	136096
Contig ID	127630_1.R1010
5'-most EST	jC-atXP24C122L17T7085a1
Method	BLASTX
NCBI GI	g3914449
BLAST score	385
E value	6.0e-37
Match length	83
% identity	89
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT 7) >gi_3172331 (AF041258) 26S proteasome subunit 7 [Prunus persica]

Seq. No.	136097
Contig ID	127643_1.R1010
5'-most EST	jC-atXP24C120P14T7089a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	38
E value	1.0e-11
Match length	65
% identity	89

NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds
Seq. No.	136098
Contig ID	127673_1.R1010
5'-most EST	jC-atXP24C120O14T7033a1
Seq. No.	136099
Contig ID	127704_1.R1010
5'-most EST	jC-atXP22C119D7T7023a1
Method	BLASTN
NCBI GI	g4165340
BLAST score	411
E value	0.0e+00
Match length	535
% identity	88
NCBI Description	Arabidopsis thaliana chromosome I BAC F11M15 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	136100
Contig ID	127705_1.R1010
5'-most EST	jC-atXP22C119D6T7015a1
Method	BLASTN
NCBI GI	g2244950
BLAST score	356
E value	0.0e+00
Match length	524
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No
Seq. No.	136101
Contig ID	127709_1.R1010
5'-most EST	jC-atXP22C119C8T7054a1
Method	BLASTX
NCBI GI	g2493482
BLAST score	259
E value	4.0e-22
Match length	135
% identity	46
NCBI Description	GLYCEROL KINASE (ATP:GLYCEROL 3-PHOSPHOTRANSFERASE) (GLYCEROKINASE) (GK) >gi_1399490 (U49666) glycerol kinase [Pseudomonas aeruginosa]
Seq. No.	136102
Contig ID	127713_1.R1010
5'-most EST	jC-atXP22C119C13T7078a1
Method	BLASTN
NCBI GI	g3859658
BLAST score	46
E value	2.0e-16
Match length	104
% identity	88
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1 (ESSAII project)
Seq. No.	136103

Contig ID	127714_1.R1010
5'-most EST	jC-atXP22C119C10T7070a1
Method	BLASTX
NCBI GI	g3046695
BLAST score	146
E value	4.0e-13
Match length	68
% identity	66
NCBI Description	(AL022224) putative protein [Arabidopsis thaliana]

Seq. No.	136104
Contig ID	127716_1.R1010
5'-most EST	g3449441
Method	BLASTX
NCBI GI	g4587610
BLAST score	60
E value	9.0e-18
Match length	69
% identity	72
NCBI Description	(AC006951) putative indole-3-glycerol phosphate synthase precursor [Arabidopsis thaliana]

Seq. No.	136105
Contig ID	127724_1.R1010
5'-most EST	jC-atXP22C116L16T7077a1
Method	BLASTX
NCBI GI	g3128168
BLAST score	287
E value	2.0e-25
Match length	86
% identity	58
NCBI Description	(AC004521) putative carboxyl-terminal peptidase [Arabidopsis thaliana]

Seq. No.	136106
Contig ID	127735_1.R1010
5'-most EST	jC-atXP22C116I7T7017a1

Seq. No.	136107
Contig ID	127738_1.R1010
5'-most EST	jC-atXP22C116H22T7001a1
Method	BLASTX
NCBI GI	g2244779
BLAST score	356
E value	1.0e-33
Match length	75
% identity	92
NCBI Description	(Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No.	136108
Contig ID	127758_1.R1010
5'-most EST	jC-atXP22C114O10T7066a1
Method	BLASTX
NCBI GI	g2098713
BLAST score	188
E value	9.0e-27
Match length	179

% identity	42
NCBI Description	(U82977) pectinesterase [Citrus sinensis]

Seq. No.	136109
Contig ID	127791_1.R1010
5'-most EST	jC-atXP19C111N8T7083a1
Method	BLASTN
NCBI GI	g598848
BLAST score	40
E value	8.0e-13
Match length	64
% identity	92
NCBI Description	Human HepG2 3' region MboI cDNA, clone hmd4h12m3

Seq. No.	136110
Contig ID	127796_1.R1010
5'-most EST	jC-atXP19C111M8T7043a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	52
E value	6.0e-20
Match length	56
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	136111
Contig ID	127809_1.R1010
5'-most EST	jC-atXP19C111I7T7026a1
Method	BLASTN
NCBI GI	g531828
BLAST score	35
E value	8.0e-10
Match length	70
% identity	90
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	136112
Contig ID	127837_1.R1010
5'-most EST	jC-atXP19C109M16T7086a1
Method	BLASTN
NCBI GI	g2245126
BLAST score	230
E value	1.0e-126
Match length	419
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	136113
Contig ID	127838_1.R1010
5'-most EST	g550218
Method	BLASTN
NCBI GI	g2760167
BLAST score	299
E value	1.0e-167
Match length	684
% identity	96

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCO15, complete sequence [Arabidopsis thaliana]
Seq. No.	136114
Contig ID	127850_1.R1010
5'-most EST	jC-atXP19C109K10T7077a1
Method	BLASTX
NCBI GI	g1495366
BLAST score	339
E value	1.0e-49
Match length	167
% identity	60
NCBI Description	(Z69370) nitrite transporter [Cucumis sativus]
Seq. No.	136115
Contig ID	127867_1.R1010
5'-most EST	jC-atXP13C104N16T7086a1
Method	BLASTX
NCBI GI	g3386604
BLAST score	299
E value	8.0e-27
Match length	56
% identity	100
NCBI Description	(AC004665) putative protein kinase [Arabidopsis thaliana]
Seq. No.	136116
Contig ID	127906_1.R1010
5'-most EST	jC-atXP13C104B13T7039a1
Method	BLASTN
NCBI GI	g3241927
BLAST score	296
E value	1.0e-165
Match length	471
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTE17, complete sequence [Arabidopsis thaliana]
Seq. No.	136117
Contig ID	127925_1.R1010
5'-most EST	jC-atXP12C99P9T7035a1
Method	BLASTX
NCBI GI	g2275196
BLAST score	702
E value	6.0e-74
Match length	219
% identity	51
NCBI Description	(AC002337) water stress-induced protein, WSI76 isolog [Arabidopsis thaliana] >gi_4630746_gb_AAD26596.1_AC007236_1 (AC007236) water stress-induced protein [Arabidopsis thaliana]
Seq. No.	136118
Contig ID	127928_1.R1010
5'-most EST	jC-atXP12C99P16T7037a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	50

E value	7.0e-19
Match length	54
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	136119
Contig ID	127952_1.R1010
5'-most EST	jC-atXP12C99F4T7006a1
Method	BLASTN
NCBI GI	g4580745
BLAST score	333
E value	0.0e+00
Match length	599
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F10O3 sequence, complete sequence

Seq. No.	136120
Contig ID	127957_1.R1010
5'-most EST	jC-atXP12C99D14T7001a1
Method	BLASTN
NCBI GI	g4510338
BLAST score	350
E value	0.0e+00
Match length	594
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC F2H17 genomic sequence, complete sequence

Seq. No.	136121
Contig ID	127976_1.R1010
5'-most EST	jC-atXP12C103J22T7078a1
Method	BLASTN
NCBI GI	g4586241
BLAST score	186
E value	1.0e-100
Match length	578
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T20K18 (ESSA project)

Seq. No.	136122
Contig ID	127986_1.R1010
5'-most EST	jC-atXP12C103G15T7072a1
Method	BLASTN
NCBI GI	g3402695
BLAST score	528
E value	0.0e+00
Match length	592
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T3K9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136123
Contig ID	128000_1.R1010
5'-most EST	jC-atXP12C103C6T7051a1
Method	BLASTX

NCBI GI	g2129698
BLAST score	423
E value	2.0e-55
Match length	153
% identity	74
NCBI Description	protein kinase ATN1 (EC 2.7.1.-) - Arabidopsis thaliana >gi_1054633_emb_CAA63387_ (X92728) protein kinase [Arabidopsis thaliana]

Seq. No.	136124
Contig ID	128004_1.R1010
5'-most EST	jC-atXP12C103B5T7046a1
Method	BLASTN
NCBI GI	g4757404
BLAST score	307
E value	1.0e-172
Match length	597
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLJ15, complete sequence

Seq. No.	136125
Contig ID	128019_1.R1010
5'-most EST	jC-atXP123C117P11T7032d1
Method	BLASTX
NCBI GI	g2506277
BLAST score	548
E value	6.0e-56
Match length	143
% identity	74
NCBI Description	RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT PRECURSOR (60 KD CHAPERONIN BETA SUBUNIT) (CPN-60 BETA) >gi_806808 (U21139) chaperonin precursor [Pisum sativum]

Seq. No.	136126
Contig ID	128081_1.R1010
5'-most EST	jC-atXP125C136F22T7049a1
Method	BLASTN
NCBI GI	g3860242
BLAST score	306
E value	1.0e-171
Match length	602
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC T13M11 genomic sequence, complete sequence

Seq. No.	136127
Contig ID	128084_1.R1010
5'-most EST	jC-atXP125C135G9T7053a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	56
E value	2.0e-22
Match length	56
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	136128
Contig ID	128119_1.R1010
5'-most EST	jC-atXP123C119N23T7058a1
Method	BLASTX
NCBI GI	g4220454
BLAST score	90
E value	4.0e-36
Match length	184
% identity	39
NCBI Description	(AC006216) Similar to gi_3413714 T19L18.21 putative myrosinase-binding protein from Arabidopsis thaliana BAC gb_AC004747. ESTs gb_65870 and gb_T20812 come from this gene. [Arabidopsis thaliana]

Seq. No.	136129
Contig ID	128126_1.R1010
5'-most EST	jC-atXP123C118M7T7007a1
Method	BLASTN
NCBI GI	g531828
BLAST score	48
E value	1.0e-17
Match length	111
% identity	93
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	136130
Contig ID	128139_2.R1010
5'-most EST	g2048438
Method	BLASTX
NCBI GI	g2252854
BLAST score	433
E value	1.0e-42
Match length	80
% identity	97
NCBI Description	(AF013294) similar to auxin-induced protein [Arabidopsis thaliana]

Seq. No.	136131
Contig ID	128161_1.R1010
5'-most EST	jC-atXP123C117F2T7076a1
Method	BLASTN
NCBI GI	g3785992
BLAST score	400
E value	0.0e+00
Match length	565
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T6A23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136132
Contig ID	128181_1.R1010
5'-most EST	jC-atXP122C159H21T7032a1
Method	BLASTX
NCBI GI	g1351747
BLAST score	752
E value	9.0e-80
Match length	219

% identity	67
NCBI Description	HYPOTHETICAL 54.3 KD PROTEIN YCF24 >gi_1016163 (U30821) ABC transporter subunit [Cyanophora paradoxa]

Seq. No.	136133
Contig ID	128187_1.R1010
5'-most EST	jC-atXP122C159B8T7063a1
Method	BLASTN
NCBI GI	g4510408
BLAST score	359
E value	0.0e+00
Match length	687
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T1E2 genomic sequence, complete sequence

Seq. No.	136134
Contig ID	128201_1.R1010
5'-most EST	jC-atXP122C156L23T7030a1
Method	BLASTX
NCBI GI	g2829896
BLAST score	152
E value	3.0e-24
Match length	227
% identity	42
NCBI Description	(AC002311) highly similar to auxin-regulated protein GH3, gp_X60033_18591 [Arabidopsis thaliana]

Seq. No.	136135
Contig ID	128219_1.R1010
5'-most EST	jC-atXP122C120G1T7076a1
Method	BLASTX
NCBI GI	g3980380
BLAST score	424
E value	2.0e-41
Match length	103
% identity	85
NCBI Description	(AC004561) putative enolase [Arabidopsis thaliana]

Seq. No.	136136
Contig ID	128225_1.R1010
5'-most EST	jC-atXP122C118I9T7035a1

Seq. No.	136137
Contig ID	128252_1.R1010
5'-most EST	jC-atXP122C117J13T7020a1
Method	BLASTX
NCBI GI	g2194126
BLAST score	300
E value	5.0e-34
Match length	112
% identity	73
NCBI Description	(AC002062) EST gb_T43335 comes from this gene. [Arabidopsis thaliana]

Seq. No.	136138
Contig ID	128323_1.R1010

5'-most EST	jC-atXP121C118B4T7038d1
Method	BLASTX
NCBI GI	g4587680
BLAST score	561
E value	1.0e-57
Match length	116
% identity	90
NCBI Description	(AC007197) putative cytochrome p450 [Arabidopsis thaliana]

Seq. No.	136139
Contig ID	128346_1.R1010
5'-most EST	jC-atXP119C209I19T7063a1
Method	BLASTN
NCBI GI	g531828
BLAST score	52
E value	5.0e-20
Match length	64
% identity	95
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	136140
Contig ID	128373_1.R1010
5'-most EST	jC-atXP119C193O23T7060a1
Method	BLASTX
NCBI GI	g2832677
BLAST score	112
E value	4.0e-27
Match length	198
% identity	44
NCBI Description	(AL021712) hypothetical protein [Arabidopsis thaliana]

Seq. No.	136141
Contig ID	128405_1.R1010
5'-most EST	jC-atXP119C156J1T7081a1

Seq. No.	136142
Contig ID	128405_2.R1010
5'-most EST	jC-atXP119C155P21T7041a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	33
E value	8.0e-09
Match length	41
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	136143
Contig ID	128441_1.R1010
5'-most EST	jC-atXP100CE3E11T7b1
Method	BLASTX
NCBI GI	g4467145
BLAST score	804
E value	5.0e-86
Match length	153
% identity	100
NCBI Description	(AL035540) farnesylated protein (ATFP6) [Arabidopsis thaliana]

Seq. No.	136144
Contig ID	128507_1.R1010
5'-most EST	jC-atXN593177r1
Method	BLASTX
NCBI GI	g2738996
BLAST score	231
E value	1.0e-18
Match length	140
% identity	75
NCBI Description	(AF022457) CYP97B2p [Glycine max]

Seq. No.	136145
Contig ID	128511_1.R1010
5'-most EST	jC-atXN567190a1
Method	BLASTN
NCBI GI	g2739021
BLAST score	33
E value	1.0e-08
Match length	37
% identity	97
NCBI Description	Rhododendron metternichii var. hondoense CT repeats, genomic sequence

Seq. No.	136146
Contig ID	128527_1.R1010
5'-most EST	jC-atXN43264d1
Method	BLASTN
NCBI GI	g432601
BLAST score	37
E value	8.0e-11
Match length	37
% identity	100
NCBI Description	MLC1c/1s=cardiac/slow skeletal alkali myosin light-chain {5' region} [chickens, liver, Genomic, 607 nt]

Seq. No.	136147
Contig ID	128533_1.R1010
5'-most EST	jC-atXN40185d1

Seq. No.	136148
Contig ID	128538_1.R1010
5'-most EST	jC-atXN392166a1
Method	BLASTX
NCBI GI	g4741187
BLAST score	406
E value	3.0e-39
Match length	186
% identity	46
NCBI Description	(AL049746) putative protein [Arabidopsis thaliana]

Seq. No.	136149
Contig ID	128540_1.R1010
5'-most EST	jC-atXN38694d1

Seq. No.	136150
Contig ID	128542_1.R1010

5'-most EST	jC-atXN373140d1
Seq. No.	136151
Contig ID	128557_1.R1010
5'-most EST	jC-atXN28071r1
Method	BLASTN
NCBI GI	g432601
BLAST score	36
E value	3.0e-10
Match length	36
% identity	100
NCBI Description	MLC1c/1s=cardiac/slow skeletal alkali myosin light-chain {5' region} [chickens, liver, Genomic, 607 nt]
Seq. No.	136152
Contig ID	128560_1.R1010
5'-most EST	jC-atXN272114r1
Method	BLASTX
NCBI GI	g1167955
BLAST score	111
E value	9.0e-18
Match length	147
% identity	39
NCBI Description	(U43497) putative 32.7 kDa jasmonate-induced protein [Hordeum vulgare] >gi_2465428 (AF021257) 32 kDa protein [Hordeum vulgare]
Seq. No.	136153
Contig ID	128574_1.R1010
5'-most EST	jC-atXN209221d1
Seq. No.	136154
Contig ID	128598_1.R1010
5'-most EST	jC-atXWAXYa1
Method	BLASTX
NCBI GI	g136757
BLAST score	293
E value	3.0e-62
Match length	186
% identity	76
NCBI Description	GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR >gi_100881_pir__S07314 UDPglucose--starch glucosyltransferase (EC 2.4.1.11) precursor - maize >gi_168653 (M24258) amyloplast-specific transit protein [Zea mays] >gi_1644339_emb_CAA27574_ (X03935) glucosyl transferase [Zea mays]
Seq. No.	136155
Contig ID	128600_1.R1010
5'-most EST	jC-atXU93r1
Method	BLASTX
NCBI GI	g3641836
BLAST score	382
E value	2.0e-47
Match length	136
% identity	68
NCBI Description	(AL023094) putative serine/threonine protein kinase

[Arabidopsis thaliana]

Seq. No.	136156
Contig ID	128602_1.R1010
5'-most EST	jC-atXU90r1

Seq. No.	136157
Contig ID	128604_1.R1010
5'-most EST	jC-atXU84d1
Method	BLASTN
NCBI GI	g1419369
BLAST score	64
E value	5.0e-27
Match length	64
% identity	100
NCBI Description	Z.mays ZmABP3 mRNA for actin depolymerizing factor

Seq. No.	136158
Contig ID	128606_1.R1010
5'-most EST	jC-atXU66r1
Method	BLASTX
NCBI GI	g4335731
BLAST score	190
E value	3.0e-29
Match length	197
% identity	43
NCBI Description	(AC006248) putative polyprotein [Arabidopsis thaliana]

Seq. No.	136159
Contig ID	128609_1.R1010
5'-most EST	jC-atXU63r1
Method	BLASTX
NCBI GI	g4415924
BLAST score	216
E value	6.0e-17
Match length	114
% identity	42
NCBI Description	(AC006282) putative glucosyl transferase [Arabidopsis thaliana]

Seq. No.	136160
Contig ID	128611_1.R1010
5'-most EST	jC-atXU60r1
Method	BLASTX
NCBI GI	g3785977
BLAST score	268
E value	7.0e-23
Match length	223
% identity	62
NCBI Description	(AC005560) putative growth regulator protein [Arabidopsis thaliana]

Seq. No.	136161
Contig ID	128613_1.R1010
5'-most EST	jC-atXU54r1
Method	BLASTX
NCBI GI	g2979554

BLAST score 198
E value 9.0e-15
Match length 107
% identity 46
NCBI Description (AC003680) CDC4 like protein [Arabidopsis thaliana]

Seq. No. 136162
Contig ID 128615_1.R1010
5'-most EST jC-atXU52r1

Seq. No. 136163
Contig ID 128617_1.R1010
5'-most EST jC-atXU48d1
Method BLASTX
NCBI GI g1184075
BLAST score 447
E value 4.0e-44
Match length 278
% identity 5
NCBI Description (U42444) Cf-2.1 [Lycopersicon pimpinellifolium] >gi_1587673_prf__2207203A Cf-2 gene [Lycopersicon esculentum]

Seq. No. 136164
Contig ID 128621_1.R1010
5'-most EST jC-atXU358r1

Seq. No. 136165
Contig ID 128623_1.R1010
5'-most EST jC-atXU34r1

Seq. No. 136166
Contig ID 128625_1.R1010
5'-most EST jC-atXU330r1
Method BLASTX
NCBI GI g4580468
BLAST score 670
E value 5.0e-70
Match length 254
% identity 50
NCBI Description (AC006081) putative protein kinase; similar to human PKX1 and Drosophila DC2 [Arabidopsis thaliana]

Seq. No. 136167
Contig ID 128627_1.R1010
5'-most EST jC-atXU32r1
Method BLASTN
NCBI GI g432601
BLAST score 36
E value 3.0e-10
Match length 36
% identity 100
NCBI Description MLC1c/1s=cardiac/slow skeletal alkali myosin light-chain {5' region} [chickens, liver, Genomic, 607 nt]

Seq. No. 136168
Contig ID 128629_1.R1010

5'-most EST	jC-atXU313r1
Method	BLASTX
NCBI GI	g100506
BLAST score	1109
E value	1.0e-121
Match length	225
% identity	95
NCBI Description	Malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) (EC 1.1.1.40) - Flaveria trinervia (fragment)

Seq. No.	136169
Contig ID	128631_1.R1010
5'-most EST	jC-atXU27r1
Method	BLASTN
NCBI GI	g468055
BLAST score	40
E value	9.0e-13
Match length	44
% identity	98
NCBI Description	Zea mays B73 QM protein mRNA, complete cds

Seq. No.	136170
Contig ID	128633_1.R1010
5'-most EST	jC-atXU254r1
Method	BLASTN
NCBI GI	g22430
BLAST score	27
E value	6.0e-05
Match length	88
% identity	93
NCBI Description	Maize pseudo-Gpa2 pseudogene for glyceraldehyde-3-phosphate dehydrogenase subunit A

Seq. No.	136171
Contig ID	128635_1.R1010
5'-most EST	jC-atXU19a1
Method	BLASTN
NCBI GI	g53723
BLAST score	50
E value	9.0e-19
Match length	75
% identity	100
NCBI Description	M.musculus extrachromosomal DNA for V kappa and J kappa coding joint (clone pKDE 34)

Seq. No.	136172
Contig ID	128636_1.R1010
5'-most EST	jC-atXU168r1

Seq. No.	136173
Contig ID	128638_1.R1010
5'-most EST	jC-atXU161r1
Method	BLASTN
NCBI GI	g209392
BLAST score	49
E value	3.0e-18
Match length	56

% identity	98
NCBI Description	Cloning vector PSU2719 DNA
Seq. No.	136174
Contig ID	128640_1.R1010
5'-most EST	jC-atXU109r1
Seq. No.	136175
Contig ID	128642_1.R1010
5'-most EST	jC-atXU104r1
Method	BLASTX
NCBI GI	g3928084
BLAST score	348
E value	2.0e-32
Match length	177
% identity	46
NCBI Description	(AC005770) retrotransposon-like protein [Arabidopsis thaliana]
Seq. No.	136176
Contig ID	128644_1.R1010
5'-most EST	jC-atXU102r1
Seq. No.	136177
Contig ID	128732_1.R1010
5'-most EST	jC-atXP92CH3H5T7031d1
Method	BLASTX
NCBI GI	g2826900
BLAST score	396
E value	3.0e-64
Match length	193
% identity	72
NCBI Description	(AB004461) DNA polymerase alpha catalytic subunit [Oryza sativa]
Seq. No.	136178
Contig ID	128735_1.R1010
5'-most EST	jC-atXP92CH3H12T7079d1
Method	BLASTN
NCBI GI	g4263642
BLAST score	138
E value	2.0e-71
Match length	538
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC T13H18 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	136179
Contig ID	128759_1.R1010
5'-most EST	jC-atXP46C174E15T7016d1
Method	BLASTX
NCBI GI	g3927836
BLAST score	555
E value	7.0e-62
Match length	156
% identity	77
NCBI Description	(AC005727) unknown protein [Arabidopsis thaliana]

Seq. No.	136180
Contig ID	128762_1.R1010
5'-most EST	jC-atXP46C174C20T7071d1
Method	BLASTX
NCBI GI	g4056482
BLAST score	481
E value	1.0e-73
Match length	213
% identity	63
NCBI Description	(AC005896) putative ABC transporter [Arabidopsis thaliana]

Seq. No.	136181
Contig ID	128772_1.R1010
5'-most EST	jC-atXP46C173N24T7062d1
Method	BLASTX
NCBI GI	g2194127
BLAST score	508
E value	2.0e-80
Match length	210
% identity	74
NCBI Description	(AC002062) Strong similarity to Arabidopsis receptor-like protein kinase (gb_ATLECGENE) and F20P5.16. [Arabidopsis thaliana]

Seq. No.	136182
Contig ID	128796_1.R1010
5'-most EST	jC-atXP46C173E14T7010d1
Method	BLASTN
NCBI GI	g3702732
BLAST score	155
E value	2.0e-81
Match length	698
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGF10, complete sequence [Arabidopsis thaliana]

Seq. No.	136183
Contig ID	128822_1.R1010
5'-most EST	jC-atXP46C172F20T7020d1
Method	BLASTX
NCBI GI	g465898
BLAST score	268
E value	4.0e-23
Match length	209
% identity	38
NCBI Description	HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III >gi_630692_pir__S44849 K12H4.8 protein - Caenorhabditis elegans >gi_289703 (L14331) homology with eukaryotic initiation factor-4A (eIF-4A) and E. coli Ribonuclease III; coded for by C. elegans cDNA GenBank:T02268; putative [Caenorhabditis elegans]

Seq. No.	136184
Contig ID	128829_1.R1010
5'-most EST	jC-atXP25C125O9T7080a1
Method	BLASTX

NCBI GI	g4490334
BLAST score	365
E value	1.0e-34
Match length	73
% identity	100
NCBI Description	(AL035656) putative protein [Arabidopsis thaliana]

Seq. No.	136185
Contig ID	128845_1.R1010
5'-most EST	jC-atXP25C125K20T7071a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	57
E value	4.0e-23
Match length	57
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	136186
Contig ID	128875_1.R1010
5'-most EST	jC-atXP25C125C21T7037a1
Method	BLASTN
NCBI GI	g2104523
BLAST score	488
E value	0.0e+00
Match length	528
% identity	98
NCBI Description	Arabidopsis thaliana BAC T10M13 from chromosome IV, from 10.8 cM to 11.6 cM, complete sequence

Seq. No.	136187
Contig ID	128879_1.R1010
5'-most EST	jC-atXP25C125B10T7044a1
Method	BLASTX
NCBI GI	g3128210
BLAST score	384
E value	7.0e-37
Match length	70
% identity	100
NCBI Description	(AC004077) putative cytochrome P450 protein [Arabidopsis thaliana] >gi_3337378 (AC004481) putative cytochrome P450 protein [Arabidopsis thaliana]

Seq. No.	136188
Contig ID	128890_2.R1010
5'-most EST	g572594
Method	BLASTX
NCBI GI	g2829918
BLAST score	180
E value	3.0e-13
Match length	38
% identity	84
NCBI Description	(AC002291) similar to "tub" protein gp_U82468_2072162 [Arabidopsis thaliana]

Seq. No.	136189
Contig ID	128898_1.R1010

5'-most EST	jC-atXP25C123O17T7025a1
Method	BLASTN
NCBI GI	g3738275
BLAST score	474
E value	0.0e+00
Match length	538
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F17A22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136190
Contig ID	128903_1.R1010
5'-most EST	jC-atXP25C123H20T7067a1
Method	BLASTN
NCBI GI	g4589411
BLAST score	277
E value	1.0e-154
Match length	620
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F5H8, complete sequence

Seq. No.	136191
Contig ID	128926_1.R1010
5'-most EST	jC-atXP123C159K15T7025d1
Method	BLASTN
NCBI GI	g298035
BLAST score	330
E value	0.0e+00
Match length	338
% identity	99
NCBI Description	A.thaliana Lhcb4 gene

Seq. No.	136192
Contig ID	128933_1.R1010
5'-most EST	jC-atXP123C119P7T7019d1
Method	BLASTX
NCBI GI	g1351869
BLAST score	308
E value	8.0e-28
Match length	153
% identity	44
NCBI Description	ACTIN >gi_508701 (U10867) actin [Filobasidiella neoformans]

Seq. No.	136193
Contig ID	129009_1.R1010
5'-most EST	jC-atXP110CG7F6T7014a1
Method	BLASTN
NCBI GI	g4580386
BLAST score	140
E value	2.0e-72
Match length	421
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC T8O18 genomic sequence, complete sequence

Seq. No. 136194

Contig ID	129014_1.R1010
5'-most EST	jC-atXP110CG7E12T7077a1
Method	BLASTX
NCBI GI	g3152587
BLAST score	704
E value	3.0e-74
Match length	214
% identity	63
NCBI Description	(AC002986) Similar to CREB-binding protein homolog gb_U88570 from D. melanogaster and contains similarity to callus-associated protein gb_U01961 from Nicotiana tabacum. EST gb_W43427 comes from this gene. [Arabidopsis thaliana]

Seq. No.	136195
Contig ID	129038_1.R1010
5'-most EST	jC-atXP110CG3H12T7078a1
Method	BLASTX
NCBI GI	g3540219
BLAST score	378
E value	2.0e-49
Match length	170
% identity	61
NCBI Description	(D87686) KIAA0017 protein [Homo sapiens]

Seq. No.	136196
Contig ID	129048_1.R1010
5'-most EST	jC-atXP110C84G7T7079a1
Method	BLASTX
NCBI GI	g4467110
BLAST score	585
E value	2.0e-60
Match length	167
% identity	71
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]

Seq. No.	136197
Contig ID	129068_1.R1010
5'-most EST	jC-atXP110C117B14T7027a1
Method	BLASTN
NCBI GI	g4757395
BLAST score	331
E value	0.0e+00
Match length	705
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L13, complete sequence

Seq. No.	136198
Contig ID	129117_1.R1010
5'-most EST	jC-atXP108C170C12T7068d1
Method	BLASTX
NCBI GI	g4115916
BLAST score	365
E value	2.0e-34
Match length	180
% identity	56
NCBI Description	(AF118222) F3H7.9 gene product [Arabidopsis thaliana]

>gi_4539441_emb_CAB40029.1_ (AL049523) putative protein [Arabidopsis thaliana]

Seq. No.	136199
Contig ID	129179_1.R1010
5'-most EST	jC-atXP3C83E7T7065a1
Method	BLASTN
NCBI GI	g4539378
BLAST score	162
E value	1.0e-85
Match length	540
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28A21 (ESSA project)

Seq. No.	136200
Contig ID	129181_1.R1010
5'-most EST	jC-atXP3C83D2T7062a1
Method	BLASTX
NCBI GI	g4522012
BLAST score	313
E value	2.0e-28
Match length	137
% identity	58
NCBI Description	(AC007069) hypothetical protein [Arabidopsis thaliana]

Seq. No.	136201
Contig ID	129212_1.R1010
5'-most EST	jC-atXP3C81E5T7033a1
Method	BLASTN
NCBI GI	g4337186
BLAST score	283
E value	1.0e-158
Match length	572
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T28I24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136202
Contig ID	129218_1.R1010
5'-most EST	jC-atXP3C81B4T7023a1
Method	BLASTX
NCBI GI	g4539440
BLAST score	319
E value	3.0e-29
Match length	140
% identity	46
NCBI Description	(AL049523) putative protein [Arabidopsis thaliana]

Seq. No.	136203
Contig ID	129234_1.R1010
5'-most EST	jC-atXP3C80D11T7006a1
Method	BLASTX
NCBI GI	g3036806
BLAST score	421
E value	5.0e-59
Match length	141

% identity	21
NCBI Description	(AL022373) glycine-rich protein [Arabidopsis thaliana]

Seq. No.	136204
Contig ID	129239_1.R1010
5'-most EST	jC-atXP74C226B4T7096d1
Method	BLASTX
NCBI GI	g1421741
BLAST score	533
E value	4.0e-54
Match length	157
% identity	66
NCBI Description	(U54770) cytochrome P450 homolog [Lycopersicon esculentum]

Seq. No.	136205
Contig ID	129239_2.R1010
5'-most EST	jC-atXP74C224H11T7081d1
Method	BLASTX
NCBI GI	g1421741
BLAST score	213
E value	7.0e-83
Match length	195
% identity	75
NCBI Description	(U54770) cytochrome P450 homolog [Lycopersicon esculentum]

Seq. No.	136206
Contig ID	129266_1.R1010
5'-most EST	jC-atXP74C225B10T7029d1
Method	BLASTX
NCBI GI	g4586117
BLAST score	328
E value	3.0e-30
Match length	237
% identity	41
NCBI Description	(AL049638) putative protein [Arabidopsis thaliana]

Seq. No.	136207
Contig ID	129307_1.R1010
5'-most EST	jC-atXP74C223N21T7036d1
Method	BLASTX
NCBI GI	g3548802
BLAST score	266
E value	1.0e-48
Match length	228
% identity	47
NCBI Description	(AC005313) axi 1-like protein [Arabidopsis thaliana] >gi_4335769_gb_AAD17446_ (AC006284) putative axi1 protein [Nicotiana tabacum] [Arabidopsis thaliana]

Seq. No.	136208
Contig ID	129416_1.R1010
5'-most EST	jC-atXP69C219M19T7055d1
Method	BLASTN
NCBI GI	g2582640
BLAST score	39
E value	3.0e-12
Match length	39

% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	136209
Contig ID	129437_1.R1010
5'-most EST	jC-atXP69C219B15T7022d1
Method	BLASTN
NCBI GI	g3941523
BLAST score	40
E value	8.0e-13
Match length	40
% identity	100
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	136210
Contig ID	129462_1.R1010
5'-most EST	jC-atXP69C217J14T7051d1
Method	BLASTX
NCBI GI	g3386600
BLAST score	582
E value	6.0e-60
Match length	167
% identity	71
NCBI Description	(AC004665) putative glycoprotein [Arabidopsis thaliana]

Seq. No.	136211
Contig ID	129474_1.R1010
5'-most EST	jC-atXP69C217C23T7001d1
Method	BLASTX
NCBI GI	g3928102
BLAST score	366
E value	1.0e-34
Match length	182
% identity	56
NCBI Description	(AC005770) putative protein kinase [Arabidopsis thaliana]

Seq. No.	136212
Contig ID	129481_1.R1010
5'-most EST	jC-atXP65C208L10T7032d1
Method	BLASTN
NCBI GI	g2582640
BLAST score	40
E value	7.0e-13
Match length	40
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	136213
Contig ID	129486_1.R1010
5'-most EST	jC-atXP65C206N17T7018d1
Method	BLASTX
NCBI GI	g3128176
BLAST score	723
E value	2.0e-76

Match length	201
% identity	72
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	136214
Contig ID	129514_1.R1010
5'-most EST	jC-atXP65C207P23T7092d1
Method	BLASTN
NCBI GI	g3941523
BLAST score	38
E value	1.0e-11
Match length	38
% identity	100
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	136215
Contig ID	129517_1.R1010
5'-most EST	jC-atXP65C208B22T7061d1
Method	BLASTN
NCBI GI	g3549651
BLAST score	349
E value	0.0e+00
Match length	603
% identity	97
NCBI Description	Arabidopsis thaliana MAP3K epsilon gene

Seq. No.	136216
Contig ID	129520_1.R1010
5'-most EST	jC-atXP65C208A7T7013d1
Method	BLASTN
NCBI GI	g2832689
BLAST score	277
E value	1.0e-154
Match length	586
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9A21 (ESSAII project)

Seq. No.	136217
Contig ID	129522_1.R1010
5'-most EST	jC-atXP65C208A11T7021d1
Method	BLASTN
NCBI GI	g3746057
BLAST score	559
E value	0.0e+00
Match length	603
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T16B12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136218
Contig ID	129524_1.R1010
5'-most EST	jC-atXP65C207P24T7005d1
Method	BLASTX
NCBI GI	g2244841
BLAST score	773

E value	2.0e-82
Match length	206
% identity	75
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	136219
Contig ID	129529_1.R1010
5'-most EST	jC-atXP65C207M8T7083d1
Method	BLASTN
NCBI GI	g2582640
BLAST score	38
E value	1.0e-11
Match length	38
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	136220
Contig ID	129539_1.R1010
5'-most EST	jC-atXP65C207K24T7059d1
Method	BLASTX
NCBI GI	g3928099
BLAST score	347
E value	2.0e-32
Match length	181
% identity	22
NCBI Description	(AC005770) unknown protein [Arabidopsis thaliana]

Seq. No.	136221
Contig ID	129624_1.R1010
5'-most EST	jC-atXP5C89E10T7032a1

Seq. No.	136222
Contig ID	129632_1.R1010
5'-most EST	jC-atXP5C89B18T7024a1

Seq. No.	136223
Contig ID	129652_1.R1010
5'-most EST	jC-atXP43C170E23T7076d1
Method	BLASTX
NCBI GI	g4337175
BLAST score	290
E value	9.0e-26
Match length	114
% identity	51
NCBI Description	(AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906, gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No.	136224
Contig ID	129684_1.R1010
5'-most EST	jC-atXP43C169I3T7041d1

Seq. No.	136225
Contig ID	129700_1.R1010
5'-most EST	jC-atXP43C169B3T7032d1

Method	BLASTX
NCBI GI	g3914467
BLAST score	699
E value	1.0e-73
Match length	215
% identity	70
NCBI Description	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7) >gi_1864003_dbj_BAA19252_ (AB001422) 21D7 [Nicotiana tabacum]

Seq. No.	136226
Contig ID	129713_1.R1010
5'-most EST	jC-atXP43C168E4T7090d1
Method	BLASTN
NCBI GI	g3860243
BLAST score	334
E value	0.0e+00
Match length	410
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F15K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136227
Contig ID	129727_1.R1010
5'-most EST	jC-atXP40C164D24T7072a1
Method	BLASTX
NCBI GI	g3445204
BLAST score	464
E value	4.0e-46
Match length	184
% identity	52
NCBI Description	(AC004786) putative GTP-binding protein [Arabidopsis thaliana]

Seq. No.	136228
Contig ID	129762_1.R1010
5'-most EST	g2749228
Method	BLASTN
NCBI GI	g3046847
BLAST score	183
E value	2.0e-98
Match length	291
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome5, TAC clone: K11J9, complete sequence [Arabidopsis thaliana]

Seq. No.	136229
Contig ID	129785_1.R1010
5'-most EST	jC-atXP40C161L14T7066a1
Method	BLASTX
NCBI GI	g3914002
BLAST score	378
E value	1.0e-64
Match length	142
% identity	94
NCBI Description	MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi_2935279 (AF033862) Lon protease [Arabidopsis thaliana]

Seq. No.	136230
Contig ID	129788_1.R1010
5'-most EST	jC-atXP40C161K20T7042a1
Method	BLASTX
NCBI GI	g3643085
BLAST score	201
E value	3.0e-40
Match length	148
% identity	61
NCBI Description	(AF075580) protein phosphatase-2C; PP2C [Mesembryanthemum crystallinum]

Seq. No.	136231
Contig ID	129795_1.R1010
5'-most EST	jC-atXP40C161J17T7057a1

Seq. No.	136232
Contig ID	129856_1.R1010
5'-most EST	jC-atXP20C114B21T7044a1
Method	BLASTX
NCBI GI	g3885331
BLAST score	286
E value	5.0e-38
Match length	148
% identity	55
NCBI Description	(AC005623) putative cytochrome p450 protein [Arabidopsis thaliana]

Seq. No.	136233
Contig ID	129881_1.R1010
5'-most EST	jC-atXP20C113E2T7081a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	37
E value	5.0e-11
Match length	37
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	136234
Contig ID	129896_1.R1010
5'-most EST	jC-atXP15C108F1T7093a1
Method	BLASTX
NCBI GI	g3955021
BLAST score	171
E value	2.0e-12
Match length	112
% identity	45
NCBI Description	(AJ010811) HB2 homeodomain protein [Populus tremula x Populus tremuloides]

Seq. No.	136235
Contig ID	129921_1.R1010
5'-most EST	jC-atXP15C107M23T7068a1
Method	BLASTN
NCBI GI	g2252639

BLAST score	334
E value	0.0e+00
Match length	693
% identity	99
NCBI Description	Genomic sequence of Arabidopsis BAC F8A5, complete sequence [Arabidopsis thaliana]

Seq. No.	136236
Contig ID	129928_1.R1010
5'-most EST	jC-atXP15C107J6T7058a1
Method	BLASTX
NCBI GI	g3212610
BLAST score	145
E value	2.0e-18
Match length	103
% identity	50
NCBI Description	Chain A, Sulfite Oxidase From Chicken Liver >gi_3212611_pdb_1SOX_B Chain B, Sulfite Oxidase From Chicken Liver

Seq. No.	136237
Contig ID	129983_1.R1010
5'-most EST	jC-atXP20728f2
Method	BLASTX
NCBI GI	g4581109
BLAST score	608
E value	5.0e-63
Match length	149
% identity	73
NCBI Description	(AC005825) unknown protein [Arabidopsis thaliana]

Seq. No.	136238
Contig ID	129987_1.R1010
5'-most EST	jC-atXP20608f2
Method	BLASTN
NCBI GI	g619522
BLAST score	45
E value	8.0e-16
Match length	53
% identity	98
NCBI Description	Synechococcus PCC 6301 genomic DNA (clone PJRSY01)

Seq. No.	136239
Contig ID	129989_1.R1010
5'-most EST	jC-atXP20581f2
Method	BLASTN
NCBI GI	g4314333
BLAST score	45
E value	8.0e-16
Match length	53
% identity	96
NCBI Description	Homo sapiens chromosome 10 clone CIT987SK-1161G12 map 10q25, complete sequence [Homo sapiens]

Seq. No.	136240
Contig ID	130005_1.R1010
5'-most EST	jC-atXN579208a2

Seq. No.	136241
Contig ID	130074_1.R1010
5'-most EST	jC-atXN25473f1
Method	BLASTX
NCBI GI	g4512263
BLAST score	190
E value	5.0e-14
Match length	58
% identity	69
NCBI Description	(AB018526) H+/Ca2+ exchanger 2 [Ipomoea nil]

Seq. No.	136242
Contig ID	130099_1.R1010
5'-most EST	jC-atXN110229f2

Seq. No.	136243
Contig ID	130107_1.R1010
5'-most EST	jC-atXB944a2

Seq. No.	136244
Contig ID	130113_1.R1010
5'-most EST	jC-atXB823a2

Seq. No.	136245
Contig ID	130115_1.R1010
5'-most EST	jC-atXB815a2

Seq. No.	136246
Contig ID	130119_1.R1010
5'-most EST	jC-atXB805f2

Seq. No.	136247
Contig ID	130123_1.R1010
5'-most EST	jC-atXB761f2
Method	BLASTX
NCBI GI	g3550436
BLAST score	228
E value	2.0e-18
Match length	69
% identity	68
NCBI Description	(AJ001317) putative transcription repressor HOTR [Hordeum vulgare]

Seq. No.	136248
Contig ID	130129_1.R1010
5'-most EST	jC-atXB632a2
Method	BLASTN
NCBI GI	g507770
BLAST score	33
E value	1.0e-08
Match length	65
% identity	89
NCBI Description	Zea mays D3L H(+)-transporting ATPase (Mha1) gene, complete cds

Seq. No.	136249

Contig ID	130132_1.R1010
5'-most EST	jC-atXB304a2
Seq. No.	136250
Contig ID	130240_1.R1010
5'-most EST	g17426
Method	BLASTX
NCBI GI	g3172538
BLAST score	179
E value	9.0e-13
Match length	113
% identity	46
NCBI Description	(AF067789) tSNARE AtTLG2p [Arabidopsis thaliana]
Seq. No.	136251
Contig ID	130243_1.R1010
5'-most EST	g935450
Method	BLASTX
NCBI GI	g4510376
BLAST score	242
E value	2.0e-20
Match length	83
% identity	54
NCBI Description	(AC007017) unknown protein [Arabidopsis thaliana]
Seq. No.	136252
Contig ID	130267_1.R1010
5'-most EST	g396890
Seq. No.	136253
Contig ID	130298_1.R1010
5'-most EST	g17298
Method	BLASTN
NCBI GI	g4455321
BLAST score	217
E value	1.0e-118
Match length	529
% identity	45
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4I10 (ESSAII project)
Seq. No.	136254
Contig ID	130308_1.R1010
5'-most EST	g17273
Method	BLASTX
NCBI GI	g1651689
BLAST score	202
E value	8.0e-16
Match length	99
% identity	44
NCBI Description	(D90899) hypothetical protein [Synechocystis sp.]
Seq. No.	136255
Contig ID	130312_1.R1010
5'-most EST	g1215939
Method	BLASTN
NCBI GI	g4454004

BLAST score	293
E value	1.0e-164
Match length	395
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F24A6 (ESSAII project)

Seq. No.	136256
Contig ID	130315_1.R1010
5'-most EST	g2748118
Method	BLASTX
NCBI GI	g479413
BLAST score	728
E value	6.0e-77
Match length	229
% identity	69
NCBI Description	myosin-like protein - Arabidopsis thaliana

Seq. No.	136257
Contig ID	130371_1.R1010
5'-most EST	g16753
Method	BLASTN
NCBI GI	g4757403
BLAST score	321
E value	0.0e+00
Match length	371
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJL12, complete sequence

Seq. No.	136258
Contig ID	130374_1.R1010
5'-most EST	g2749713

Seq. No.	136259
Contig ID	130391_1.R1010
5'-most EST	g2749235
Method	BLASTN
NCBI GI	g2864607
BLAST score	259
E value	1.0e-143
Match length	428
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6 (ESSAII project)

Seq. No.	136260
Contig ID	130392_1.R1010
5'-most EST	g16804
Method	BLASTN
NCBI GI	g4757399
BLAST score	302
E value	1.0e-169
Match length	318
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MEE13, complete sequence

Seq. No.	136261
Contig ID	130435_1.R1010
5'-most EST	g16850
Method	BLASTN
NCBI GI	g4531433
BLAST score	366
E value	0.0e+00
Match length	416
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II P1 MFL8 genomic sequence, complete sequence

Seq. No.	136262
Contig ID	130477_1.R1010
5'-most EST	g2580825
Method	BLASTN
NCBI GI	g3228389
BLAST score	409
E value	0.0e+00
Match length	517
% identity	98
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17L21, complete sequence [Arabidopsis thaliana]

Seq. No.	136263
Contig ID	130491_1.R1010
5'-most EST	g2756764
Method	BLASTN
NCBI GI	g2618677
BLAST score	272
E value	1.0e-151
Match length	474
% identity	96
NCBI Description	Arabidopsis thaliana BAC F21B7 chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	136264
Contig ID	130527_1.R1010
5'-most EST	g2723103
Method	BLASTN
NCBI GI	g3236234
BLAST score	216
E value	1.0e-118
Match length	468
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F13M22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136265
Contig ID	130553_1.R1010
5'-most EST	g2722809
Method	BLASTX
NCBI GI	g3152585
BLAST score	329
E value	2.0e-30
Match length	121

% identity	57
NCBI Description	(AC002986) Contains similarity to auxin-induced protein TM018A10.6 from A. thaliana BAC gb_AF013294. [Arabidopsis thaliana]

Seq. No.	136266
Contig ID	130584_1.R1010
5'-most EST	g501985
Method	BLASTN
NCBI GI	g2244901
BLAST score	186
E value	1.0e-100
Match length	380
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	136267
Contig ID	130693_1.R1010
5'-most EST	g17134
Method	BLASTN
NCBI GI	g3738313
BLAST score	282
E value	1.0e-157
Match length	453
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T29E15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136268
Contig ID	130702_1.R1010
5'-most EST	g17146
Method	BLASTN
NCBI GI	g3128137
BLAST score	311
E value	1.0e-175
Match length	360
% identity	77
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9I9, complete sequence [Arabidopsis thaliana]

Seq. No.	136269
Contig ID	130789_1.R1010
5'-most EST	g906739
Method	BLASTX
NCBI GI	g1841357
BLAST score	291
E value	5.0e-26
Match length	128
% identity	50
NCBI Description	(D85382) mitochondrial ribosomal protein S11 (nuclear encoded) [Oryza sativa]

Seq. No.	136270
Contig ID	130806_1.R1010
5'-most EST	g506521
Method	BLASTN

NCBI GI	g4734003
BLAST score	54
E value	1.0e-21
Match length	62
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F3L12 genomic sequence, complete sequence

Seq. No.	136271
Contig ID	130811_1.R1010
5'-most EST	g16667
Method	BLASTX
NCBI GI	g4689108
BLAST score	422
E value	2.0e-41
Match length	113
% identity	63
NCBI Description	(AF077030) hypothetical 43.2 kDa protein [Homo sapiens]

Seq. No.	136272
Contig ID	130825_1.R1010
5'-most EST	g394887
Method	BLASTX
NCBI GI	g2827637
BLAST score	250
E value	2.0e-21
Match length	64
% identity	72
NCBI Description	(AL021636) putative protein [Arabidopsis thaliana]

Seq. No.	136273
Contig ID	130910_1.R1010
5'-most EST	g16655
Method	BLASTX
NCBI GI	g543565
BLAST score	226
E value	2.0e-18
Match length	94
% identity	49
NCBI Description	hypothetical 10.0K protein - Zinnia elegans >gi_493721_dbj_BAA06462_ (D30802) TED4 [Zinnia elegans] >gi_641903 (U19266) putative nonspecific lipid transfer; auxin induced gene [Zinnia elegans]

Seq. No.	136274
Contig ID	130938_1.R1010
5'-most EST	g17599
Method	BLASTN
NCBI GI	g4235150
BLAST score	149
E value	3.0e-78
Match length	306
% identity	97
NCBI Description	Arabidopsis thaliana chromosome I BAC T25B24 genomic sequence, complete sequence

Seq. No. 136275

Contig ID	130993_1.R1010
5'-most EST	g17573
Method	BLASTN
NCBI GI	g2213606
BLAST score	194
E value	1.0e-105
Match length	395
% identity	98
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F21J9, complete sequence [Arabidopsis thaliana]

Seq. No.	136276
Contig ID	131015_1.R1010
5'-most EST	g2393174
Method	BLASTN
NCBI GI	g2924653
BLAST score	200
E value	1.0e-108
Match length	412
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDA7, complete sequence [Arabidopsis thaliana]

Seq. No.	136277
Contig ID	131074_1.R1010
5'-most EST	g315162

Seq. No.	136278
Contig ID	131075_1.R1010
5'-most EST	g315175
Method	BLASTX
NCBI GI	g2979549
BLAST score	285
E value	2.0e-51
Match length	130
% identity	88
NCBI Description	(AC003680) putative 7-ethoxycoumarin O-deethylase [Arabidopsis thaliana]

Seq. No.	136279
Contig ID	131077_1.R1010
5'-most EST	g1223592
Method	BLASTN
NCBI GI	g4309747
BLAST score	334
E value	0.0e+00
Match length	448
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T13E11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136280
Contig ID	131080_1.R1010
5'-most EST	g315213
Method	BLASTX
NCBI GI	g1946365
BLAST score	108

E value 2.0e-36
Match length 93
% identity 85
NCBI Description (U93215) glutaredoxin isolog [Arabidopsis thaliana]

Seq. No. 136281
Contig ID 131083_1.R1010
5'-most EST g315217

Seq. No. 136282
Contig ID 131169_1.R1010
5'-most EST g315386

Seq. No. 136283
Contig ID 131175_1.R1010
5'-most EST g315392
Method BLASTX
NCBI GI g3882203
BLAST score 298
E value 2.0e-33
Match length 150
% identity 51
NCBI Description (AB018284) KIAA0741 protein [Homo sapiens]

Seq. No. 136284
Contig ID 131180_1.R1010
5'-most EST g2756818
Method BLASTX
NCBI GI g1621268
BLAST score 197
E value 4.0e-15
Match length 120
% identity 41
NCBI Description (Z81012) unknown [Ricinus communis]

Seq. No. 136285
Contig ID 131198_1.R1010
5'-most EST g2757313
Method BLASTX
NCBI GI g4753655
BLAST score 449
E value 1.0e-44
Match length 93
% identity 84
NCBI Description (AL049751) pectate lyase like protein [Arabidopsis thaliana]

Seq. No. 136286
Contig ID 131208_1.R1010
5'-most EST g315428
Method BLASTX
NCBI GI g4678943
BLAST score 446
E value 6.0e-66
Match length 156
% identity 74
NCBI Description (AL049711) putative protein [Arabidopsis thaliana]

Seq. No.	136287
Contig ID	131223_1.R1010
5'-most EST	g315444
Method	BLASTN
NCBI GI	g4580386
BLAST score	438
E value	0.0e+00
Match length	530
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T8O18 genomic sequence, complete sequence

Seq. No.	136288
Contig ID	131236_1.R1010
5'-most EST	g315643
Method	BLASTN
NCBI GI	g4220510
BLAST score	142
E value	5.0e-74
Match length	403
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18 (ESSAII project)

Seq. No.	136289
Contig ID	131246_1.R1010
5'-most EST	g315476

Seq. No.	136290
Contig ID	131311_1.R1010
5'-most EST	g315547

Seq. No.	136291
Contig ID	131318_1.R1010
5'-most EST	g2763303
Method	BLASTX
NCBI GI	g3618320
BLAST score	249
E value	3.0e-21
Match length	93
% identity	48
NCBI Description	(AB001888) zinc finger protein [Oryza sativa]

Seq. No.	136292
Contig ID	131335_1.R1010
5'-most EST	g315576
Method	BLASTX
NCBI GI	g3892701
BLAST score	211
E value	7.0e-17
Match length	93
% identity	46
NCBI Description	(AL033545) hypothetical protein [Arabidopsis thaliana]

Seq. No.	136293
Contig ID	131417_1.R1010

5'-most EST	g958178
Method	BLASTN
NCBI GI	g3510345
BLAST score	90
E value	6.0e-43
Match length	391
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNJ8, complete sequence [Arabidopsis thaliana]

Seq. No.	136294
Contig ID	131476_1.R1010
5'-most EST	g2758438
Method	BLASTX
NCBI GI	g3482919
BLAST score	403
E value	8.0e-40
Match length	102
% identity	82
NCBI Description	(AC003970) Putative protein kinase [Arabidopsis thaliana]

Seq. No.	136295
Contig ID	131480_1.R1010
5'-most EST	g2393412
Method	BLASTX
NCBI GI	g4567304
BLAST score	561
E value	1.0e-57
Match length	129
% identity	89
NCBI Description	(AC005956) unknown protein [Arabidopsis thaliana]

Seq. No.	136296
Contig ID	131498_1.R1010
5'-most EST	g2758078
Method	BLASTX
NCBI GI	g2494041
BLAST score	245
E value	1.0e-20
Match length	164
% identity	43
NCBI Description	DIAMINOPIMELATE EPIMERASE >gi_1653875_dbj_BAA18785_ (D90917) diaminopimelate epimerase [Synechocystis sp.]

Seq. No.	136297
Contig ID	131560_1.R1010
5'-most EST	g2763468
Method	BLASTX
NCBI GI	g2160166
BLAST score	82
E value	2.0e-15
Match length	186
% identity	36
NCBI Description	(AC000132) No definition line found [Arabidopsis thaliana]

Seq. No.	136298
Contig ID	131644_1.R1010

5'-most EST	g2762822
Method	BLASTN
NCBI GI	g4678291
BLAST score	277
E value	1.0e-154
Match length	330
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F28P10 (ESSA project)

Seq. No.	136299
Contig ID	131653_1.R1010
5'-most EST	g315976
Method	BLASTX
NCBI GI	g1706714
BLAST score	297
E value	8.0e-27
Match length	92
% identity	63
NCBI Description	ELECTRON TRANSFER FLAVOPROTEIN BETA-SUBUNIT (BETA-ETF) (ELECTRON TRANSFER FLAVOPROTEIN SMALL SUBUNIT) (ETFSS) >gi_1209054 (U32230) EtfS [Bradyrhizobium japonicum]

Seq. No.	136300
Contig ID	131702_1.R1010
5'-most EST	g2047618

Seq. No.	136301
Contig ID	131748_1.R1010
5'-most EST	g394894
Method	BLASTX
NCBI GI	g4512667
BLAST score	330
E value	5.0e-52
Match length	116
% identity	84
NCBI Description	(AC006931) putative MAP kinase [Arabidopsis thaliana]

Seq. No.	136302
Contig ID	131755_1.R1010
5'-most EST	g396604
Method	BLASTN
NCBI GI	g4586098
BLAST score	339
E value	0.0e+00
Match length	383
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F16J13 (ESSA project)

Seq. No.	136303
Contig ID	131795_1.R1010
5'-most EST	g396867
Method	BLASTX
NCBI GI	g99771
BLAST score	279
E value	7.0e-25

Match length	86
% identity	62
NCBI Description	ubiquitin 81-aa extension protein 1 - Arabidopsis thaliana >gi_166934 (J05539) ubiquitin extension protein (UBQ5) [Arabidopsis thaliana]

Seq. No.	136304
Contig ID	131800_1.R1010
5'-most EST	g396873
Method	BLASTN
NCBI GI	g4159699
BLAST score	447
E value	0.0e+00
Match length	459
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K16E1, complete sequence

Seq. No.	136305
Contig ID	131803_1.R1010
5'-most EST	g396891

Seq. No.	136306
Contig ID	131837_1.R1010
5'-most EST	g397188
Method	BLASTX
NCBI GI	g3128200
BLAST score	247
E value	6.0e-21
Match length	84
% identity	62
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	136307
Contig ID	131839_1.R1010
5'-most EST	g397190
Method	BLASTX
NCBI GI	g4490297
BLAST score	554
E value	7.0e-57
Match length	184
% identity	62
NCBI Description	(AL035678) putative protein [Arabidopsis thaliana]

Seq. No.	136308
Contig ID	131906_1.R1010
5'-most EST	g397266
Method	BLASTN
NCBI GI	g2244991
BLAST score	261
E value	1.0e-145
Match length	328
% identity	87
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No. 136309

Contig ID	131941_1.R1010
5'-most EST	g397310
Method	BLASTX
NCBI GI	g4220474
BLAST score	497
E value	6.0e-50
Match length	156
% identity	72
NCBI Description	(AC006069) putative myosin heavy chain [Arabidopsis thaliana]

Seq. No.	136310
Contig ID	131980_1.R1010
5'-most EST	g2576801

Seq. No.	136311
Contig ID	132104_1.R1010
5'-most EST	g406618
Method	BLASTN
NCBI GI	g3080430
BLAST score	427
E value	0.0e+00
Match length	590
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T19P19 (ESSAII project)

Seq. No.	136312
Contig ID	132107_1.R1010
5'-most EST	g2722678
Method	BLASTX
NCBI GI	g4589974
BLAST score	559
E value	2.0e-57
Match length	118
% identity	92
NCBI Description	(AC007195) unknown protein [Arabidopsis thaliana]

Seq. No.	136313
Contig ID	132169_1.R1010
5'-most EST	g2048503
Method	BLASTN
NCBI GI	g3449326
BLAST score	375
E value	0.0e+00
Match length	429
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M22, complete sequence [Arabidopsis thaliana]

Seq. No.	136314
Contig ID	132179_1.R1010
5'-most EST	g2749492
Method	BLASTN
NCBI GI	g3869074
BLAST score	343
E value	0.0e+00

Match length	422
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMI9, complete sequence [Arabidopsis thaliana]

Seq. No.	136315
Contig ID	132186_1.R1010
5'-most EST	g398883
Method	BLASTN
NCBI GI	g2828180
BLAST score	366
E value	0.0e+00
Match length	442
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDK4, complete sequence [Arabidopsis thaliana]

Seq. No.	136316
Contig ID	132229_1.R1010
5'-most EST	g435205
Method	BLASTN
NCBI GI	g4558656
BLAST score	323
E value	0.0e+00
Match length	387
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T10F5 genomic sequence, complete sequence

Seq. No.	136317
Contig ID	132312_1.R1010
5'-most EST	g402945
Method	BLASTN
NCBI GI	g3046856
BLAST score	301
E value	1.0e-169
Match length	381
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXI22, complete sequence [Arabidopsis thaliana]

Seq. No.	136318
Contig ID	132375_1.R1010
5'-most EST	g2708350

Seq. No.	136319
Contig ID	132394_1.R1010
5'-most EST	g2580949
Method	BLASTX
NCBI GI	g2811048
BLAST score	174
E value	2.0e-12
Match length	80
% identity	50
NCBI Description	DEVB PROTEIN HOMOLOG >gi_2131051_emb_CAB09261_ (Z95844) devB [Mycobacterium tuberculosis]

Seq. No.	136320
Contig ID	132488_1.R1010
5'-most EST	g406691
Method	BLASTN
NCBI GI	g3046854
BLAST score	448
E value	0.0e+00
Match length	509
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRG7, complete sequence [Arabidopsis thaliana]

Seq. No.	136321
Contig ID	132499_1.R1010
5'-most EST	g2048229
Method	BLASTX
NCBI GI	g4586576
BLAST score	239
E value	5.0e-20
Match length	65
% identity	69
NCBI Description	(AB024992) multidrug resistance protein [Cicer arietinum]

Seq. No.	136322
Contig ID	132537_1.R1010
5'-most EST	g406811
Method	BLASTN
NCBI GI	g1785729
BLAST score	353
E value	0.0e+00
Match length	391
% identity	98
NCBI Description	A.thaliana mitochondrial genome, part B

Seq. No.	136323
Contig ID	132591_1.R1010
5'-most EST	g410350
Method	BLASTN
NCBI GI	g4220631
BLAST score	328
E value	0.0e+00
Match length	368
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K5J14, complete sequence [Arabidopsis thaliana]

Seq. No.	136324
Contig ID	132603_1.R1010
5'-most EST	g410365

Seq. No.	136325
Contig ID	132608_1.R1010
5'-most EST	g410372

Seq. No.	136326
Contig ID	132628_1.R1010
5'-most EST	g410397

Method	BLASTN
NCBI GI	g3128140
BLAST score	218
E value	1.0e-119
Match length	226
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJE4, complete sequence [Arabidopsis thaliana]

Seq. No.	136327
Contig ID	132646_1.R1010
5'-most EST	g416434
Method	BLASTX
NCBI GI	g3335336
BLAST score	612
E value	7.0e-64
Match length	127
% identity	94
NCBI Description	(AC004512) Contains similarity to DnaJ gene YM8520.10 gb_825566 from from S. cerevisiae cosmid gb_Z49705. ESTs gb_Z47720 and gb_Z29879 come from this gene. [Arabidopsis thaliana]

Seq. No.	136328
Contig ID	132667_1.R1010
5'-most EST	g3450623
Method	BLASTN
NCBI GI	g3047060
BLAST score	36
E value	1.0e-10
Match length	83
% identity	87
NCBI Description	Arabidopsis thaliana BAC F7N22

Seq. No.	136329
Contig ID	132668_1.R1010
5'-most EST	g416463
Method	BLASTN
NCBI GI	g1785673
BLAST score	549
E value	0.0e+00
Match length	572
% identity	61
NCBI Description	A.thaliana mitochondrial genome, part A

Seq. No.	136330
Contig ID	132695_1.R1010
5'-most EST	g2413491
Method	BLASTN
NCBI GI	g3894179
BLAST score	304
E value	1.0e-170
Match length	357
% identity	38
NCBI Description	Arabidopsis thaliana chromosome II BAC F13H10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136331
Contig ID	132713_1.R1010
5'-most EST	g635224
Method	BLASTN
NCBI GI	g3241925
BLAST score	176
E value	4.0e-94
Match length	387
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK9, complete sequence [Arabidopsis thaliana]

Seq. No.	136332
Contig ID	132722_1.R1010
5'-most EST	g2764255

Seq. No.	136333
Contig ID	132750_1.R1010
5'-most EST	g634171
Method	BLASTN
NCBI GI	g3212846
BLAST score	281
E value	1.0e-157
Match length	309
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136334
Contig ID	132752_1.R1010
5'-most EST	g2062883
Method	BLASTN
NCBI GI	g1050427
BLAST score	345
E value	0.0e+00
Match length	400
% identity	98
NCBI Description	A.thaliana mRNA for an exon from SNAP25A protein

Seq. No.	136335
Contig ID	132790_1.R1010
5'-most EST	g2759858
Method	BLASTN
NCBI GI	g2098816
BLAST score	243
E value	1.0e-134
Match length	361
% identity	96
NCBI Description	Arabidopsis thaliana BAC F19G10, complete sequence

Seq. No.	136336
Contig ID	132798_1.R1010
5'-most EST	g435234
Method	BLASTX
NCBI GI	g2244926
BLAST score	269
E value	1.0e-23

Match length	62
% identity	87
NCBI Description	(Z97339) glutaredoxin [Arabidopsis thaliana]

Seq. No.	136337
Contig ID	132799_1.R1010
5'-most EST	g435235
Method	BLASTX
NCBI GI	g3377841
BLAST score	201
E value	5.0e-35
Match length	90
% identity	86
NCBI Description	(AF075598) contains similarity to phosphofructokinases (Pfam; PFK.hmm, score; 36.60) [Arabidopsis thaliana]

Seq. No.	136338
Contig ID	132885_1.R1010
5'-most EST	g906333
Method	BLASTX
NCBI GI	g1620898
BLAST score	192
E value	2.0e-14
Match length	73
% identity	60
NCBI Description	(D87957) protein involved in sexual development [Homo sapiens]

Seq. No.	136339
Contig ID	132951_1.R1010
5'-most EST	g2749660
Method	BLASTN
NCBI GI	g4220643
BLAST score	212
E value	1.0e-115
Match length	409
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD22, complete sequence [Arabidopsis thaliana]

Seq. No.	136340
Contig ID	132969_1.R1010
5'-most EST	g453739
Method	BLASTN
NCBI GI	g3873174
BLAST score	301
E value	1.0e-169
Match length	305
% identity	79
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14N23, complete sequence [Arabidopsis thaliana]

Seq. No.	136341
Contig ID	132996_1.R1010
5'-most EST	g453766
Method	BLASTN
NCBI GI	g2264315

BLAST score	320
E value	1.0e-180
Match length	383
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRN17, complete sequence [Arabidopsis thaliana]

Seq. No.	136342
Contig ID	132997_1.R1010
5'-most EST	g2445924
Method	BLASTN
NCBI GI	g2264315
BLAST score	238
E value	1.0e-131
Match length	367
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRN17, complete sequence [Arabidopsis thaliana]

Seq. No.	136343
Contig ID	133004_1.R1010
5'-most EST	g936377

Seq. No.	136344
Contig ID	133086_1.R1010
5'-most EST	g453875
Method	BLASTX
NCBI GI	g3935151
BLAST score	312
E value	1.0e-28
Match length	68
% identity	90
NCBI Description	(AC005106) T25N20.15 [Arabidopsis thaliana]

Seq. No.	136345
Contig ID	133110_1.R1010
5'-most EST	g3450014

Seq. No.	136346
Contig ID	133152_1.R1010
5'-most EST	g454213
Method	BLASTX
NCBI GI	g4567279
BLAST score	565
E value	2.0e-62
Match length	156
% identity	74
NCBI Description	(AC006841) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	136347
Contig ID	133170_1.R1010
5'-most EST	g458747
Method	BLASTN
NCBI GI	g3128166
BLAST score	364
E value	0.0e+00

Match length	599
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F4I1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136348
Contig ID	133196_1.R1010
5'-most EST	g2393161
Method	BLASTX
NCBI GI	g4559380
BLAST score	581
E value	6.0e-60
Match length	110
% identity	100
NCBI Description	(AC006526) putative auxin-responsive GH3 protein [Arabidopsis thaliana]

Seq. No.	136349
Contig ID	133218_1.R1010
5'-most EST	g458795
Method	BLASTN
NCBI GI	g2618677
BLAST score	219
E value	1.0e-120
Match length	299
% identity	95
NCBI Description	Arabidopsis thaliana BAC F21B7 chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	136350
Contig ID	133355_1.R1010
5'-most EST	g460474

Seq. No.	136351
Contig ID	133357_1.R1010
5'-most EST	g2596380
Method	BLASTX
NCBI GI	g3980379
BLAST score	460
E value	6.0e-46
Match length	92
% identity	99
NCBI Description	(AC004561) putative cyclin, PCNA [Arabidopsis thaliana]

Seq. No.	136352
Contig ID	133359_1.R1010
5'-most EST	g460478

Seq. No.	136353
Contig ID	133459_1.R1010
5'-most EST	g496460

Seq. No.	136354
Contig ID	133460_1.R1010
5'-most EST	g496461
Method	BLASTX
NCBI GI	g2497913

BLAST score	500
E value	1.0e-50
Match length	82
% identity	99
NCBI Description	EC PROTEIN HOMOLOG

Seq. No.	136355
Contig ID	133467_1.R1010
5'-most EST	g473296
Method	BLASTX
NCBI GI	g3738325
BLAST score	331
E value	7.0e-31
Match length	90
% identity	74
NCBI Description	(AC005170) putative CaMB-channel protein [Arabidopsis thaliana]

Seq. No.	136356
Contig ID	133473_1.R1010
5'-most EST	g496463
Method	BLASTN
NCBI GI	g3128137
BLAST score	281
E value	1.0e-157
Match length	494
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9I9, complete sequence [Arabidopsis thaliana]

Seq. No.	136357
Contig ID	133492_1.R1010
5'-most EST	g2048883
Method	BLASTN
NCBI GI	g4678291
BLAST score	294
E value	1.0e-164
Match length	411
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F28P10 (ESSA project)

Seq. No.	136358
Contig ID	133497_1.R1010
5'-most EST	g2393352

Seq. No.	136359
Contig ID	133510_1.R1010
5'-most EST	g473347
Method	BLASTN
NCBI GI	g1785729
BLAST score	488
E value	0.0e+00
Match length	513
% identity	99
NCBI Description	A.thaliana mitochondrial genome, part B

Seq. No.	136360
Contig ID	133526_1.R1010
5'-most EST	g493266
Method	BLASTX
NCBI GI	g4063733
BLAST score	964
E value	1.0e-105
Match length	203
% identity	92
NCBI Description	(AC006259) putative P450 [Arabidopsis thaliana]

Seq. No.	136361
Contig ID	133529_1.R1010
5'-most EST	g493310

Seq. No.	136362
Contig ID	133546_1.R1010
5'-most EST	g2413968
Method	BLASTX
NCBI GI	g4582436
BLAST score	233
E value	3.0e-19
Match length	90
% identity	56
NCBI Description	(AC007196) unknown protein [Arabidopsis thaliana]

Seq. No.	136363
Contig ID	133554_1.R1010
5'-most EST	g1328262
Method	BLASTN
NCBI GI	g2351067
BLAST score	361
E value	0.0e+00
Match length	396
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPO12, complete sequence [Arabidopsis thaliana]

Seq. No.	136364
Contig ID	133559_1.R1010
5'-most EST	g2414146
Method	BLASTX
NCBI GI	g1220453
BLAST score	408
E value	1.0e-39
Match length	124
% identity	60
NCBI Description	(M79328) alpha-amylase [Solanum tuberosum]

Seq. No.	136365
Contig ID	133571_1.R1010
5'-most EST	g493312
Method	BLASTN
NCBI GI	g940179
BLAST score	224
E value	1.0e-123
Match length	423

% identity	94
NCBI Description	Arabidopsis thaliana floral homeotic (AP3) gene, promoter region and partial cds

Seq. No.	136366
Contig ID	133572_1.R1010
5'-most EST	g2393354
Method	BLASTN
NCBI GI	g4580386
BLAST score	278
E value	1.0e-155
Match length	383
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T8O18 genomic sequence, complete sequence

Seq. No.	136367
Contig ID	133677_1.R1010
5'-most EST	g507094

Seq. No.	136368
Contig ID	133723_1.R1010
5'-most EST	g496401
Method	BLASTX
NCBI GI	g2583129
BLAST score	303
E value	1.0e-27
Match length	56
% identity	98
NCBI Description	(AC002387) putative methionine aminopeptidase [Arabidopsis thaliana]

Seq. No.	136369
Contig ID	133760_1.R1010
5'-most EST	g496439
Method	BLASTX
NCBI GI	g3164138
BLAST score	144
E value	1.0e-13
Match length	102
% identity	43
NCBI Description	(D78604) cytochrome p450 monooxygenase [Arabidopsis thaliana] >gi_4115378 (AC005967) cytochrome p450 monooxygenase [Arabidopsis thaliana]

Seq. No.	136370
Contig ID	133761_1.R1010
5'-most EST	g506948
Method	BLASTN
NCBI GI	g2351063
BLAST score	104
E value	2.0e-51
Match length	224
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCL19, complete sequence [Arabidopsis thaliana]

Seq. No.	136371
Contig ID	133772_1.R1010
5'-most EST	g623727

Seq. No.	136372
Contig ID	133881_1.R1010
5'-most EST	g2047759
Method	BLASTN
NCBI GI	g2280508
BLAST score	284
E value	1.0e-158
Match length	388
% identity	97
NCBI Description	Arabidopsis thaliana tRNA-Glu gene

Seq. No.	136373
Contig ID	133887_1.R1010
5'-most EST	g1158841
Method	BLASTN
NCBI GI	g3355463
BLAST score	233
E value	1.0e-128
Match length	436
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136374
Contig ID	133900_1.R1010
5'-most EST	g498476

Seq. No.	136375
Contig ID	133906_1.R1010
5'-most EST	g498482
Method	BLASTN
NCBI GI	g4519197
BLAST score	44
E value	1.0e-15
Match length	135
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MTC11, complete sequence

Seq. No.	136376
Contig ID	133939_1.R1010
5'-most EST	g498515
Method	BLASTX
NCBI GI	g4567304
BLAST score	462
E value	1.0e-122
Match length	233
% identity	93
NCBI Description	(AC005956) unknown protein [Arabidopsis thaliana]

Seq. No.	136377
Contig ID	134082_1.R1010
5'-most EST	g2747650

Method	BLASTX
NCBI GI	g3413703
BLAST score	471
E value	4.0e-47
Match length	148
% identity	70
NCBI Description	(AC004747) unknown protein [Arabidopsis thaliana]

Seq. No.	136378
Contig ID	134095_1.R1010
5'-most EST	g957900
Method	BLASTX
NCBI GI	g4646206
BLAST score	617
E value	3.0e-64
Match length	172
% identity	72
NCBI Description	(AC007230) Contains similarity to gb_D13630 KIAA0005 gene from Homo sapiens. ESTs gb_T45345, gb_T21086, gb_R90360, gb_T20468, gb_T45191 and gb_AI100459 come from this gene. [Arabidopsis thaliana]

Seq. No.	136379
Contig ID	134128_1.R1010
5'-most EST	g2733521
Method	BLASTX
NCBI GI	g4309681
BLAST score	331
E value	1.0e-30
Match length	120
% identity	51
NCBI Description	(AC006930) R33423_1 [Homo sapiens]

Seq. No.	136380
Contig ID	134131_1.R1010
5'-most EST	g2757674
Method	BLASTX
NCBI GI	g2213600
BLAST score	430
E value	3.0e-42
Match length	161
% identity	58
NCBI Description	(AC000348) T7N9.20 [Arabidopsis thaliana]

Seq. No.	136381
Contig ID	134132_1.R1010
5'-most EST	g2733523
Method	BLASTN
NCBI GI	g3873174
BLAST score	363
E value	0.0e+00
Match length	410
% identity	98
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14N23, complete sequence [Arabidopsis thaliana]

Seq. No.	136382

Contig ID	134189_1.R1010
5'-most EST	g3450386
Method	BLASTX
NCBI GI	g4689473
BLAST score	522
E value	4.0e-53
Match length	139
% identity	73
NCBI Description	(AC007213) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	136383
Contig ID	134276_1.R1010
5'-most EST	g1217058
Method	BLASTX
NCBI GI	g2062155
BLAST score	390
E value	2.0e-37
Match length	200
% identity	38
NCBI Description	(AC001645) mitochondrial processing peptidase alpha subunit precusor isolog [Arabidopsis thaliana]

Seq. No.	136384
Contig ID	134280_1.R1010
5'-most EST	g502144
Method	BLASTN
NCBI GI	g3985957
BLAST score	513
E value	0.0e+00
Match length	547
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN8, complete sequence [Arabidopsis thaliana]

Seq. No.	136385
Contig ID	134318_1.R1010
5'-most EST	g502195
Method	BLASTX
NCBI GI	g1617274
BLAST score	441
E value	3.0e-44
Match length	233
% identity	55
NCBI Description	(Z72152) AMP-binding protein [Brassica napus]

Seq. No.	136386
Contig ID	134347_1.R1010
5'-most EST	g1217184
Method	BLASTN
NCBI GI	g4580386
BLAST score	126
E value	2.0e-64
Match length	403
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T8O18 genomic sequence, complete sequence

Seq. No.	136387
Contig ID	134377_1.R1010
5'-most EST	g557621
Method	BLASTN
NCBI GI	g2564046
BLAST score	172
E value	7.0e-92
Match length	408
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MGI19, complete sequence [Arabidopsis thaliana]

Seq. No.	136388
Contig ID	134431_1.R1010
5'-most EST	g2446139

Seq. No.	136389
Contig ID	134494_1.R1010
5'-most EST	g506591
Method	BLASTN
NCBI GI	g2191126
BLAST score	93
E value	1.0e-44
Match length	149
% identity	97
NCBI Description	Arabidopsis thaliana BAC IG002N01

Seq. No.	136390
Contig ID	134543_1.R1010
5'-most EST	g1517266
Method	BLASTX
NCBI GI	g4580391
BLAST score	162
E value	6.0e-11
Match length	75
% identity	49
NCBI Description	(AC007171) unknown protein [Arabidopsis thaliana]

Seq. No.	136391
Contig ID	134546_1.R1010
5'-most EST	g506934
Method	BLASTN
NCBI GI	g3201608
BLAST score	211
E value	1.0e-115
Match length	495
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F7F1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136392
Contig ID	134554_1.R1010
5'-most EST	g509100
Method	BLASTX
NCBI GI	g4539337
BLAST score	165

E value	1.0e-12
Match length	43
% identity	78
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	136393
Contig ID	134559_1.R1010
5'-most EST	g506952
Method	BLASTX
NCBI GI	g1903357
BLAST score	249
E value	3.0e-21
Match length	73
% identity	66
NCBI Description	(AC000104) Strong similarity to Arabidopsis 2A6 (gb_X83096). [Arabidopsis thaliana]

Seq. No.	136394
Contig ID	134568_1.R1010
5'-most EST	g506963
Method	BLASTX
NCBI GI	g2979549
BLAST score	472
E value	2.0e-47
Match length	89
% identity	99
NCBI Description	(AC003680) putative 7-ethoxycoumarin O-deethylase [Arabidopsis thaliana]

Seq. No.	136395
Contig ID	134626_1.R1010
5'-most EST	g957935

Seq. No.	136396
Contig ID	134655_1.R1010
5'-most EST	g507104
Method	BLASTN
NCBI GI	g3241924
BLAST score	102
E value	4.0e-50
Match length	359
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNC6, complete sequence [Arabidopsis thaliana]

Seq. No.	136397
Contig ID	134820_1.R1010
5'-most EST	g937858
Method	BLASTX
NCBI GI	g3548808
BLAST score	220
E value	4.0e-20
Match length	128
% identity	45
NCBI Description	(AC005313) unknown protein [Arabidopsis thaliana]

Seq. No. 136398

Contig ID	134864_1.R1010
5'-most EST	g511167
Method	BLASTX
NCBI GI	g3024666
BLAST score	341
E value	5.0e-32
Match length	81
% identity	75
NCBI Description	STRICTOSIDINE SYNTHASE 1/2 PRECURSOR >gi_1754983 (U43713) strictosidine synthase [Arabidopsis thaliana] >gi_1754985 (U43945) strictosidine synthase [Arabidopsis thaliana]

Seq. No.	136399
Contig ID	134866_1.R1010
5'-most EST	g511169
Method	BLASTX
NCBI GI	g4263715
BLAST score	669
E value	2.0e-70
Match length	130
% identity	100
NCBI Description	(AC006223) putative alanine acetyl transferase [Arabidopsis thaliana]

Seq. No.	136400
Contig ID	134881_1.R1010
5'-most EST	g511184
Method	BLASTN
NCBI GI	g3046848
BLAST score	489
E value	0.0e+00
Match length	569
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18C1, complete sequence [Arabidopsis thaliana]

Seq. No.	136401
Contig ID	134932_1.R1010
5'-most EST	g515433
Method	BLASTN
NCBI GI	g3980263
BLAST score	42
E value	3.0e-14
Match length	42
% identity	100
NCBI Description	Cicer arietinum mRNA for 20S proteasome beta subunit

Seq. No.	136402
Contig ID	134971_1.R1010
5'-most EST	g2763682

Seq. No.	136403
Contig ID	135056_1.R1010
5'-most EST	g550167
Method	BLASTX
NCBI GI	g4539601
BLAST score	146

E value 4.0e-09
Match length 108
% identity 35
NCBI Description (AL049522) serine/threonine-protein kinase [Schizosaccharomyces pombe]

Seq. No. 136404
Contig ID 135072_1.R1010
5'-most EST g550184
Method BLASTN
NCBI GI g4584531
BLAST score 317
E value 1.0e-178
Match length 329
% identity 82
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T9E8 (ESSA project)

Seq. No. 136405
Contig ID 135092_1.R1010
5'-most EST g550204

Seq. No. 136406
Contig ID 135097_1.R1010
5'-most EST g2722958

Seq. No. 136407
Contig ID 135136_1.R1010
5'-most EST g550248
Method BLASTX
NCBI GI g4506399
BLAST score 142
E value 1.0e-08
Match length 87
% identity 40
NCBI Description homolog of yeast Rae1 (Bharathi) mRNA-associated protein of 41 kDa (Kraemer) >gi_3122666_sp_P78406_RA1L_HUMAN MRNA-ASSOCIATED PROTEIN MRNP41 (RAE1 PROTEIN HOMOLOG) >gi_1903456 (U84720) mRNA export protein [Homo sapiens]

Seq. No. 136408
Contig ID 135137_1.R1010
5'-most EST g935677
Method BLASTX
NCBI GI g3122671
BLAST score 470
E value 2.0e-59
Match length 125
% identity 91
NCBI Description HYPOTHETICAL RAE1-LIKE PROTEIN >gi_2129676_pir__S71241 probable export protein - Arabidopsis thaliana >gi_1297188 (U53501) Theoretical protein with similarity to Swiss-Prot Accession Number P41838 poly A+ RNA export protein [Arabidopsis thaliana]

Seq. No. 136409
Contig ID 135138_1.R1010

5'-most EST	g550250
Method	BLASTX
NCBI GI	g4741927
BLAST score	409
E value	5.0e-40
Match length	82
% identity	96
NCBI Description	(AF130252) calcium dependent protein kinase CP4 [Arabidopsis thaliana]

Seq. No.	136410
Contig ID	135199_1.R1010
5'-most EST	g572552
Method	BLASTN
NCBI GI	g2828185
BLAST score	519
E value	0.0e+00
Match length	527
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUD21, complete sequence [Arabidopsis thaliana]

Seq. No.	136411
Contig ID	135208_1.R1010
5'-most EST	g557631
Method	BLASTN
NCBI GI	g2924651
BLAST score	406
E value	0.0e+00
Match length	446
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana]

Seq. No.	136412
Contig ID	135288_1.R1010
5'-most EST	g2393345
Method	BLASTN
NCBI GI	g3859658
BLAST score	305
E value	1.0e-171
Match length	412
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1 (ESSAII project)

Seq. No.	136413
Contig ID	135327_1.R1010
5'-most EST	g572590

Seq. No.	136414
Contig ID	135342_1.R1010
5'-most EST	g2062800
Method	BLASTN
NCBI GI	g4097544
BLAST score	249
E value	1.0e-138

Match length	369
% identity	94
NCBI Description	Arabidopsis thaliana farnesylated protein ATFP2 mRNA, partial cds

Seq. No.	136415
Contig ID	135411_1.R1010
5'-most EST	g586964
Method	BLASTN
NCBI GI	g4580514
BLAST score	407
E value	0.0e+00
Match length	431
% identity	99
NCBI Description	Arabidopsis thaliana scarecrow-like 3 (SCL3) mRNA, partial cds

Seq. No.	136416
Contig ID	135420_1.R1010
5'-most EST	g586973
Method	BLASTX
NCBI GI	g4510406
BLAST score	275
E value	3.0e-24
Match length	66
% identity	77
NCBI Description	(AC006587) putative protein kinase [Arabidopsis thaliana]

Seq. No.	136417
Contig ID	135468_1.R1010
5'-most EST	g587024
Method	BLASTN
NCBI GI	g4757395
BLAST score	360
E value	0.0e+00
Match length	363
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L13, complete sequence

Seq. No.	136418
Contig ID	135469_1.R1010
5'-most EST	g2749280
Method	BLASTN
NCBI GI	g4757395
BLAST score	292
E value	1.0e-163
Match length	383
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L13, complete sequence

Seq. No.	136419
Contig ID	135481_1.R1010
5'-most EST	g587042

Seq. No. 136420

Contig ID 135528_1.R1010
5'-most EST g623005

Seq. No. 136421
Contig ID 135698_1.R1010
5'-most EST g634190
Method BLASTN
NCBI GI g2656024
BLAST score 350
E value 0.0e+00
Match length 406
% identity 97
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15E6

Seq. No. 136422
Contig ID 135702_1.R1010
5'-most EST g634242
Method BLASTN
NCBI GI g3869074
BLAST score 273
E value 1.0e-152
Match length 305
% identity 97
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMI9, complete sequence [Arabidopsis thaliana]

Seq. No. 136423
Contig ID 135726_1.R1010
5'-most EST g634434
Method BLASTX
NCBI GI g4115934
BLAST score 587
E value 1.0e-60
Match length 139
% identity 69
NCBI Description (AF118223) contains similarity to Methanobacterium thermoautotrophicum transcriptional regulator (GB:AE000850) [Arabidopsis thaliana]

Seq. No. 136424
Contig ID 135805_1.R1010
5'-most EST g634781
Method BLASTX
NCBI GI g3047127
BLAST score 256
E value 6.0e-22
Match length 110
% identity 57
NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]

Seq. No. 136425
Contig ID 135837_1.R1010
5'-most EST g634880

Seq. No. 136426
Contig ID 135926_1.R1010

5'-most EST	g671760
Seq. No.	136427
Contig ID	135927_1.R1010
5'-most EST	g957936
Method	BLASTX
NCBI GI	g2702283
BLAST score	510
E value	8.0e-52
Match length	124
% identity	76
NCBI Description	(AC003033) unknown protein [Arabidopsis thaliana]
Seq. No.	136428
Contig ID	135963_1.R1010
5'-most EST	g671802
Method	BLASTN
NCBI GI	g2618602
BLAST score	51
E value	1.0e-19
Match length	143
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]
Seq. No.	136429
Contig ID	135986_1.R1010
5'-most EST	g683513
Seq. No.	136430
Contig ID	136066_1.R1010
5'-most EST	g773438
Method	BLASTX
NCBI GI	g1168530
BLAST score	304
E value	5.0e-39
Match length	99
% identity	90
NCBI Description	SERINE/THREONINE-PROTEIN KINASE ASK2 >gi_99748_pir__S24586 probable serine/threonine-specific protein kinase (EC 2.7.1.-) (clone ASK2) - Arabidopsis thaliana >gi_16443_emb_CAA78106_ (Z12120) protein kinase [Arabidopsis thaliana]
Seq. No.	136431
Contig ID	136100_1.R1010
5'-most EST	g1158897
Method	BLASTX
NCBI GI	g2275210
BLAST score	271
E value	1.0e-23
Match length	134
% identity	46
NCBI Description	(AC002337) peptidyl-prolyl cis-trans isomerase isolog [Arabidopsis thaliana]
Seq. No.	136432

Contig ID	136129_1.R1010
5'-most EST	g2762996
Method	BLASTX
NCBI GI	g3080428
BLAST score	541
E value	2.0e-55
Match length	101
% identity	99
NCBI Description	(AL022604) putative protein [Arabidopsis thaliana]

Seq. No.	136433
Contig ID	136142_1.R1010
5'-most EST	g1216770
Method	BLASTN
NCBI GI	g2264312
BLAST score	360
E value	0.0e+00
Match length	424
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK16, complete sequence [Arabidopsis thaliana]

Seq. No.	136434
Contig ID	136156_1.R1010
5'-most EST	g2759115
Method	BLASTX
NCBI GI	g3738302
BLAST score	467
E value	9.0e-52
Match length	168
% identity	65
NCBI Description	(AC005309) tubby-like protein [Arabidopsis thaliana] >gi_4249398 (AC006072) putative tubby protein [Arabidopsis thaliana]

Seq. No.	136435
Contig ID	136199_1.R1010
5'-most EST	g757597

Seq. No.	136436
Contig ID	136211_1.R1010
5'-most EST	g757609

Seq. No.	136437
Contig ID	136297_1.R1010
5'-most EST	g1932914
Method	BLASTN
NCBI GI	g3402671
BLAST score	304
E value	1.0e-170
Match length	339
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T16B24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136438
Contig ID	136332_1.R1010

5'-most EST	g773491
Seq. No.	136439
Contig ID	136369_1.R1010
5'-most EST	g1054483
Method	BLASTX
NCBI GI	g2642444
BLAST score	325
E value	2.0e-39
Match length	130
% identity	67
NCBI Description	(AC002391) putative cytochrome P450 [Arabidopsis thaliana]
Seq. No.	136440
Contig ID	136462_1.R1010
5'-most EST	g860757
Method	BLASTN
NCBI GI	g3128166
BLAST score	377
E value	0.0e+00
Match length	498
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC F4I1 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	136441
Contig ID	136467_1.R1010
5'-most EST	g860763
Seq. No.	136442
Contig ID	136468_1.R1010
5'-most EST	g895730
Seq. No.	136443
Contig ID	136518_1.R1010
5'-most EST	g895726
Method	BLASTN
NCBI GI	g3927822
BLAST score	518
E value	0.0e+00
Match length	595
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F8N16 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	136444
Contig ID	136532_1.R1010
5'-most EST	g872008
Method	BLASTX
NCBI GI	g3738333
BLAST score	62
E value	5.0e-49
Match length	168
% identity	64
NCBI Description	(AC005170) unknown protein [Arabidopsis thaliana]
Seq. No.	136445

Contig ID	136538_1.R1010
5'-most EST	g872007
Method	BLASTN
NCBI GI	g3738313
BLAST score	294
E value	1.0e-164
Match length	356
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T29E15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136446
Contig ID	136552_1.R1010
5'-most EST	g935991
Method	BLASTX
NCBI GI	g2244984
BLAST score	514
E value	3.0e-52
Match length	132
% identity	81
NCBI Description	(Z97340) strong similarity to beta-1,3-glucanase class I precursor [Arabidopsis thaliana]

Seq. No.	136447
Contig ID	136574_1.R1010
5'-most EST	g895738
Method	BLASTN
NCBI GI	g2337888
BLAST score	336
E value	0.0e+00
Match length	455
% identity	95
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14J16, complete sequence [Arabidopsis thaliana]

Seq. No.	136448
Contig ID	136585_1.R1010
5'-most EST	g897686

Seq. No.	136449
Contig ID	136626_1.R1010
5'-most EST	g899190
Method	BLASTN
NCBI GI	g4733952
BLAST score	228
E value	1.0e-125
Match length	280
% identity	96
NCBI Description	Arabidopsis thaliana chromosome I BAC F23H11 genomic sequence, complete sequence

Seq. No.	136450
Contig ID	136713_1.R1010
5'-most EST	g1158562

Seq. No.	136451
Contig ID	136726_1.R1010

5'-most EST	g905495
Method	BLASTX
NCBI GI	g4538901
BLAST score	216
E value	3.0e-17
Match length	133
% identity	40
NCBI Description	(AL049482) RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]

Seq. No.	136452
Contig ID	136735_1.R1010
5'-most EST	g905505
Method	BLASTX
NCBI GI	g4531434
BLAST score	81
E value	5.0e-41
Match length	127
% identity	76
NCBI Description	(AC006224) unknown protein [Arabidopsis thaliana]

Seq. No.	136453
Contig ID	136754_1.R1010
5'-most EST	g905526
Method	BLASTN
NCBI GI	g1707006
BLAST score	366
E value	0.0e+00
Match length	472
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T1B8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136454
Contig ID	136849_1.R1010
5'-most EST	g905631
Method	BLASTX
NCBI GI	g2213594
BLAST score	273
E value	5.0e-24
Match length	77
% identity	65
NCBI Description	(AC000348) T7N9.14 [Arabidopsis thaliana]

Seq. No.	136455
Contig ID	136882_1.R1010
5'-most EST	g2596326

Seq. No.	136456
Contig ID	136930_1.R1010
5'-most EST	g930930
Method	BLASTN
NCBI GI	g3461810
BLAST score	45
E value	5.0e-16
Match length	77
% identity	90

NCBI Description	Arabidopsis thaliana chromosome II BAC T17M13 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	136457
Contig ID	137008_1.R1010
5'-most EST	g906898
Method	BLASTX
NCBI GI	g478809
BLAST score	564
E value	5.0e-61
Match length	170
% identity	67
NCBI Description	protein kinase 6 (EC 2.7.1.-) - soybean >gi_170047 (M67449) protein kinase [Glycine max] >gi_444789_prf__1908223A protein kinase [Glycine max]
Seq. No.	136458
Contig ID	137217_1.R1010
5'-most EST	g2758405
Method	BLASTN
NCBI GI	g3702734
BLAST score	294
E value	1.0e-164
Match length	411
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNB8, complete sequence [Arabidopsis thaliana]
Seq. No.	136459
Contig ID	137259_1.R1010
5'-most EST	g906112
Method	BLASTN
NCBI GI	g2673901
BLAST score	176
E value	3.0e-94
Match length	298
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T24P15 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	136460
Contig ID	137356_1.R1010
5'-most EST	g906215
Method	BLASTX
NCBI GI	g466022
BLAST score	183
E value	2.0e-13
Match length	162
% identity	30
NCBI Description	HYPOTHETICAL 77.3 KD PROTEIN T05G5.8 IN CHROMOSOME III >gi_482214_pir__S41008 hypothetical protein T05G5.8 - Caenorhabditis elegans
Seq. No.	136461
Contig ID	137455_1.R1010
5'-most EST	g906330
Method	BLASTX

NCBI GI	g4262154
BLAST score	282
E value	4.0e-26
Match length	125
% identity	58
NCBI Description	(AC005275) putative protein phosphatase regulatory subunit [Arabidopsis thaliana]

Seq. No.	136462
Contig ID	137534_1.R1010
5'-most EST	g906429
Method	BLASTN
NCBI GI	g2924733
BLAST score	34
E value	3.0e-09
Match length	142
% identity	81
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]

Seq. No.	136463
Contig ID	137592_1.R1010
5'-most EST	g906494
Method	BLASTN
NCBI GI	g3510340
BLAST score	118
E value	1.0e-59
Match length	396
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDN11, complete sequence [Arabidopsis thaliana]

Seq. No.	136464
Contig ID	137739_1.R1010
5'-most EST	g2596714
Method	BLASTX
NCBI GI	g4262234
BLAST score	683
E value	8.0e-72
Match length	195
% identity	55
NCBI Description	(AC006200) unknown protein [Arabidopsis thaliana]

Seq. No.	136465
Contig ID	137810_1.R1010
5'-most EST	g2756677
Method	BLASTX
NCBI GI	g3582340
BLAST score	160
E value	9.0e-11
Match length	58
% identity	53
NCBI Description	(AC005496) unknown protein [Arabidopsis thaliana]

Seq. No.	136466
Contig ID	137872_1.R1010
5'-most EST	g906815

Method	BLASTN
NCBI GI	g2760168
BLAST score	185
E value	2.0e-99
Match length	593
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MEE6, complete sequence [Arabidopsis thaliana]

Seq. No.	136467
Contig ID	137929_1.R1010
5'-most EST	g2747839

Seq. No.	136468
Contig ID	137938_1.R1010
5'-most EST	g957765

Seq. No.	136469
Contig ID	137986_1.R1010
5'-most EST	g906949
Method	BLASTX
NCBI GI	g4586039
BLAST score	249
E value	3.0e-21
Match length	76
% identity	67
NCBI Description	(AC007109) unknown protein [Arabidopsis thaliana]

Seq. No.	136470
Contig ID	138035_1.R1010
5'-most EST	g907005

Seq. No.	136471
Contig ID	138096_1.R1010
5'-most EST	g937520
Method	BLASTX
NCBI GI	g3176687
BLAST score	558
E value	1.0e-100
Match length	198
% identity	92
NCBI Description	(AC003671) Strong similarity to trehalose-6-phosphate synthase homolog from A. thaliana chromosome 4 contig gb_Z97344. ESTs gb_H37594, gb_R65023, gb_H37578 and gb_R64855 come from this gene. [Arabidopsis thaliana]

Seq. No.	136472
Contig ID	138132_1.R1010
5'-most EST	g2758070
Method	BLASTX
NCBI GI	g1903360
BLAST score	391
E value	1.0e-37
Match length	160
% identity	49
NCBI Description	(AC000104) Similar to Arabidopsis 2A6 (gb_X83096). EST gb_T76913 comes from this gene. [Arabidopsis thaliana]

Seq. No.	136473
Contig ID	138198_1.R1010
5'-most EST	g907192
Method	BLASTX
NCBI GI	g4454044
BLAST score	363
E value	8.0e-35
Match length	89
% identity	80
NCBI Description	(AL035394) putative Ap2 domain protein [Arabidopsis thaliana]

Seq. No.	136474
Contig ID	138206_1.R1010
5'-most EST	g2759446
Method	BLASTX
NCBI GI	g115783
BLAST score	89
E value	2.0e-48
Match length	110
% identity	93
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	136475
Contig ID	138287_1.R1010
5'-most EST	g930373
Method	BLASTX
NCBI GI	g2129471
BLAST score	394
E value	3.0e-38
Match length	101
% identity	79
NCBI Description	glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) precursor - Scotch pine >gi_1100223 (L32560) glyceraldehyde-3-phosphate dehydrogenase [Pinus sylvestris]

Seq. No.	136476
Contig ID	138309_1.R1010
5'-most EST	g930491

Seq. No.	136477
Contig ID	138377_1.R1010
5'-most EST	g930645
Method	BLASTX
NCBI GI	g2190550
BLAST score	258
E value	2.0e-22
Match length	73
% identity	66
NCBI Description	(AC001229) ESTs gb_T45673,gb_N37512 come from this gene. [Arabidopsis thaliana]

Seq. No. 136478

Contig ID	138391_1.R1010
5'-most EST	g930655
Method	BLASTX
NCBI GI	g3894191
BLAST score	290
E value	9.0e-26
Match length	175
% identity	48
NCBI Description	(AC005662) unknown protein [Arabidopsis thaliana]

Seq. No.	136479
Contig ID	138391_2.R1010
5'-most EST	g2393408
Method	BLASTX
NCBI GI	g3894191
BLAST score	269
E value	2.0e-23
Match length	132
% identity	48
NCBI Description	(AC005662) unknown protein [Arabidopsis thaliana]

Seq. No.	136480
Contig ID	138435_1.R1010
5'-most EST	g2393429

Seq. No.	136481
Contig ID	138438_1.R1010
5'-most EST	g930720

Seq. No.	136482
Contig ID	138445_1.R1010
5'-most EST	g930729

Seq. No.	136483
Contig ID	138494_1.R1010
5'-most EST	g930783

Seq. No.	136484
Contig ID	138613_1.R1010
5'-most EST	g930941
Method	BLASTN
NCBI GI	g3641835
BLAST score	204
E value	1.0e-111
Match length	400
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T4L20 (ESSAII project)

Seq. No.	136485
Contig ID	138696_1.R1010
5'-most EST	g931047
Method	BLASTX
NCBI GI	g4587540
BLAST score	546
E value	3.0e-56
Match length	124

% identity	87
NCBI Description	(AC006577) Belongs to the PF_00657 Lipase/Acylhydrolase with GDSL-motif family. [Arabidopsis thaliana]

Seq. No.	136486
Contig ID	138705_1.R1010
5'-most EST	g931059

Seq. No.	136487
Contig ID	138706_1.R1010
5'-most EST	g931060
Method	BLASTN
NCBI GI	g4027862
BLAST score	232
E value	1.0e-127
Match length	367
% identity	90
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T7A14 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136488
Contig ID	138860_1.R1010
5'-most EST	g2764066
Method	BLASTN
NCBI GI	g3327922
BLAST score	335
E value	0.0e+00
Match length	343
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T31E10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136489
Contig ID	138862_1.R1010
5'-most EST	g931243
Method	BLASTX
NCBI GI	g4468803
BLAST score	351
E value	2.0e-33
Match length	107
% identity	70
NCBI Description	(AL035601) cytochrome P450-like protein [Arabidopsis thaliana]

Seq. No.	136490
Contig ID	138969_1.R1010
5'-most EST	g1158777

Seq. No.	136491
Contig ID	139006_1.R1010
5'-most EST	g931937
Method	BLASTX
NCBI GI	g2827625
BLAST score	478
E value	6.0e-48
Match length	147
% identity	71

NCBI Description	(AL021636) putative protein [Arabidopsis thaliana]
Seq. No.	136492
Contig ID	139067_1.R1010
5'-most EST	g2048954
Seq. No.	136493
Contig ID	139077_1.R1010
5'-most EST	g931928
Method	BLASTX
NCBI GI	g4220485
BLAST score	556
E value	4.0e-57
Match length	155
% identity	77
NCBI Description	(AC006069) putative beta-1,3-glucanase [Arabidopsis thaliana]
Seq. No.	136494
Contig ID	139209_1.R1010
5'-most EST	g933367
Method	BLASTN
NCBI GI	g2696018
BLAST score	519
E value	0.0e+00
Match length	643
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC9, complete sequence [Arabidopsis thaliana]
Seq. No.	136495
Contig ID	139232_1.R1010
5'-most EST	g933465
Method	BLASTX
NCBI GI	g3746060
BLAST score	322
E value	5.0e-42
Match length	134
% identity	65
NCBI Description	(AC005311) unknown protein [Arabidopsis thaliana]
Seq. No.	136496
Contig ID	139404_1.R1010
5'-most EST	g933694
Seq. No.	136497
Contig ID	139459_1.R1010
5'-most EST	g935200
Method	BLASTX
NCBI GI	g629561
BLAST score	449
E value	1.0e-44
Match length	142
% identity	63
NCBI Description	SRG1 protein - Arabidopsis thaliana >gi_479047_emb_CAA55654_ (X79052) SRG1 [Arabidopsis thaliana]

Seq. No. 136498
Contig ID 139499_1.R1010
5'-most EST g1159576

Seq. No. 136499
Contig ID 139594_1.R1010
5'-most EST g2762216
Method BLASTX
NCBI GI g2281088
BLAST score 174
E value 2.0e-12
Match length 104
% identity 38
NCBI Description (AC002333) indole-3-acetate beta-glucosyltransferase isolog [Arabidopsis thaliana]

Seq. No. 136500
Contig ID 139605_1.R1010
5'-most EST g1565873
Method BLASTX
NCBI GI g2911059
BLAST score 541
E value 2.0e-55
Match length 151
% identity 79
NCBI Description (AL021961) putative protein [Arabidopsis thaliana]

Seq. No. 136501
Contig ID 139804_1.R1010
5'-most EST g2048118

Seq. No. 136502
Contig ID 139826_1.R1010
5'-most EST g2763398
Method BLASTX
NCBI GI g3582341
BLAST score 699
E value 7.0e-74
Match length 171
% identity 75
NCBI Description (AC005496) putative flavonol 3-o-glucosyltransferase [Arabidopsis thaliana]

Seq. No. 136503
Contig ID 139830_1.R1010
5'-most EST g935087

Seq. No. 136504
Contig ID 139889_1.R1010
5'-most EST g935154

Seq. No. 136505
Contig ID 139933_1.R1010
5'-most EST g935210
Method BLASTX
NCBI GI g3236247

BLAST score	75
E value	4.0e-51
Match length	104
% identity	94
NCBI Description	(AC004684) SCARECROW-like protein [Arabidopsis thaliana]

Seq. No.	136506
Contig ID	140158_1.R1010
5'-most EST	g935479
Method	BLASTX
NCBI GI	g4455033
BLAST score	182
E value	2.0e-13
Match length	86
% identity	45
NCBI Description	(AF116237) pseudouridine synthase 1 [Mus musculus]

Seq. No.	136507
Contig ID	140230_1.R1010
5'-most EST	g935567
Method	BLASTN
NCBI GI	g2656024
BLAST score	143
E value	1.0e-74
Match length	312
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15E6

Seq. No.	136508
Contig ID	140642_1.R1010
5'-most EST	g936045

Seq. No.	136509
Contig ID	140665_1.R1010
5'-most EST	g936071
Method	BLASTX
NCBI GI	g4063752
BLAST score	454
E value	5.0e-45
Match length	114
% identity	79
NCBI Description	(AC005851) unknown protein [Arabidopsis thaliana] >gi_4510410_gb_AAD21496.1_ (AC006929) unknown protein [Arabidopsis thaliana]

Seq. No.	136510
Contig ID	140722_1.R1010
5'-most EST	g2733339
Method	BLASTN
NCBI GI	g2815404
BLAST score	59
E value	4.0e-24
Match length	154
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMG4, complete sequence [Arabidopsis thaliana]

Seq. No.	136511
Contig ID	140833_1.R1010
5'-most EST	g2759079

Seq. No.	136512
Contig ID	140946_1.R1010
5'-most EST	g936416
Method	BLASTN
NCBI GI	g4733953
BLAST score	90
E value	7.0e-43
Match length	393
% identity	97
NCBI Description	Arabidopsis thaliana chromosome I BAC F13O11 genomic sequence, complete sequence

Seq. No.	136513
Contig ID	141052_1.R1010
5'-most EST	g2748467
Method	BLASTN
NCBI GI	g3212102
BLAST score	114
E value	4.0e-57
Match length	477
% identity	97
NCBI Description	Arabidopsis Thaliana BAC F6A4, Chromosome IV, near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	136514
Contig ID	141143_1.R1010
5'-most EST	g936645
Method	BLASTN
NCBI GI	g1785729
BLAST score	261
E value	1.0e-145
Match length	299
% identity	96
NCBI Description	A.thaliana mitochondrial genome, part B

Seq. No.	136515
Contig ID	141280_1.R1010
5'-most EST	g958000
Method	BLASTN
NCBI GI	g2564048
BLAST score	367
E value	0.0e+00
Match length	452
% identity	49
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKD15, complete sequence [Arabidopsis thaliana]

Seq. No.	136516
Contig ID	141318_1.R1010
5'-most EST	g3228571
Method	BLASTN
NCBI GI	g2656028

BLAST score 345
E value 0.0e+00
Match length 699
% identity 98
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNF13

Seq. No. 136517
Contig ID 141384_1.R1010
5'-most EST g936936
Method BLASTX
NCBI GI g4522009
BLAST score 852
E value 1.0e-91
Match length 169
% identity 99
NCBI Description (AC007069) unknown protein [Arabidopsis thaliana]

Seq. No. 136518
Contig ID 141471_1.R1010
5'-most EST g937041

Seq. No. 136519
Contig ID 141649_1.R1010
5'-most EST g2749255

Seq. No. 136520
Contig ID 141712_1.R1010
5'-most EST g937327

Seq. No. 136521
Contig ID 141793_1.R1010
5'-most EST g957634
Method BLASTX
NCBI GI g2739382
BLAST score 313
E value 1.0e-28
Match length 131
% identity 58
NCBI Description (AC002505) myosin heavy chain-like protein [Arabidopsis thaliana]

Seq. No. 136522
Contig ID 141871_1.R1010
5'-most EST g937526
Method BLASTN
NCBI GI g4467131
BLAST score 300
E value 1.0e-168
Match length 342
% identity 97
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F20M13 (ESSA project)

Seq. No. 136523
Contig ID 141945_1.R1010
5'-most EST g2758876

Seq. No.	136524
Contig ID	142148_1.R1010
5'-most EST	g937881
Method	BLASTX
NCBI GI	g4510406
BLAST score	176
E value	1.0e-12
Match length	80
% identity	54
NCBI Description	(AC006587) putative protein kinase [Arabidopsis thaliana]

Seq. No.	136525
Contig ID	142273_1.R1010
5'-most EST	g928952

Seq. No.	136526
Contig ID	142297_1.R1010
5'-most EST	g1015432
Method	BLASTX
NCBI GI	g4406778
BLAST score	358
E value	1.0e-57
Match length	130
% identity	86
NCBI Description	(AC006532) putative brassinosteroid insensitive protein [Arabidopsis thaliana]

Seq. No.	136527
Contig ID	142373_1.R1010
5'-most EST	g2048111

Seq. No.	136528
Contig ID	142447_1.R1010
5'-most EST	g949067
Method	BLASTX
NCBI GI	g3249105
BLAST score	210
E value	2.0e-16
Match length	128
% identity	40
NCBI Description	(AC003114) Contains similarity to protein phosphatase 2C (ABI1) gb_X78886 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	136529
Contig ID	142471_1.R1010
5'-most EST	g949304

Seq. No.	136530
Contig ID	142552_1.R1010
5'-most EST	g1217096
Method	BLASTN
NCBI GI	g1785673
BLAST score	433
E value	0.0e+00
Match length	544
% identity	95

NCBI Description	A.thaliana mitochondrial genome, part A
Seq. No.	136531
Contig ID	142658_1.R1010
5'-most EST	g957585
Seq. No.	136532
Contig ID	142680_1.R1010
5'-most EST	g957612
Method	BLASTN
NCBI GI	g3449334
BLAST score	326
E value	0.0e+00
Match length	441
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH9, complete sequence [Arabidopsis thaliana]
Seq. No.	136533
Contig ID	142749_1.R1010
5'-most EST	g957698
Method	BLASTN
NCBI GI	g4220638
BLAST score	220
E value	1.0e-120
Match length	374
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIF21, complete sequence [Arabidopsis thaliana]
Seq. No.	136534
Contig ID	142787_1.R1010
5'-most EST	g2759501
Method	BLASTN
NCBI GI	g4159712
BLAST score	259
E value	1.0e-143
Match length	470
% identity	81
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWI23, complete sequence
Seq. No.	136535
Contig ID	142793_1.R1010
5'-most EST	g957745
Method	BLASTN
NCBI GI	g2264310
BLAST score	240
E value	1.0e-132
Match length	264
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKP11, complete sequence [Arabidopsis thaliana]
Seq. No.	136536
Contig ID	142802_1.R1010
5'-most EST	g2047435

Method	BLASTX
NCBI GI	g2244860
BLAST score	210
E value	1.0e-16
Match length	126
% identity	39
NCBI Description	(Z97337) cucumisin [Arabidopsis thaliana]

Seq. No.	136537
Contig ID	142912_1.R1010
5'-most EST	g2749692
Method	BLASTX
NCBI GI	g4558558
BLAST score	601
E value	1.0e-62
Match length	116
% identity	97
NCBI Description	(AC007138) putative polygalacturonidase [Arabidopsis thaliana]

Seq. No.	136538
Contig ID	143072_1.R1010
5'-most EST	g958049
Method	BLASTN
NCBI GI	g4589439
BLAST score	338
E value	0.0e+00
Match length	491
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQM1, complete sequence

Seq. No.	136539
Contig ID	143139_1.R1010
5'-most EST	g958126
Method	BLASTN
NCBI GI	g4006885
BLAST score	161
E value	2.0e-85
Match length	300
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	136540
Contig ID	143198_1.R1010
5'-most EST	g958191
Method	BLASTX
NCBI GI	g3047104
BLAST score	285
E value	2.0e-25
Match length	140
% identity	55
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	136541
Contig ID	143209_1.R1010

5'-most EST	g3719146
Method	BLASTX
NCBI GI	g3386611
BLAST score	253
E value	5.0e-22
Match length	90
% identity	50
NCBI Description	(AC004665) unknown protein [Arabidopsis thaliana]

Seq. No.	136542
Contig ID	143277_1.R1010
5'-most EST	g2749268

Seq. No.	136543
Contig ID	143305_1.R1010
5'-most EST	g1328084

Seq. No.	136544
Contig ID	143442_1.R1010
5'-most EST	g1041270

Seq. No.	136545
Contig ID	143511_1.R1010
5'-most EST	g2722388
Method	BLASTX
NCBI GI	g3242723
BLAST score	44
E value	2.0e-39
Match length	95
% identity	97
NCBI Description	(AC003040) putative acetone-cyanohydrin lyase [Arabidopsis thaliana]

Seq. No.	136546
Contig ID	143566_1.R1010
5'-most EST	g1565829
Method	BLASTX
NCBI GI	g4006886
BLAST score	508
E value	2.0e-51
Match length	152
% identity	59
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	136547
Contig ID	143599_1.R1010
5'-most EST	g1053411

Seq. No.	136548
Contig ID	143646_1.R1010
5'-most EST	g2412911

Seq. No.	136549
Contig ID	143650_1.R1010
5'-most EST	g1053472

Seq. No.	136550

Contig ID	143684_1.R1010
5'-most EST	g1053767
Method	BLASTN
NCBI GI	g3702732
BLAST score	325
E value	0.0e+00
Match length	365
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGF10, complete sequence [Arabidopsis thaliana]

Seq. No.	136551
Contig ID	143696_1.R1010
5'-most EST	g1053523
Method	BLASTX
NCBI GI	g4455361
BLAST score	504
E value	6.0e-51
Match length	111
% identity	87
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	136552
Contig ID	143707_1.R1010
5'-most EST	g1053540
Method	BLASTN
NCBI GI	g4582411
BLAST score	173
E value	2.0e-92
Match length	326
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T23K8 sequence, complete sequence

Seq. No.	136553
Contig ID	143708_1.R1010
5'-most EST	g1053789
Method	BLASTN
NCBI GI	g2191126
BLAST score	291
E value	1.0e-163
Match length	366
% identity	95
NCBI Description	Arabidopsis thaliana BAC IG002N01

Seq. No.	136554
Contig ID	143733_1.R1010
5'-most EST	g2047566
Method	BLASTX
NCBI GI	g3927825
BLAST score	120
E value	4.0e-50
Match length	170
% identity	74
NCBI Description	(AC005727) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No.	136555
Contig ID	143742_1.R1010
5'-most EST	g1053581

Seq. No.	136556
Contig ID	143757_1.R1010
5'-most EST	g1053599
Method	BLASTX
NCBI GI	g4558564
BLAST score	462
E value	5.0e-46
Match length	116
% identity	78
NCBI Description	(AC007138) predicted protein of unknown function [Arabidopsis thaliana]

Seq. No.	136557
Contig ID	143844_1.R1010
5'-most EST	g2412725

Seq. No.	136558
Contig ID	143849_1.R1010
5'-most EST	g1053705
Method	BLASTX
NCBI GI	g2558938
BLAST score	202
E value	1.0e-29
Match length	206
% identity	42
NCBI Description	(AF024625) arm repeat containing protein [Brassica napus]

Seq. No.	136559
Contig ID	143971_1.R1010
5'-most EST	g1053856
Method	BLASTN
NCBI GI	g3522932
BLAST score	473
E value	0.0e+00
Match length	494
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136560
Contig ID	143987_1.R1010
5'-most EST	g1053879
Method	BLASTN
NCBI GI	g1785673
BLAST score	378
E value	0.0e+00
Match length	487
% identity	95
NCBI Description	A.thaliana mitochondrial genome, part A

Seq. No.	136561
Contig ID	144001_1.R1010
5'-most EST	g2393643

Seq. No.	136562
Contig ID	144026_1.R1010
5'-most EST	g2580750
Method	BLASTX
NCBI GI	g3132477
BLAST score	550
E value	2.0e-56
Match length	110
% identity	99
NCBI Description	(AC003096) unknown protein [Arabidopsis thaliana]

Seq. No.	136563
Contig ID	144165_1.R1010
5'-most EST	g2757263
Method	BLASTX
NCBI GI	g2982458
BLAST score	595
E value	1.0e-61
Match length	127
% identity	98
NCBI Description	(AL022223) putative protein [Arabidopsis thaliana]

Seq. No.	136564
Contig ID	144238_1.R1010
5'-most EST	g2047442
Method	BLASTX
NCBI GI	g3892057
BLAST score	379
E value	9.0e-37
Match length	99
% identity	78
NCBI Description	(AC002330) hypothetical protein [Arabidopsis thaliana]

Seq. No.	136565
Contig ID	144532_1.R1010
5'-most EST	g1103334

Seq. No.	136566
Contig ID	144561_1.R1010
5'-most EST	g1158881

Seq. No.	136567
Contig ID	144612_1.R1010
5'-most EST	g1103362
Method	BLASTX
NCBI GI	g4468804
BLAST score	417
E value	7.0e-41
Match length	123
% identity	61
NCBI Description	(AL035601) putative protein [Arabidopsis thaliana]

Seq. No.	136568
Contig ID	144616_1.R1010
5'-most EST	g1103366
Method	BLASTN

NCBI GI	g2853071
BLAST score	217
E value	1.0e-119
Match length	235
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F24J7 (ESSA project)

Seq. No.	136569
Contig ID	144631_1.R1010
5'-most EST	g1149442

Seq. No.	136570
Contig ID	144635_1.R1010
5'-most EST	g1109707
Method	BLASTX
NCBI GI	g3287494
BLAST score	333
E value	7.0e-31
Match length	139
% identity	52
NCBI Description	(D78504) similar to yeast SRP1 [Oryza sativa]

Seq. No.	136571
Contig ID	144641_1.R1010
5'-most EST	g1109713
Method	BLASTX
NCBI GI	g3980386
BLAST score	735
E value	4.0e-78
Match length	143
% identity	99
NCBI Description	(AC004561) putative glutathione S-transferase [Arabidopsis thaliana]

Seq. No.	136572
Contig ID	144654_1.R1010
5'-most EST	g1109726
Method	BLASTN
NCBI GI	g3869067
BLAST score	199
E value	1.0e-108
Match length	245
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCK7, complete sequence [Arabidopsis thaliana]

Seq. No.	136573
Contig ID	144684_1.R1010
5'-most EST	g2748813

Seq. No.	136574
Contig ID	144724_1.R1010
5'-most EST	g1158274
Method	BLASTX
NCBI GI	g3885341
BLAST score	532

E value	3.0e-54
Match length	162
% identity	53
NCBI Description	(AC005623) unknown protein [Arabidopsis thaliana]

Seq. No.	136575
Contig ID	144729_1.R1010
5'-most EST	g1158279
Method	BLASTN
NCBI GI	g2564045
BLAST score	312
E value	1.0e-175
Match length	502
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K8K14, complete sequence [Arabidopsis thaliana]

Seq. No.	136576
Contig ID	144747_1.R1010
5'-most EST	g1158299
Method	BLASTX
NCBI GI	g4415931
BLAST score	454
E value	6.0e-49
Match length	115
% identity	87
NCBI Description	(AC006418) unknown protein [Arabidopsis thaliana] >gi_4559393_gb_AAD23053.1_AC006526_18 (AC006526) unknown protein [Arabidopsis thaliana]

Seq. No.	136577
Contig ID	145411_1.R1010
5'-most EST	g2580944
Method	BLASTN
NCBI GI	g4220468
BLAST score	294
E value	1.0e-164
Match length	337
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T8O11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136578
Contig ID	145460_1.R1010
5'-most EST	g2757384
Method	BLASTX
NCBI GI	g2982452
BLAST score	572
E value	5.0e-59
Match length	132
% identity	87
NCBI Description	(AL022223) receptor protein kinase-like protein [Arabidopsis thaliana]

Seq. No.	136579
Contig ID	145670_1.R1010
5'-most EST	g1159324

Method	BLASTN
NCBI GI	g4519195
BLAST score	147
E value	5.0e-77
Match length	225
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MQC12, complete sequence

Seq. No.	136580
Contig ID	145923_1.R1010
5'-most EST	g3450082
Method	BLASTN
NCBI GI	g3641835
BLAST score	350
E value	0.0e+00
Match length	519
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T4L20 (ESSAII project)

Seq. No.	136581
Contig ID	145938_1.R1010
5'-most EST	g1159662
Method	BLASTN
NCBI GI	g4557061
BLAST score	225
E value	1.0e-123
Match length	449
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC F23M2 genomic sequence, complete sequence

Seq. No.	136582
Contig ID	146227_1.R1010
5'-most EST	g1215839
Method	BLASTN
NCBI GI	g2253009
BLAST score	340
E value	0.0e+00
Match length	411
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for MAP3K delta-1 protein kinase, partial

Seq. No.	136583
Contig ID	146233_1.R1010
5'-most EST	g1225918

Seq. No.	136584
Contig ID	146245_1.R1010
5'-most EST	g2393146

Seq. No.	136585
Contig ID	146259_1.R1010
5'-most EST	g1215872
Method	BLASTX

NCBI GI g3319340
BLAST score 480
E value 3.0e-48
Match length 95
% identity 100
NCBI Description (AF077407) contains similarity to E. coli cation transport protein ChaC (GB:D90756) [Arabidopsis thaliana]

Seq. No. 136586
Contig ID 146331_1.R1010
5'-most EST g1215944
Method BLASTX
NCBI GI g4490297
BLAST score 71
E value 3.0e+00
Match length 109
% identity 17
NCBI Description (AL035678) putative protein [Arabidopsis thaliana]

Seq. No. 136587
Contig ID 146338_1.R1010
5'-most EST g2749520

Seq. No. 136588
Contig ID 146352_1.R1010
5'-most EST g1215969
Method BLASTX
NCBI GI g2462832
BLAST score 484
E value 1.0e-48
Match length 125
% identity 65
NCBI Description (AF000657) similar to Bacillus CotA [Arabidopsis thaliana]

Seq. No. 136589
Contig ID 146455_1.R1010
5'-most EST g2758462
Method BLASTX
NCBI GI g2351097
BLAST score 391
E value 2.0e-55
Match length 206
% identity 60
NCBI Description (AB006810) ATMRK1 [Arabidopsis thaliana]

Seq. No. 136590
Contig ID 146965_1.R1010
5'-most EST g2048076

Seq. No. 136591
Contig ID 147359_1.R1010
5'-most EST g2047652
Method BLASTN
NCBI GI g2827538
BLAST score 275
E value 1.0e-153
Match length 315

% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T12H17 (ESSAII project)

Seq. No.	136592
Contig ID	147553_1.R1010
5'-most EST	g2748193
Method	BLASTN
NCBI GI	g3510341
BLAST score	325
E value	0.0e+00
Match length	416
% identity	50
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFC16, complete sequence [Arabidopsis thaliana]

Seq. No.	136593
Contig ID	147669_1.R1010
5'-most EST	g2749065
Method	BLASTX
NCBI GI	g4559329
BLAST score	279
E value	1.0e-24
Match length	91
% identity	60
NCBI Description	(AC007087) putative protein kinase MAP3K [Arabidopsis thaliana]

Seq. No.	136594
Contig ID	147984_1.R1010
5'-most EST	g2048181
Method	BLASTX
NCBI GI	g4753648
BLAST score	692
E value	5.0e-73
Match length	137
% identity	99
NCBI Description	(AL049751) putative protein [Arabidopsis thaliana]

Seq. No.	136595
Contig ID	148213_1.R1010
5'-most EST	g1327623
Method	BLASTX
NCBI GI	g2795806
BLAST score	741
E value	1.0e-78
Match length	170
% identity	88
NCBI Description	(AC003674) unknown protein [Arabidopsis thaliana]

Seq. No.	136596
Contig ID	148442_1.R1010
5'-most EST	g2748790
Method	BLASTN
NCBI GI	g3510339
BLAST score	356
E value	0.0e+00

Match length	440
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K3K7, complete sequence [Arabidopsis thaliana]

Seq. No.	136597
Contig ID	148493_1.R1010
5'-most EST	g1328128
Method	BLASTN
NCBI GI	g4757678
BLAST score	110
E value	7.0e-55
Match length	325
% identity	97
NCBI Description	Arabidopsis thaliana chromosome I BAC F9H16 genomic sequence, complete sequence

Seq. No.	136598
Contig ID	148539_1.R1010
5'-most EST	g2393179
Method	BLASTN
NCBI GI	g4662647
BLAST score	186
E value	1.0e-100
Match length	450
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F3K12 genomic sequence, complete sequence

Seq. No.	136599
Contig ID	148602_1.R1010
5'-most EST	g2596170
Method	BLASTX
NCBI GI	g2494123
BLAST score	397
E value	3.0e-38
Match length	77
% identity	99
NCBI Description	(AC002376) Contains similarity to Saccharomyces hypothetical 52.1 KD protein (gb_Z28075). EST gb_T04617 comes from this gene. [Arabidopsis thaliana]

Seq. No.	136600
Contig ID	148635_1.R1010
5'-most EST	g2597530
Method	BLASTX
NCBI GI	g2621798
BLAST score	303
E value	2.0e-27
Match length	80
% identity	70
NCBI Description	(AE000850) transcriptional regulator [Methanobacterium thermoautotrophicum]

Seq. No.	136601
Contig ID	148719_1.R1010
5'-most EST	g2445923

Method	BLASTN
NCBI GI	g4417264
BLAST score	246
E value	1.0e-136
Match length	387
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136602
Contig ID	148840_1.R1010
5'-most EST	g1520923
Method	BLASTN
NCBI GI	g343347
BLAST score	261
E value	1.0e-145
Match length	432
% identity	91
NCBI Description	Soybean 18S ribosomal RNA gene

Seq. No.	136603
Contig ID	149018_1.R1010
5'-most EST	g1565836
Method	BLASTN
NCBI GI	g2618603
BLAST score	175
E value	2.0e-93
Match length	212
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSL3, complete sequence [Arabidopsis thaliana]

Seq. No.	136604
Contig ID	149158_1.R1010
5'-most EST	g1932922
Method	BLASTX
NCBI GI	g2245053
BLAST score	231
E value	4.0e-19
Match length	81
% identity	59
NCBI Description	(Z97342) resistance gene homolog [Arabidopsis thaliana]

Seq. No.	136605
Contig ID	149262_1.R1010
5'-most EST	g2759078
Method	BLASTN
NCBI GI	g2088638
BLAST score	361
E value	0.0e+00
Match length	426
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T28M21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136606
Contig ID	149299_1.R1010

5'-most EST	g2047603
Method	BLASTN
NCBI GI	g4220640
BLAST score	160
E value	8.0e-85
Match length	320
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPE11, complete sequence [Arabidopsis thaliana]

Seq. No.	136607
Contig ID	149346_1.R1010
5'-most EST	g2047481

Seq. No.	136608
Contig ID	149348_1.R1010
5'-most EST	g2758665
Method	BLASTN
NCBI GI	g4589428
BLAST score	174
E value	6.0e-93
Match length	408
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFH8, complete sequence

Seq. No.	136609
Contig ID	149351_1.R1010
5'-most EST	g2576672
Method	BLASTX
NCBI GI	g2213595
BLAST score	178
E value	6.0e-13
Match length	51
% identity	63
NCBI Description	(AC000348) T7N9.15 [Arabidopsis thaliana]

Seq. No.	136610
Contig ID	149368_1.R1010
5'-most EST	g2047510
Method	BLASTX
NCBI GI	g2392772
BLAST score	163
E value	7.0e-21
Match length	69
% identity	80
NCBI Description	(AC002534) putative chloroplast prephenate dehydratase [Arabidopsis thaliana]

Seq. No.	136611
Contig ID	149383_1.R1010
5'-most EST	g2580669
Method	BLASTX
NCBI GI	g3193292
BLAST score	529
E value	7.0e-54
Match length	125

% identity	84
NCBI Description	(AF069298) similar to ATPases associated with various cellular activites (Pfam: AAA.hmm, score: 230.91) [Arabidopsis thaliana]

Seq. No.	136612
Contig ID	149678_1.R1010
5'-most EST	g2047882
Method	BLASTX
NCBI GI	g4006872
BLAST score	169
E value	5.0e-19
Match length	106
% identity	52
NCBI Description	(Z99707) methionyl aminopeptidase-like protein [Arabidopsis thaliana]

Seq. No.	136613
Contig ID	149769_1.R1010
5'-most EST	g2047980
Method	BLASTN
NCBI GI	g4757414
BLAST score	205
E value	1.0e-111
Match length	367
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYF24, complete sequence

Seq. No.	136614
Contig ID	149779_1.R1010
5'-most EST	g2047991
Method	BLASTN
NCBI GI	g4585952
BLAST score	188
E value	1.0e-101
Match length	362
% identity	91
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F26F24, complete sequence

Seq. No.	136615
Contig ID	149785_1.R1010
5'-most EST	g2580872

Seq. No.	136616
Contig ID	149791_1.R1010
5'-most EST	g2580759

Seq. No.	136617
Contig ID	149795_1.R1010
5'-most EST	g2393442
Method	BLASTN
NCBI GI	g4757399
BLAST score	196
E value	1.0e-106
Match length	438

% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MEE13, complete sequence
Seq. No.	136618
Contig ID	149823_1.R1010
5'-most EST	g2413308
Seq. No.	136619
Contig ID	149862_1.R1010
5'-most EST	g2048096
Seq. No.	136620
Contig ID	149879_1.R1010
5'-most EST	g2048113
Method	BLASTX
NCBI GI	g2829889
BLAST score	376
E value	4.0e-36
Match length	85
% identity	88
NCBI Description	(AC002396) Hypothetical protein [Arabidopsis thaliana]
Seq. No.	136621
Contig ID	149897_1.R1010
5'-most EST	g2048133
Seq. No.	136622
Contig ID	150114_1.R1010
5'-most EST	g2048366
Method	BLASTN
NCBI GI	g2191181
BLAST score	176
E value	4.0e-94
Match length	200
% identity	96
NCBI Description	Arabidopsis thaliana BAC TM021B04
Seq. No.	136623
Contig ID	150204_1.R1010
5'-most EST	g2445909
Method	BLASTN
NCBI GI	g2182285
BLAST score	318
E value	1.0e-179
Match length	387
% identity	96
NCBI Description	Sequence of BAC F5I14 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]
Seq. No.	136624
Contig ID	150254_1.R1010
5'-most EST	g2758810
Seq. No.	136625
Contig ID	150422_1.R1010
5'-most EST	g2749090

Method	BLASTN
NCBI GI	g2335089
BLAST score	332
E value	0.0e+00
Match length	407
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T11A7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136626
Contig ID	150464_1.R1010
5'-most EST	g2412933
Method	BLASTN
NCBI GI	g2828183
BLAST score	42
E value	2.0e-14
Match length	99
% identity	55
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPL12, complete sequence [Arabidopsis thaliana]

Seq. No.	136627
Contig ID	150482_1.R1010
5'-most EST	g2048777
Method	BLASTX
NCBI GI	g3702333
BLAST score	163
E value	1.0e-11
Match length	40
% identity	65
NCBI Description	(AC005397) hypothetical protein [Arabidopsis thaliana]

Seq. No.	136628
Contig ID	150492_1.R1010
5'-most EST	g2749179
Method	BLASTN
NCBI GI	g4220643
BLAST score	348
E value	0.0e+00
Match length	421
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD22, complete sequence [Arabidopsis thaliana]

Seq. No.	136629
Contig ID	150594_1.R1010
5'-most EST	g2048900
Method	BLASTN
NCBI GI	g2645198
BLAST score	231
E value	1.0e-127
Match length	302
% identity	95
NCBI Description	Arabidopsis thaliana chromosome I BAC T26J12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136630

Contig ID	150643_1.R1010
5'-most EST	g2048950
Method	BLASTX
NCBI GI	g2651307
BLAST score	74
E value	7.0e-25
Match length	91
% identity	55
NCBI Description	(AC002336) putative uroporphyinogen decarboxylase [Arabidopsis thaliana]

Seq. No.	136631
Contig ID	150743_1.R1010
5'-most EST	g2414001
Method	BLASTN
NCBI GI	g3004543
BLAST score	296
E value	1.0e-166
Match length	445
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F19F24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136632
Contig ID	150833_1.R1010
5'-most EST	g2446032
Method	BLASTN
NCBI GI	g2894591
BLAST score	59
E value	2.0e-24
Match length	324
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T6K21 (ESSAII project)

Seq. No.	136633
Contig ID	150889_1.R1010
5'-most EST	g2393163
Method	BLASTN
NCBI GI	g3894179
BLAST score	370
E value	0.0e+00
Match length	453
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F13H10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136634
Contig ID	150921_1.R1010
5'-most EST	g3450256
Method	BLASTN
NCBI GI	g3869075
BLAST score	78
E value	1.0e-35
Match length	226
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MXK3, complete sequence [Arabidopsis thaliana]

Seq. No.	136635
Contig ID	150953_1.R1010
5'-most EST	g2393227
Method	BLASTX
NCBI GI	g4510381
BLAST score	392
E value	6.0e-38
Match length	134
% identity	67
NCBI Description	(AC007017) unknown protein [Arabidopsis thaliana]

Seq. No.	136636
Contig ID	150985_1.R1010
5'-most EST	g2393259
Method	BLASTN
NCBI GI	g4159706
BLAST score	222
E value	1.0e-121
Match length	284
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGL6, complete sequence

Seq. No.	136637
Contig ID	151059_1.R1010
5'-most EST	g2393333
Method	BLASTN
NCBI GI	g2924652
BLAST score	334
E value	0.0e+00
Match length	406
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9L2, complete sequence [Arabidopsis thaliana]

Seq. No.	136638
Contig ID	151061_1.R1010
5'-most EST	g2393335
Method	BLASTN
NCBI GI	g2182289
BLAST score	106
E value	2.0e-52
Match length	281
% identity	93
NCBI Description	Arabidopsis thaliana chromosome I BAC F11P17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136639
Contig ID	151062_1.R1010
5'-most EST	g2747491
Method	BLASTN
NCBI GI	g4587986
BLAST score	216
E value	1.0e-118
Match length	518

% identity	92
NCBI Description	Arabidopsis thaliana ABA-regulated gene cluster, complete sequence
Seq. No.	136640
Contig ID	151069_1.R1010
5'-most EST	g2445934
Seq. No.	136641
Contig ID	151076_1.R1010
5'-most EST	g2393350
Seq. No.	136642
Contig ID	151099_1.R1010
5'-most EST	g2393373
Method	BLASTN
NCBI GI	g4538949
BLAST score	306
E value	1.0e-171
Match length	443
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F24G24 (ESSA project)
Seq. No.	136643
Contig ID	151118_1.R1010
5'-most EST	g2393392
Seq. No.	136644
Contig ID	151128_1.R1010
5'-most EST	g2393402
Method	BLASTX
NCBI GI	g3859659
BLAST score	307
E value	6.0e-28
Match length	64
% identity	92
NCBI Description	(AL031394) putative potassium transporter AtKT5p (AtKT5) [Arabidopsis thaliana]
Seq. No.	136645
Contig ID	151136_1.R1010
5'-most EST	g2393410
Seq. No.	136646
Contig ID	151322_1.R1010
5'-most EST	g3449405
Method	BLASTX
NCBI GI	g2262113
BLAST score	372
E value	2.0e-35
Match length	76
% identity	96
NCBI Description	(AC002343) unknown protein [Arabidopsis thaliana]
Seq. No.	136647
Contig ID	151359_1.R1010

5'-most EST	g2756851
Method	BLASTN
NCBI GI	g3492818
BLAST score	39
E value	2.0e-12
Match length	86
% identity	86
NCBI Description	Quercus suber cDNA for a ribosomal protein RPL41

Seq. No.	136648
Contig ID	151401_1.R1010
5'-most EST	g2393676
Method	BLASTN
NCBI GI	g4415928
BLAST score	281
E value	1.0e-157
Match length	432
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC F13A10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136649
Contig ID	151444_1.R1010
5'-most EST	g2412726
Method	BLASTX
NCBI GI	g2443885
BLAST score	388
E value	1.0e-37
Match length	83
% identity	90
NCBI Description	(AC002294) Unknown protein [Arabidopsis thaliana]

Seq. No.	136650
Contig ID	151444_2.R1010
5'-most EST	g2722213
Method	BLASTN
NCBI GI	g2182289
BLAST score	152
E value	3.0e-80
Match length	216
% identity	94
NCBI Description	Arabidopsis thaliana chromosome I BAC F11P17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136651
Contig ID	151445_1.R1010
5'-most EST	g2413317
Method	BLASTX
NCBI GI	g2191131
BLAST score	367
E value	3.0e-35
Match length	68
% identity	100
NCBI Description	(AF007269) A_IG002N01.8 gene product [Arabidopsis thaliana]

Seq. No.	136652
Contig ID	151447_1.R1010

5'-most EST	g2412917
Seq. No.	136653
Contig ID	151495_1.R1010
5'-most EST	g2412777
Method	BLASTN
NCBI GI	g3522932
BLAST score	272
E value	1.0e-151
Match length	287
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	136654
Contig ID	151552_1.R1010
5'-most EST	g2412834
Seq. No.	136655
Contig ID	151629_1.R1010
5'-most EST	g3450126
Seq. No.	136656
Contig ID	151649_1.R1010
5'-most EST	g2749574
Method	BLASTX
NCBI GI	g2288999
BLAST score	397
E value	2.0e-38
Match length	112
% identity	71
NCBI Description	(AC002335) electron transfer flavoprotein ubiquinone oxidoreductase isolog [Arabidopsis thaliana]
Seq. No.	136657
Contig ID	151680_1.R1010
5'-most EST	g2576631
Method	BLASTX
NCBI GI	g4388834
BLAST score	304
E value	1.0e-27
Match length	114
% identity	18
NCBI Description	(AC006528) putative disease resistance protein RPP1, 3' partial [Arabidopsis thaliana]
Seq. No.	136658
Contig ID	151724_1.R1010
5'-most EST	g2413011
Method	BLASTN
NCBI GI	g2160132
BLAST score	21
E value	5.8e-02
Match length	273
% identity	62
NCBI Description	Sequence of BAC F19K23 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	136659
Contig ID	151734_1.R1010
5'-most EST	g2413021

Seq. No.	136660
Contig ID	151822_1.R1010
5'-most EST	g2413110
Method	BLASTX
NCBI GI	g548485
BLAST score	175
E value	5.0e-13
Match length	64
% identity	27
NCBI Description	POLYGALACTURONASE INHIBITOR PRECURSOR (POLYGALACTURONASE-INHIBITING PROTEIN) >gi_478677_pir__S23764 polygalacturanase-inhibiting protein precursor - kidney bean >gi_21029_emb_CAA46016_ (X64769) polygalacturanase-inhibiting protein [Phaseolus vulgaris]

Seq. No.	136661
Contig ID	151858_1.R1010
5'-most EST	g2747915
Method	BLASTN
NCBI GI	g2244747
BLAST score	54
E value	2.0e-21
Match length	414
% identity	67
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	136662
Contig ID	151860_1.R1010
5'-most EST	g2749543
Method	BLASTN
NCBI GI	g3128166
BLAST score	415
E value	0.0e+00
Match length	459
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F4I1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136663
Contig ID	151866_1.R1010
5'-most EST	g2413154

Seq. No.	136664
Contig ID	151952_1.R1010
5'-most EST	g2580778
Method	BLASTX
NCBI GI	g2245014
BLAST score	280
E value	9.0e-25
Match length	82
% identity	68

NCBI Description (Z97341) glucosyltransferase homolog [Arabidopsis thaliana]

Seq. No. 136665
Contig ID 151964_1.R1010
5'-most EST g3449732
Method BLASTN
NCBI GI g2924733
BLAST score 107
E value 4.0e-53
Match length 287
% identity 98
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]

Seq. No. 136666
Contig ID 151980_1.R1010
5'-most EST g2580711
Method BLASTN
NCBI GI g4757403
BLAST score 283
E value 1.0e-158
Match length 291
% identity 99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJL12, complete sequence

Seq. No. 136667
Contig ID 152004_1.R1010
5'-most EST g2580734
Method BLASTX
NCBI GI g2497753
BLAST score 238
E value 7.0e-20
Match length 85
% identity 51
NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3) >gi_1321915_emb_CAA65477_ (X96716) lipid transfer protein [Prunus dulcis]

Seq. No. 136668
Contig ID 152077_1.R1010
5'-most EST g2722217

Seq. No. 136669
Contig ID 152119_1.R1010
5'-most EST g2580655
Method BLASTN
NCBI GI g16472
BLAST score 178
E value 2.0e-95
Match length 355
% identity 98
NCBI Description A.thaliana rRNA repeat unit, most frequent IGR type

Seq. No. 136670
Contig ID 152119_2.R1010
5'-most EST g2756756

Method	BLASTN
NCBI GI	g3402671
BLAST score	269
E value	1.0e-149
Match length	288
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T16B24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136671
Contig ID	152232_1.R1010
5'-most EST	g3450076
Method	BLASTX
NCBI GI	g2129755
BLAST score	184
E value	1.0e-13
Match length	103
% identity	39
NCBI Description	tryptophan synthase (EC 4.2.1.20) alpha chain - Arabidopsis thaliana >gi_619753 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana] >gi_1585768_prf__2201482A Trp synthase:SUBUNIT=alpha [Arabidopsis thaliana]

Seq. No.	136672
Contig ID	152400_1.R1010
5'-most EST	g2413832
Method	BLASTX
NCBI GI	g4127458
BLAST score	492
E value	9.0e-52
Match length	160
% identity	71
NCBI Description	(AJ011669) myb cov1 protein [Arabidopsis thaliana]

Seq. No.	136673
Contig ID	152647_1.R1010
5'-most EST	g2748592
Method	BLASTN
NCBI GI	g3510345
BLAST score	108
E value	2.0e-53
Match length	435
% identity	48
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNJ8, complete sequence [Arabidopsis thaliana]

Seq. No.	136674
Contig ID	152931_1.R1010
5'-most EST	g2749420
Method	BLASTN
NCBI GI	g2760170
BLAST score	174
E value	7.0e-93
Match length	484
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIO24, complete sequence [Arabidopsis thaliana]

Seq. No. 136675
Contig ID 153137_1.R1010
5'-most EST g2722350

Seq. No. 136676
Contig ID 153146_1.R1010
5'-most EST g2733960
Method BLASTX
NCBI GI g2239089
BLAST score 156
E value 3.0e-16
Match length 132
% identity 45
NCBI Description (Z84386) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus] >gi_3288180_emb_CAB11466_ (Z98758) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus]

Seq. No. 136677
Contig ID 153248_1.R1010
5'-most EST g2576745

Seq. No. 136678
Contig ID 153317_1.R1010
5'-most EST g2757289
Method BLASTX
NCBI GI g1809259
BLAST score 229
E value 8.0e-19
Match length 96
% identity 48
NCBI Description (U59318) serine/threonine protein kinase Fen [Lycopersicon esculentum]

Seq. No. 136679
Contig ID 153419_1.R1010
5'-most EST g2580751
Method BLASTX
NCBI GI g488573
BLAST score 500
E value 1.0e-50
Match length 103
% identity 97
NCBI Description (U09463) histone H3.2 [Medicago sativa]

Seq. No. 136680
Contig ID 153480_1.R1010
5'-most EST g2722207

Seq. No. 136681
Contig ID 153613_1.R1010
5'-most EST g2580960
Method BLASTX
NCBI GI g4007792
BLAST score 232
E value 4.0e-19

Match length	93
% identity	55
NCBI Description	(AL034463) Xenopus 14s cohesin smc1 subunit homolog [Schizosaccharomyces pombe]

Seq. No.	136682
Contig ID	153842_1.R1010
5'-most EST	g2749495
Method	BLASTN
NCBI GI	g3510340
BLAST score	271
E value	1.0e-151
Match length	332
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDN11, complete sequence [Arabidopsis thaliana]

Seq. No.	136683
Contig ID	153885_1.R1010
5'-most EST	g2763414
Method	BLASTN
NCBI GI	g4079614
BLAST score	337
E value	0.0e+00
Match length	399
% identity	97
NCBI Description	Arabidopsis thaliana chromosome I BAC F21M11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136684
Contig ID	153924_1.R1010
5'-most EST	g3449536

Seq. No.	136685
Contig ID	154192_1.R1010
5'-most EST	g2757269

Seq. No.	136686
Contig ID	154410_1.R1010
5'-most EST	g2763029
Method	BLASTN
NCBI GI	g4056429
BLAST score	68
E value	5.0e-30
Match length	240
% identity	4
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F5O8 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136687
Contig ID	154481_1.R1010
5'-most EST	g2597256
Method	BLASTX
NCBI GI	g3193287
BLAST score	368
E value	2.0e-44
Match length	136

% identity	62
NCBI Description	(AF069298) Arabidopsis predicted protein of unknown function T10P11.19 (GB:AC002330) [Arabidopsis thaliana]

Seq. No.	136688
Contig ID	154513_1.R1010
5'-most EST	g2596786
Method	BLASTN
NCBI GI	g2088638
BLAST score	360
E value	0.0e+00
Match length	461
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T28M21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136689
Contig ID	154646_1.R1010
5'-most EST	g2757411
Method	BLASTX
NCBI GI	g115783
BLAST score	274
E value	4.0e-26
Match length	65
% identity	97
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	136690
Contig ID	154648_1.R1010
5'-most EST	g2762897
Method	BLASTX
NCBI GI	g2760839
BLAST score	475
E value	9.0e-48
Match length	97
% identity	95
NCBI Description	(AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq. No.	136691
Contig ID	154940_1.R1010
5'-most EST	g2764223
Method	BLASTX
NCBI GI	g4467142
BLAST score	191
E value	8.0e-30
Match length	89
% identity	84
NCBI Description	(AL035540) Phospholipase like protein [Arabidopsis thaliana]

Seq. No.	136692
Contig ID	154959_1.R1010
5'-most EST	g2597234

Seq. No. 136693
Contig ID 155142_1.R1010
5'-most EST g2597417
Method BLASTN
NCBI GI g2191126
BLAST score 339
E value 0.0e+00
Match length 422
% identity 96
NCBI Description Arabidopsis thaliana BAC IG002N01

Seq. No. 136694
Contig ID 155259_1.R1010
5'-most EST g2597534

Seq. No. 136695
Contig ID 155446_1.R1010
5'-most EST g2733822
Method BLASTX
NCBI GI g2979551
BLAST score 298
E value 3.0e-27
Match length 75
% identity 81
NCBI Description (AC003680) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No. 136696
Contig ID 155547_1.R1010
5'-most EST g2619116
Method BLASTN
NCBI GI g3650026
BLAST score 182
E value 5.0e-98
Match length 281
% identity 99
NCBI Description Arabidopsis thaliana chromosome II BAC T26I20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 136697
Contig ID 155756_1.R1010
5'-most EST g2763201
Method BLASTX
NCBI GI g3548801
BLAST score 316
E value 5.0e-29
Match length 79
% identity 76
NCBI Description (AC005313) putative transmembrane protein [Arabidopsis thaliana] >gi_4335768_gb_AAD17445_ (AC006284) putative integral membrane protein [Arabidopsis thaliana]

Seq. No. 136698
Contig ID 155836_1.R1010
5'-most EST g2763181
Method BLASTX
NCBI GI g4206122

BLAST score	453
E value	4.0e-45
Match length	106
% identity	79
NCBI Description	(AF097667) protein phosphatase 2C homolog [Mesembryanthemum crystallinum]

Seq. No.	136699
Contig ID	155927_1.R1010
5'-most EST	g2722281
Method	BLASTX
NCBI GI	g3021266
BLAST score	556
E value	4.0e-57
Match length	105
% identity	100
NCBI Description	(AL022347) serine/threonine kinase - like protein [Arabidopsis thaliana] >gi_3292840_emb_CAA19830_ (AL031018) serine/threonine kinase - like protein [Arabidopsis thaliana]

Seq. No.	136700
Contig ID	156076_1.R1010
5'-most EST	g2722689
Method	BLASTX
NCBI GI	g4490336
BLAST score	445
E value	4.0e-44
Match length	99
% identity	88
NCBI Description	(AL035656) auxin-induced protein-like [Arabidopsis thaliana]

Seq. No.	136701
Contig ID	156128_1.R1010
5'-most EST	g2722938
Method	BLASTN
NCBI GI	g2645198
BLAST score	271
E value	1.0e-151
Match length	319
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC T26J12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136702
Contig ID	156576_1.R1010
5'-most EST	g2722992
Method	BLASTN
NCBI GI	g3242700
BLAST score	249
E value	1.0e-138
Match length	303
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F26B6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136703
Contig ID	156646_1.R1010
5'-most EST	g2723014
Method	BLASTN
NCBI GI	g3449314
BLAST score	243
E value	1.0e-134
Match length	321
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K22F20, complete sequence [Arabidopsis thaliana]

Seq. No.	136704
Contig ID	156705_1.R1010
5'-most EST	g2723073
Method	BLASTN
NCBI GI	g3241917
BLAST score	232
E value	1.0e-127
Match length	443
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19B1, complete sequence [Arabidopsis thaliana]

Seq. No.	136705
Contig ID	156930_1.R1010
5'-most EST	g2757807
Method	BLASTN
NCBI GI	g4490324
BLAST score	323
E value	0.0e+00
Match length	394
% identity	61
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14 (ESSA project)

Seq. No.	136706
Contig ID	156959_1.R1010
5'-most EST	g3719094
Method	BLASTN
NCBI GI	g2351064
BLAST score	384
E value	0.0e+00
Match length	442
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDJ22, complete sequence [Arabidopsis thaliana]

Seq. No.	136707
Contig ID	157055_1.R1010
5'-most EST	g2733237

Seq. No.	136708
Contig ID	157153_1.R1010
5'-most EST	g2733336
Method	BLASTX
NCBI GI	g2827549

BLAST score	598
E value	4.0e-62
Match length	139
% identity	87
NCBI Description	(AL021635) glycoprotein endopeptidase - like protein [Arabidopsis thaliana]

Seq. No.	136709
Contig ID	157252_1.R1010
5'-most EST	g2749423

Seq. No.	136710
Contig ID	157333_1.R1010
5'-most EST	g2733518
Method	BLASTX
NCBI GI	g4263795
BLAST score	313
E value	4.0e-48
Match length	100
% identity	95
NCBI Description	(AC006068) putative glucosyltransferase [Arabidopsis thaliana]

Seq. No.	136711
Contig ID	157478_1.R1010
5'-most EST	g2733662
Method	BLASTN
NCBI GI	g4432829
BLAST score	252
E value	1.0e-139
Match length	256
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T1B3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136712
Contig ID	157665_1.R1010
5'-most EST	g2747888
Method	BLASTN
NCBI GI	g2564050
BLAST score	207
E value	1.0e-113
Match length	321
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUA22, complete sequence [Arabidopsis thaliana]

Seq. No.	136713
Contig ID	157724_1.R1010
5'-most EST	g2733913
Method	BLASTX
NCBI GI	g2924785
BLAST score	231
E value	4.0e-19
Match length	118
% identity	47
NCBI Description	(AC002334) similar to disease resistance protein

[Arabidopsis thaliana]

Seq. No.	136714
Contig ID	157758_1.R1010
5'-most EST	g2747822
Method	BLASTN
NCBI GI	g3449327
BLAST score	303
E value	1.0e-170
Match length	402
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCA23, complete sequence [Arabidopsis thaliana]

Seq. No.	136715
Contig ID	157847_1.R1010
5'-most EST	g2739561
Method	BLASTX
NCBI GI	g3184292
BLAST score	292
E value	3.0e-26
Match length	52
% identity	90
NCBI Description	(AC004136) putative nucleic acid binding protein, 5' partial [Arabidopsis thaliana]

Seq. No.	136716
Contig ID	157935_1.R1010
5'-most EST	g2748061
Method	BLASTN
NCBI GI	g3128166
BLAST score	277
E value	1.0e-154
Match length	339
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F4I1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136717
Contig ID	158087_1.R1010
5'-most EST	g3450414
Method	BLASTX
NCBI GI	g3043426
BLAST score	83
E value	1.6e-01
Match length	83
% identity	62
NCBI Description	(AJ005345) hypothetical protein [Cicer arietinum]

Seq. No.	136718
Contig ID	158102_1.R1010
5'-most EST	g2747516

Seq. No.	136719
Contig ID	158219_1.R1010
5'-most EST	g2747633

Seq. No.	136720
Contig ID	158286_1.R1010
5'-most EST	g2759018
Method	BLASTN
NCBI GI	g2351068
BLAST score	273
E value	1.0e-152
Match length	319
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRH10, complete sequence [Arabidopsis thaliana]

Seq. No.	136721
Contig ID	158439_1.R1010
5'-most EST	g2747855
Method	BLASTN
NCBI GI	g2656026
BLAST score	74
E value	2.0e-33
Match length	195
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDF20

Seq. No.	136722
Contig ID	158493_1.R1010
5'-most EST	g2749539
Method	BLASTX
NCBI GI	g3395440
BLAST score	233
E value	3.0e-19
Match length	78
% identity	56
NCBI Description	(AC004683) hypothetical protein [Arabidopsis thaliana]

Seq. No.	136723
Contig ID	159057_1.R1010
5'-most EST	g3228580
Method	BLASTX
NCBI GI	g3033400
BLAST score	195
E value	2.0e-14
Match length	141
% identity	68
NCBI Description	(AC004238) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No.	136724
Contig ID	159570_1.R1010
5'-most EST	g2748992

Seq. No.	136725
Contig ID	159862_1.R1010
5'-most EST	g2749505
Method	BLASTN
NCBI GI	g3406034
BLAST score	78

E value	1.0e-35
Match length	125
% identity	92
NCBI Description	BAC F18A17 from chromosome V containing TINY at 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	136726
Contig ID	159870_1.R1010
5'-most EST	g2749293

Seq. No.	136727
Contig ID	160574_1.R1010
5'-most EST	g2756835
Method	BLASTX
NCBI GI	g2335099
BLAST score	355
E value	3.0e-35
Match length	75
% identity	91
NCBI Description	(AC002339) unknown protein [Arabidopsis thaliana]

Seq. No.	136728
Contig ID	160711_1.R1010
5'-most EST	g2756973
Method	BLASTX
NCBI GI	g3860250
BLAST score	301
E value	3.0e-27
Match length	104
% identity	58
NCBI Description	(AC005824) putative chloroplast prephenate dehydratase [Arabidopsis thaliana]

Seq. No.	136729
Contig ID	160869_1.R1010
5'-most EST	g2757133
Method	BLASTN
NCBI GI	g2815519
BLAST score	153
E value	2.0e-80
Match length	328
% identity	98
NCBI Description	Arabidopsis thaliana BAC T5J8 from chromosome IV, top arm, complete sequence [Arabidopsis thaliana]

Seq. No.	136730
Contig ID	161344_1.R1010
5'-most EST	g2759232
Method	BLASTX
NCBI GI	g2342686
BLAST score	397
E value	6.0e-43
Match length	96
% identity	96
NCBI Description	(AC000106) Similar to Saccharomyces hypothetical protein YDR051c (gb_Z49209). ESTs gb_T44436,gb_42252 come from this gene. [Arabidopsis thaliana]

Seq. No.	136731
Contig ID	161391_1.R1010
5'-most EST	g2764347
Method	BLASTX
NCBI GI	g3850585
BLAST score	445
E value	3.0e-44
Match length	109
% identity	81
NCBI Description	(AC005278) ESTs gb_H36966, gb_R65511, gb_T42324 and gb_T20569 come from this gene. [Arabidopsis thaliana]

Seq. No.	136732
Contig ID	161493_1.R1010
5'-most EST	g2759093
Method	BLASTX
NCBI GI	g4220452
BLAST score	524
E value	2.0e-53
Match length	117
% identity	44
NCBI Description	(AC006216) Similar to gi_3413714 T19L18.21 putative myrosinase-binding protein from Arabidopsis thaliana BAC gb_AC004747. ESTs gb_T44298, gb_T42447, gb_R64761 and gb_I100206 come from this gene. [Arabidopsis thaliana]

Seq. No.	136733
Contig ID	161946_1.R1010
5'-most EST	g2763477
Method	BLASTX
NCBI GI	g2062159
BLAST score	512
E value	4.0e-52
Match length	126
% identity	47
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	136734
Contig ID	163021_1.R1010
5'-most EST	g3449561
Method	BLASTX
NCBI GI	g3928543
BLAST score	48
E value	3.0e-09
Match length	52
% identity	67
NCBI Description	(AB016819) UDP-glucose glucosyltransferase [Arabidopsis thaliana]

Seq. No.	136735
Contig ID	163311_1.R1010
5'-most EST	g2759588

Seq. No.	136736
Contig ID	163603_1.R1010

5'-most EST	g2762416
Method	BLASTN
NCBI GI	g4335744
BLAST score	263
E value	1.0e-146
Match length	354
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T4M8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136737
Contig ID	164898_1.R1010
5'-most EST	g2763371
Method	BLASTN
NCBI GI	g3449329
BLAST score	352
E value	0.0e+00
Match length	452
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDH9, complete sequence [Arabidopsis thaliana]

Seq. No.	136738
Contig ID	164933_1.R1010
5'-most EST	g2763405
Method	BLASTX
NCBI GI	g3445210
BLAST score	549
E value	3.0e-56
Match length	119
% identity	87
NCBI Description	(AC004786) putative flavonol 3-o-glucosyltransferase [Arabidopsis thaliana]

Seq. No.	136739
Contig ID	165000_1.R1010
5'-most EST	g2763473
Method	BLASTN
NCBI GI	g4263774
BLAST score	362
E value	0.0e+00
Match length	438
% identity	59
NCBI Description	Arabidopsis thaliana chromosome II BAC T20F21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136740
Contig ID	165223_1.R1010
5'-most EST	g2763770
Method	BLASTX
NCBI GI	g3297820
BLAST score	149
E value	2.0e-09
Match length	66
% identity	55
NCBI Description	(AL031032) putative protein [Arabidopsis thaliana]

Seq. No.	136741
Contig ID	167194_1.R1010
5'-most EST	g3719179
Method	BLASTN
NCBI GI	g2351064
BLAST score	393
E value	0.0e+00
Match length	440
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDJ22, complete sequence [Arabidopsis thaliana]

Seq. No.	136742
Contig ID	167214_1.R1010
5'-most EST	g3719121
Method	BLASTN
NCBI GI	g2351064
BLAST score	260
E value	1.0e-144
Match length	310
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDJ22, complete sequence [Arabidopsis thaliana]

Seq. No.	136743
Contig ID	167372_1.R1010
5'-most EST	g3868952
Method	BLASTX
NCBI GI	g4262237
BLAST score	351
E value	3.0e-33
Match length	109
% identity	67
NCBI Description	(AC006200) hypothetical protein [Arabidopsis thaliana]

Seq. No.	136744
Seq. ID	ARABL1-01-Q1-B1-F4
Method	BLASTX
NCBI GI	g549063
BLAST score	225
E value	4.0e-19
Match length	53
% identity	81
NCBI Description	TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) >gi_1072464_pir__A38958 IgE-dependent histamine-releasing factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626) 21kd polypeptide [Oryza sativa]

Seq. No.	136745
Seq. ID	ARABL1-01-Q1-B2-B2
Method	BLASTX
NCBI GI	g1172872
BLAST score	290
E value	2.0e-26
Match length	89
% identity	69
NCBI Description	CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718

	drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_ (D13042) thiol protease [Arabidopsis thaliana] >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]
Seq. No.	136746
Seq. ID	ARABL1-01-Q1-B2-D2
Method	BLASTX
NCBI GI	g3688799
BLAST score	670
E value	1.0e-70
Match length	134
% identity	99
NCBI Description	(AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis thaliana]
Seq. No.	136747
Seq. ID	ARABL1-01-Q1-B2-E6
Method	BLASTX
NCBI GI	g4056456
BLAST score	276
E value	2.0e-24
Match length	57
% identity	98
NCBI Description	(AC005990) Strong similarity to gb_U20808 auxin-induced protein from Vigna radiata and a member of the zinc-binding dehydrogenase family PF_00107. ESTs gb_T43674, gb_H77006 and gb_AA395179 come from this gene. [Arabidopsis thaliana]
Seq. No.	136748
Seq. ID	ARABL1-01-Q1-B2-E8
Method	BLASTN
NCBI GI	g4512656
BLAST score	353
E value	0.0e+00
Match length	407
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence
Seq. No.	136749
Seq. ID	ARABL1-01-Q1-B2-F5
Method	BLASTN
NCBI GI	g2351065
BLAST score	78
E value	1.0e-36
Match length	78
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHF15, complete sequence [Arabidopsis thaliana]
Seq. No.	136750
Seq. ID	ARABL1-01-Q1-B2-F6
Method	BLASTX
NCBI GI	g131398
BLAST score	533

E value	1.0e-54
Match length	123
% identity	88
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No.	136751
Seq. ID	ARABL1-01-Q1-B2-G2
Method	BLASTN
NCBI GI	g3868723
BLAST score	208
E value	1.0e-113
Match length	394
% identity	98
NCBI Description	Arabidopsis thaliana chromosome V map 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	136752
Seq. ID	ARABL1-01-Q1-E1-B6
Method	BLASTN
NCBI GI	g3449331
BLAST score	133
E value	5.0e-69
Match length	173
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNC17, complete sequence [Arabidopsis thaliana]

Seq. No.	136753
Seq. ID	ARABL1-01-Q1-E1-B9
Method	BLASTX
NCBI GI	g3123296
BLAST score	244
E value	9.0e-21
Match length	59
% identity	85
NCBI Description	CALMODULIN-RELATED PROTEIN 3, TOUCH-INDUCED >gi_598067 (L34546) calmodulin-related protein [Arabidopsis thaliana]

Seq. No.	136754
Seq. ID	ARABL1-01-Q1-E1-E12
Method	BLASTN
NCBI GI	g2564045
BLAST score	364
E value	0.0e+00
Match length	393
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K8K14, complete sequence [Arabidopsis thaliana]

Seq. No.	136755
Seq. ID	ARABL1-01-Q1-E1-E8
Method	BLASTN
NCBI GI	g4512656
BLAST score	163
E value	7.0e-87
Match length	179
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	136756
Seq. ID	ARABL1-01-Q1-E1-F1
Method	BLASTN
NCBI GI	g2564051
BLAST score	187
E value	1.0e-101
Match length	203
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD9, complete sequence [Arabidopsis thaliana]

Seq. No.	136757
Seq. ID	ARABL1-01-Q1-E1-F5
Method	BLASTN
NCBI GI	g2351065
BLAST score	62
E value	5.0e-27
Match length	78
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHF15, complete sequence [Arabidopsis thaliana]

Seq. No.	136758
Seq. ID	ARABL1-019-Q1-B1-B10
Method	BLASTN
NCBI GI	g2262097
BLAST score	339
E value	0.0e+00
Match length	339
% identity	100
NCBI Description	Arabidopsis thaliana chromosome IV BAC T19F6 genomic sequence, complete sequence

Seq. No.	136759
Seq. ID	ARABL1-019-Q1-B1-C3
Method	BLASTN
NCBI GI	g4325340
BLAST score	299
E value	1.0e-167
Match length	299
% identity	100
NCBI Description	Arabidopsis thaliana BAC T1J1

Seq. No.	136760
Seq. ID	ARABL1-019-Q1-B1-C5
Method	BLASTX

NCBI GI	g2388577
BLAST score	609
E value	1.0e-63
Match length	120
% identity	98
NCBI Description	(AC000098) Similar to Arabidopsis putative ion-channel PID:g2262157 (gb_AC002329). [Arabidopsis thaliana]

Seq. No.	136761
Seq. ID	ARABL1-019-Q1-B1-E12
Method	BLASTN
NCBI GI	g3492855
BLAST score	320
E value	1.0e-180
Match length	320
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F20N2, complete sequence [Arabidopsis thaliana]

Seq. No.	136762
Seq. ID	ARABL1-019-Q1-B1-E7
Method	BLASTN
NCBI GI	g3869070
BLAST score	216
E value	1.0e-118
Match length	251
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MGO3, complete sequence [Arabidopsis thaliana]

Seq. No.	136763
Seq. ID	ARABL1-019-Q1-B1-F3
Method	BLASTX
NCBI GI	g2832717
BLAST score	445
E value	3.0e-44
Match length	104
% identity	77
NCBI Description	(AJ003114) alkaline/neutral invertase [Lolium temulentum]

Seq. No.	136764
Seq. ID	ARABL1-019-Q1-B1-F6
Method	BLASTX
NCBI GI	g2924509
BLAST score	251
E value	2.0e-21
Match length	105
% identity	48
NCBI Description	(AL022023) subtilisin proteinase-like [Arabidopsis thaliana]

Seq. No.	136765
Seq. ID	ARABL1-019-Q1-B1-F8
Method	BLASTX
NCBI GI	g2119846
BLAST score	723
E value	7.0e-77

Match length	139
% identity	100
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	136766
Seq. ID	ARABL1-019-Q1-B1-F9
Method	BLASTX
NCBI GI	g3236237
BLAST score	335
E value	1.0e-31
Match length	61
% identity	100
NCBI Description	(AC004684) putative ribotol dehydrogenase [Arabidopsis thaliana]

Seq. No.	136767
Seq. ID	ARABL1-019-Q1-B1-H8
Method	BLASTN
NCBI GI	g4193383
BLAST score	81
E value	4.0e-38
Match length	140
% identity	93
NCBI Description	Arabidopsis thaliana ribosomal protein S27 (ARS27A) gene, complete cds

Seq. No.	136768
Seq. ID	ARABL1-02-Q1-B1-E7
Method	BLASTN
NCBI GI	g4757392
BLAST score	136
E value	6.0e-71
Match length	136
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K14A17, complete sequence

Seq. No.	136769
Seq. ID	ARABL1-02-Q1-B1-E9
Method	BLASTN
NCBI GI	g4263753
BLAST score	237
E value	1.0e-131
Match length	237
% identity	100
NCBI Description	Arabidopsis thaliana chromosome V map near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	136770
Seq. ID	ARABL1-02-Q1-B1-G5
Method	BLASTN

NCBI GI	g3869066
BLAST score	127
E value	2.0e-65
Match length	148
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBM17, complete sequence [Arabidopsis thaliana]

Seq. No.	136771
Seq. ID	ARABL1-02-Q1-B1-H5
Method	BLASTN
NCBI GI	g887938
BLAST score	30
E value	2.0e-07
Match length	169
% identity	95
NCBI Description	Arabidopsis thaliana clone YAP317 GAST1 protein homolog mRNA, complete cds

Seq. No.	136772
Seq. ID	ARABL1-02-Q1-E1-B10
Method	BLASTN
NCBI GI	g4314374
BLAST score	235
E value	1.0e-129
Match length	247
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136773
Seq. ID	ARABL1-02-Q1-E1-B3
Method	BLASTX
NCBI GI	g2507587
BLAST score	235
E value	1.0e-19
Match length	41
% identity	100
NCBI Description	METALLOTHIONEIN-LIKE PROTEIN 2A (MT-2A) (MT-K) (MT-1G) >gi_1361998_pir__S57861 metallothionein 2a - Arabidopsis thaliana >gi_555976 (U15108) metallothionein-like protein [Arabidopsis thaliana] >gi_1580892_prf__2116236A metallothionein 1 [Arabidopsis thaliana]

Seq. No.	136774
Seq. ID	ARABL1-02-Q1-E1-D11
Method	BLASTN
NCBI GI	g2262155
BLAST score	212
E value	1.0e-116
Match length	256
% identity	95
NCBI Description	DNA sequence of Arabidopsis thaliana BAC F5J6 from chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No.	136775
Seq. ID	ARABL1-02-Q1-E1-D5

Method	BLASTN
NCBI GI	g3402745
BLAST score	160
E value	4.0e-85
Match length	180
% identity	67
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F18E5 (ESSAII project)

Seq. No.	136776
Seq. ID	ARABL1-02-Q1-E1-D8
Method	BLASTN
NCBI GI	g4757392
BLAST score	124
E value	9.0e-64
Match length	136
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K14A17, complete sequence

Seq. No.	136777
Seq. ID	ARABL1-02-Q1-E1-F5
Method	BLASTX
NCBI GI	g1174850
BLAST score	203
E value	5.0e-16
Match length	69
% identity	64
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-21 KD 2 (UBIQUITIN-PROTEIN LIGASE 5) (UBIQUITIN CARRIER PROTEIN 5)

Seq. No.	136778
Seq. ID	ARABL1-02-Q1-E1-G11
Method	BLASTN
NCBI GI	g4512690
BLAST score	102
E value	1.0e-50
Match length	126
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F11A3 genomic sequence, complete sequence

Seq. No.	136779
Seq. ID	ARABL1-02-Q1-E1-G5
Method	BLASTN
NCBI GI	g3869066
BLAST score	119
E value	1.0e-60
Match length	148
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBM17, complete sequence [Arabidopsis thaliana]

Seq. No.	136780
Seq. ID	ARABL1-020-Q1-B1-A4
Method	BLASTX
NCBI GI	g4490330

BLAST score	467
E value	4.0e-47
Match length	90
% identity	93
NCBI Description	(AL035656) splicing factor-like protein [Arabidopsis thaliana]

Seq. No.	136781
Seq. ID	ARABL1-020-Q1-B1-B5
Method	BLASTN
NCBI GI	g4539448
BLAST score	110
E value	3.0e-55
Match length	175
% identity	90
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T5C23 (ESSA project)

Seq. No.	136782
Seq. ID	ARABL1-020-Q1-B1-E12
Method	BLASTX
NCBI GI	g2914700
BLAST score	500
E value	8.0e-51
Match length	117
% identity	85
NCBI Description	(AC003974) tRNA-processing protein SEN3-like [Arabidopsis thaliana]

Seq. No.	136783
Seq. ID	ARABL1-020-Q1-B1-G8
Method	BLASTX
NCBI GI	g2911060
BLAST score	312
E value	7.0e-29
Match length	75
% identity	57
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana] >gi_3297826_emb_CAA19884.1_ (AL031032) putative protein [Arabidopsis thaliana]

Seq. No.	136784
Seq. ID	ARABL1-020-Q1-B1-H4
Method	BLASTN
NCBI GI	g4589427
BLAST score	129
E value	3.0e-66
Match length	337
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFG13, complete sequence

Seq. No.	136785
Seq. ID	ARABL1-020-Q1-B1-H8
Method	BLASTX
NCBI GI	g2879811
BLAST score	204

E value	2.0e-16
Match length	39
% identity	95
NCBI Description	(AJ223316) ribosomal protein L30 [Lupinus luteus]

Seq. No.	136786
Seq. ID	ARABL1-021-Q1-B1-B4
Method	BLASTX
NCBI GI	g2829910
BLAST score	242
E value	1.0e-20
Match length	115
% identity	14
NCBI Description	(AC002291) Unknown protein, contains regulator of chromosome condensation motifs [Arabidopsis thaliana]

Seq. No.	136787
Seq. ID	ARABL1-021-Q1-B1-D10
Method	BLASTX
NCBI GI	g445612
BLAST score	199
E value	1.0e-15
Match length	86
% identity	74
NCBI Description	ribosomal protein S19 [Solanum tuberosum]

Seq. No.	136788
Seq. ID	ARABL1-021-Q1-B1-D8
Method	BLASTN
NCBI GI	g4544405
BLAST score	155
E value	8.0e-82
Match length	327
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F28I8 genomic sequence, complete sequence

Seq. No.	136789
Seq. ID	ARABL1-021-Q1-B1-D9
Method	BLASTN
NCBI GI	g3738313
BLAST score	308
E value	1.0e-173
Match length	312
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T29E15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136790
Seq. ID	ARABL1-021-Q1-B1-E1
Method	BLASTX
NCBI GI	g1773014
BLAST score	233
E value	8.0e-20
Match length	82
% identity	59
NCBI Description	(Y10338) chloride channel Stclc1 [Solanum tuberosum]

Seq. No.	136791
Seq. ID	ARABL1-021-Q1-B1-E2
Method	BLASTX
NCBI GI	g131398
BLAST score	288
E value	7.0e-26
Match length	85
% identity	69
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No.	136792
Seq. ID	ARABL1-021-Q1-B1-E7
Method	BLASTX
NCBI GI	g464987
BLAST score	199
E value	2.0e-15
Match length	125
% identity	100
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10) >gi_421858_pir__S32672 ubiquitin--protein ligase (EC 6.3.2.19) UBC10 - Arabidopsis thaliana >gi_297878_emb_CAA78715_ (Z14991) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_349213 (L00640) ubiquitin conjugating enzyme [Arabidopsis thaliana]

Seq. No.	136793
Seq. ID	ARABL1-021-Q1-B1-F2
Method	BLASTX
NCBI GI	g3080389
BLAST score	542
E value	1.0e-55
Match length	107
% identity	100
NCBI Description	(AL022603) putative membrane associated protein [Arabidopsis thaliana]

Seq. No.	136794
Seq. ID	ARABL1-021-Q1-B1-F4
Method	BLASTN
NCBI GI	g3327922
BLAST score	49
E value	7.0e-19
Match length	137
% identity	84
NCBI Description	Arabidopsis thaliana chromosome II BAC T31E10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136795
Seq. ID	ARABL1-021-Q1-B1-G2
Method	BLASTX
NCBI GI	g3142294
BLAST score	281
E value	5.0e-25
Match length	68
% identity	97
NCBI Description	(AC002411) Strong similarity to initiation factor eIF-2, gb_U37354 from S. pombe. ESTs gb_T41979, gb_N37284 and gb_N37529 come from this gene. [Arabidopsis thaliana]

Seq. No.	136796
Seq. ID	ARABL1-021-Q1-B1-G5
Method	BLASTX
NCBI GI	g2392895
BLAST score	703
E value	2.0e-74
Match length	134
% identity	100
NCBI Description	(AF017056) brassinosteroid insensitive 1 [Arabidopsis thaliana]

Seq. No.	136797
Seq. ID	ARABL1-021-Q1-B1-H12
Method	BLASTX
NCBI GI	g733554
BLAST score	114
E value	8.0e-22
Match length	87
% identity	55
NCBI Description	(U23450) similar to RNA-binding protein [Caenorhabditis elegans]

Seq. No.	136798
Seq. ID	ARABL1-021-Q1-B1-H4
Method	BLASTX
NCBI GI	g166410
BLAST score	334
E value	3.0e-31
Match length	101
% identity	64
NCBI Description	(L07291) Alfin-1 [Medicago sativa]

Seq. No.	136799
Seq. ID	ARABL1-021-Q1-B1-H8
Method	BLASTX
NCBI GI	g115767
BLAST score	261
E value	5.0e-23
Match length	49
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana]

>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	136800
Seq. ID	ARABL1-022-Q1-B1-A10
Method	BLASTN
NCBI GI	g4734011
BLAST score	195
E value	1.0e-105
Match length	403
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F24C20 genomic sequence, complete sequence

Seq. No.	136801
Seq. ID	ARABL1-022-Q1-B1-A7
Method	BLASTX
NCBI GI	g3212859
BLAST score	394
E value	1.0e-38
Match length	81
% identity	96
NCBI Description	(AC004005) hypothetical protein [Arabidopsis thaliana]

Seq. No.	136802
Seq. ID	ARABL1-022-Q1-B1-B7
Method	BLASTN
NCBI GI	g4079614
BLAST score	20
E value	1.4e-01
Match length	168
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC F21M11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136803
Seq. ID	ARABL1-022-Q1-B1-C7
Method	BLASTN
NCBI GI	g2656028
BLAST score	169
E value	3.0e-90
Match length	247
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNF13

Seq. No.	136804
Seq. ID	ARABL1-022-Q1-B1-G3
Method	BLASTN
NCBI GI	g3367500
BLAST score	100
E value	5.0e-49
Match length	289
% identity	100
NCBI Description	REVERSE-COMPLEMENT OF: F23J3.GCG.SEQ CHECK: 2754 FROM: 1 TO: 93489, complete sequence [Arabidopsis thaliana]

Seq. No.	136805
Seq. ID	ARABL1-022-Q1-B1-H1
Method	BLASTX
NCBI GI	g2119846
BLAST score	584
E value	9.0e-61
Match length	108
% identity	100
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	136806
Seq. ID	ARABL1-023-Q1-B1-A11
Method	BLASTX
NCBI GI	g3924594
BLAST score	535
E value	7.0e-55
Match length	123
% identity	60
NCBI Description	(AF069442) putative ribonucleoprotein [Arabidopsis thaliana] >gi_4262139_gb_AAD14439_ (AC005275) putative ribonucleoprotein [Arabidopsis thaliana]

Seq. No.	136807
Seq. ID	ARABL1-023-Q1-B1-A12
Method	BLASTX
NCBI GI	g1168201
BLAST score	598
E value	3.0e-62
Match length	122
% identity	100
NCBI Description	14-3-3-LIKE PROTEIN RCI2 >gi_1076394_pir__S47970 RCI1B protein - Arabidopsis thaliana >gi_531379_emb_CAA52238_ (X74141) RCI1B [Arabidopsis thaliana]

Seq. No.	136808
Seq. ID	ARABL1-023-Q1-B1-A4
Method	BLASTX
NCBI GI	g3046696
BLAST score	400
E value	2.0e-39
Match length	78
% identity	100
NCBI Description	(AL022224) CTP synthase like protein [Arabidopsis thaliana]

Seq. No.	136809
Seq. ID	ARABL1-023-Q1-B1-A5
Method	BLASTX
NCBI GI	g2493129
BLAST score	398
E value	3.0e-39
Match length	79

% identity	97
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 1 (V-ATPASE B SUBUNIT) >gi_459198 (U07052) vacuolar H+-ATPase subunit B [Gossypium hirsutum]
Seq. No.	136810
Seq. ID	ARABL1-023-Q1-B1-C3
Method	BLASTX
NCBI GI	g3738340
BLAST score	221
E value	2.0e-18
Match length	60
% identity	72
NCBI Description	(AC005170) GMP synthase-like protein [Arabidopsis thaliana]
Seq. No.	136811
Seq. ID	ARABL1-023-Q1-B1-D8
Method	BLASTX
NCBI GI	g115783
BLAST score	276
E value	7.0e-25
Match length	56
% identity	96
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]
Seq. No.	136812
Seq. ID	ARABL1-023-Q1-B1-H3
Method	BLASTN
NCBI GI	g2138315
BLAST score	137
E value	3.0e-71
Match length	242
% identity	98
NCBI Description	Arabidopsis thaliana root hair defective 3 (RHD3) gene, complete cds
Seq. No.	136813
Seq. ID	ARABL1-023-Q1-B1-H5
Method	BLASTX
NCBI GI	g131143
BLAST score	454
E value	1.0e-45
Match length	86
% identity	94
NCBI Description	PHOTOSYSTEM I P700 CHLOROPHYLL A APOPROTEIN A1 >gi_72670_pir__A1NTP7 photosystem I P700 apoprotein A1 - common tobacco chloroplast >gi_11830_emb_CAA77352_ (Z00044) PSI P700 apoprotein A1 [Nicotiana tabacum] >gi_225198_prf__1211235AC photosystem I P700 apoprotein A1 [Nicotiana tabacum]
Seq. No.	136814
Seq. ID	ARABL1-024-Q1-B1-B5
Method	BLASTX

09604506.960704

NCBI GI	g544424
BLAST score	215
E value	2.0e-17
Match length	42
% identity	100
NCBI Description	GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi_419755_pir__S30147 glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana >gi_16301_emb_CAA78711_ (Z14987) glycine rich protein [Arabidopsis thaliana] >gi_166837 (L00648) RNA-binding protein [Arabidopsis thaliana] >gi_4567224_gb_AAD23639.1_AC007119_5 (AC007119) glycine-rich RNA binding protein 7 [Arabidopsis thaliana]

Seq. No.	136815
Seq. ID	ARABL1-024-Q1-B1-E3
Method	BLASTN
NCBI GI	g1532162
BLAST score	138
E value	1.0e-71
Match length	348
% identity	97
NCBI Description	Arabidopsis thaliana AT.I.24-1, AT.I.24-2, AT.I.24-3, AT.I.24-4, AT.I.24-5, AT.I.24-6, AT.I.24-9 and AT.I.24-14 genes, partial cds, AT.I.24-7, ascorbate peroxidase (ATHAPX1), EF-1alpha-A1, -A2 and -A3 (EF-1alpha) and AT.I

Seq. No.	136816
Seq. ID	ARABL1-024-Q1-B1-E7
Method	BLASTN
NCBI GI	g4589439
BLAST score	41
E value	3.0e-14
Match length	105
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQM1, complete sequence

Seq. No.	136817
Seq. ID	ARABL1-024-Q1-B1-E9
Method	BLASTN
NCBI GI	g3702731
BLAST score	103
E value	3.0e-51
Match length	126
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFC19, complete sequence [Arabidopsis thaliana]

Seq. No.	136818
Seq. ID	ARABL1-024-Q1-B1-F8
Method	BLASTN
NCBI GI	g3449313
BLAST score	229
E value	1.0e-126
Match length	333
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K21P3, complete sequence [Arabidopsis thaliana]

Seq. No.	136819
Seq. ID	ARABL1-024-Q1-B1-F9
Method	BLASTN
NCBI GI	g3869068
BLAST score	148
E value	1.0e-77
Match length	344
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC16, complete sequence [Arabidopsis thaliana]

Seq. No.	136820
Seq. ID	ARABL1-024-Q1-B1-G6
Method	BLASTN
NCBI GI	g298035
BLAST score	67
E value	7.0e-30
Match length	67
% identity	100
NCBI Description	A.thaliana Lhcb4 gene

Seq. No.	136821
Seq. ID	ARABL1-024-Q1-B1-H6
Method	BLASTX
NCBI GI	g2119846
BLAST score	546
E value	2.0e-56
Match length	101
% identity	100
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	136822
Seq. ID	ARABL1-025-Q1-B1-A8
Method	BLASTX
NCBI GI	g115783
BLAST score	557
E value	2.0e-57
Match length	105
% identity	99
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	136823
Seq. ID	ARABL1-025-Q1-B1-C12
Method	BLASTX
NCBI GI	g4741954
BLAST score	153

E value	1.0e-10
Match length	28
% identity	100
NCBI Description	(AF134127) Lhcb4.2 protein [Arabidopsis thaliana]

Seq. No.	136824
Seq. ID	ARABL1-025-Q1-B1-C4
Method	BLASTN
NCBI GI	g4539331
BLAST score	155
E value	8.0e-82
Match length	331
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22I13 (ESSA project)

Seq. No.	136825
Seq. ID	ARABL1-025-Q1-B1-D1
Method	BLASTX
NCBI GI	g4415912
BLAST score	369
E value	2.0e-35
Match length	109
% identity	63
NCBI Description	(AC006282) putative protease [Arabidopsis thaliana]

Seq. No.	136826
Seq. ID	ARABL1-025-Q1-B1-D3
Method	BLASTN
NCBI GI	g4388816
BLAST score	163
E value	1.0e-86
Match length	288
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F9B22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136827
Seq. ID	ARABL1-025-Q1-B1-F9
Method	BLASTX
NCBI GI	g2118220
BLAST score	388
E value	1.0e-37
Match length	113
% identity	50
NCBI Description	H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P1) - Arabidopsis thaliana >gi_926929 (L44581) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana] >gi_926933 (L44583) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana] >gi_3096941_emb_CAA18851.1_ (AL023094) vacuolar H+-transporting ATPase 16K chain [Arabidopsis thaliana] >gi_4539311_emb_CAB38812.1_ (AL035679) H+-transporting ATPase 16K chain P2, vacuolar [Arabidopsis thaliana] >gi_4589976_gb_AAD26493.1_AC007195_7 (AC007195) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]

Seq. No.	136828
Seq. ID	ARABL1-025-Q1-B1-G9
Method	BLASTN
NCBI GI	g790686
BLAST score	92
E value	1.0e-44
Match length	100
% identity	98
NCBI Description	Arabidopsis thaliana zinc finger protein (ZFP8) mRNA, complete cds

Seq. No.	136829
Seq. ID	ARABL1-026-Q1-B1-A1
Method	BLASTN
NCBI GI	g3309259
BLAST score	162
E value	4.0e-86
Match length	272
% identity	99
NCBI Description	Arabidopsis thaliana BAC F4H6, chromosome IV, complete sequence

Seq. No.	136830
Seq. ID	ARABL1-026-Q1-B1-A12
Method	BLASTX
NCBI GI	g1651828
BLAST score	294
E value	1.0e-26
Match length	99
% identity	60
NCBI Description	(D90900) dihydrolipoamide dehydrogenase [Synechocystis sp.]

Seq. No.	136831
Seq. ID	ARABL1-026-Q1-B1-C6
Method	BLASTN
NCBI GI	g4220468
BLAST score	260
E value	1.0e-144
Match length	260
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T8O11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136832
Seq. ID	ARABL1-026-Q1-B1-D5
Method	BLASTN
NCBI GI	g16375
BLAST score	99
E value	9.0e-49
Match length	103
% identity	99
NCBI Description	A.thaliana gene (LHCP AB 140) for chlorophyll a/b binding protein

Seq. No.	136833
Seq. ID	ARABL1-026-Q1-B1-F4
Method	BLASTN

NCBI GI	g4589421
BLAST score	183
E value	2.0e-98
Match length	319
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K5K13, complete sequence

Seq. No.	136834
Seq. ID	ARABL1-026-Q1-B1-F5
Method	BLASTX
NCBI GI	g3738316
BLAST score	209
E value	9.0e-17
Match length	50
% identity	80
NCBI Description	(AC005170) unknown protein [Arabidopsis thaliana]

Seq. No.	136835
Seq. ID	ARABL1-026-Q1-B1-H9
Method	BLASTN
NCBI GI	g2335089
BLAST score	235
E value	1.0e-129
Match length	357
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T11A7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136836
Seq. ID	ARABL1-027-Q1-B1-A1
Method	BLASTN
NCBI GI	g2924734
BLAST score	21
E value	8.2e-02
Match length	377
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXE10, complete sequence [Arabidopsis thaliana]

Seq. No.	136837
Seq. ID	ARABL1-027-Q1-B1-B7
Method	BLASTN
NCBI GI	g3402671
BLAST score	209
E value	1.0e-114
Match length	209
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T16B24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136838
Seq. ID	ARABL1-027-Q1-B1-C3
Method	BLASTN
NCBI GI	g4586349
BLAST score	55
E value	4.0e-22

Match length	97
% identity	90
NCBI Description	Arabidopsis thaliana DNA for glucose-1-phosphate adenylyltransferase, complete cds

Seq. No.	136839
Seq. ID	ARABL1-027-Q1-B1-C6
Method	BLASTN
NCBI GI	g3702737
BLAST score	126
E value	1.0e-64
Match length	210
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSN2, complete sequence [Arabidopsis thaliana]

Seq. No.	136840
Seq. ID	ARABL1-027-Q1-B1-E11
Method	BLASTX
NCBI GI	g4567268
BLAST score	359
E value	2.0e-34
Match length	78
% identity	100
NCBI Description	(AC006841) putative fructose biphosphate aldolase [Arabidopsis thaliana]

Seq. No.	136841
Seq. ID	ARABL1-027-Q1-B1-E2
Method	BLASTX
NCBI GI	g4581201
BLAST score	192
E value	7.0e-15
Match length	55
% identity	71
NCBI Description	(Y17911) cyclic nucleotide and calmodulin-regulated ion channel [Arabidopsis thaliana]

Seq. No.	136842
Seq. ID	ARABL1-027-Q1-B1-E5
Method	BLASTX
NCBI GI	g2618725
BLAST score	244
E value	7.0e-21
Match length	45
% identity	100
NCBI Description	(U49074) IAA18 [Arabidopsis thaliana]

Seq. No.	136843
Seq. ID	ARABL1-027-Q1-B1-E6
Method	BLASTN
NCBI GI	g2351069
BLAST score	152
E value	4.0e-80
Match length	285
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MSH12, complete sequence [Arabidopsis thaliana]

Seq. No.	136844
Seq. ID	ARABL1-027-Q1-B1-E9
Method	BLASTN
NCBI GI	g4220637
BLAST score	283
E value	1.0e-158
Match length	304
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MIE1, complete sequence [Arabidopsis thaliana]

Seq. No.	136845
Seq. ID	ARABL1-027-Q1-B1-G12
Method	BLASTX
NCBI GI	g3451075
BLAST score	351
E value	2.0e-33
Match length	102
% identity	62
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	136846
Seq. ID	ARABL1-027-Q1-B1-G6
Method	BLASTX
NCBI GI	g4510348
BLAST score	511
E value	2.0e-52
Match length	89
% identity	100
NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]

Seq. No.	136847
Seq. ID	ARABL1-027-Q1-B1-G7
Method	BLASTN
NCBI GI	g4159706
BLAST score	54
E value	7.0e-22
Match length	155
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGL6, complete sequence

Seq. No.	136848
Seq. ID	ARABL1-027-Q1-B1-G8
Method	BLASTX
NCBI GI	g1086252
BLAST score	337
E value	7.0e-32
Match length	91
% identity	60
NCBI Description	sucrose cleavage protein - Potato >gi_707001_bbs_157931 (S74161) sucrolytic enzyme/ferredoxin homolog [Solanum tuberosum=potatoes, cv. Cara, leaf, Peptide, 322 aa] [Solanum tuberosum]

Seq. No.	136849
Seq. ID	ARABL1-028-Q1-B1-A2
Method	BLASTN
NCBI GI	g1490552
BLAST score	294
E value	1.0e-165
Match length	297
% identity	100
NCBI Description	Arabidopsis thaliana S-adenosylmethionine decarboxylase (SAMdc) mRNA, complete cds

Seq. No.	136850
Seq. ID	ARABL1-028-Q1-B1-B11
Method	BLASTX
NCBI GI	g4646206
BLAST score	411
E value	2.0e-40
Match length	107
% identity	71
NCBI Description	(AC007230) Contains similarity to gb_D13630 KIAA0005 gene from Homo sapiens. ESTs gb_T45345, gb_T21086, gb_R90360, gb_T20468, gb_T45191 and gb_AI100459 come from this gene. [Arabidopsis thaliana]

Seq. No.	136851
Seq. ID	ARABL1-028-Q1-B1-B3
Method	BLASTX
NCBI GI	g421929
BLAST score	365
E value	4.0e-35
Match length	98
% identity	11
NCBI Description	ubiquitin - tomato >gi_312160_emb_CAA51679_ (X73156) ubiquitin [Lycopersicon esculentum]

Seq. No.	136852
Seq. ID	ARABL1-028-Q1-B1-B6
Method	BLASTX
NCBI GI	g2494041
BLAST score	182
E value	2.0e-16
Match length	77
% identity	57
NCBI Description	DIAMINOPIMELATE EPIMERASE >gi_1653875_dbj_BAA18785_ (D90917) diaminopimelate epimerase [Synechocystis sp.]

Seq. No.	136853
Seq. ID	ARABL1-028-Q1-B1-B7
Method	BLASTX
NCBI GI	g2119848
BLAST score	450
E value	4.0e-45
Match length	91
% identity	92
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B1 - Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459) photosystem II type I chlorophyll a /b binding protein

[Arabidopsis thaliana] >gi_3128229 (AC004077) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	136854
Seq. ID	ARABL1-028-Q1-B1-C5
Method	BLASTX
NCBI GI	g166410
BLAST score	226
E value	9.0e-19
Match length	59
% identity	71
NCBI Description	(L07291) Alfin-1 [Medicago sativa]

Seq. No.	136855
Seq. ID	ARABL1-028-Q1-B1-D5
Method	BLASTX
NCBI GI	g4469020
BLAST score	322
E value	7.0e-30
Match length	76
% identity	79
NCBI Description	(AL035602) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	136856
Seq. ID	ARABL1-028-Q1-B1-F1
Method	BLASTN
NCBI GI	g2894591
BLAST score	133
E value	8.0e-69
Match length	247
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T6K21 (ESSAII project)

Seq. No.	136857
Seq. ID	ARABL1-028-Q1-B1-F7
Method	BLASTX
NCBI GI	g2160175
BLAST score	458
E value	4.0e-46
Match length	91
% identity	100
NCBI Description	(AC000132) Strong similarity to Dianthus cysteine proteinase (gb_U17135). [Arabidopsis thaliana]

Seq. No.	136858
Seq. ID	ARABL1-028-Q1-B1-G8
Method	BLASTN
NCBI GI	g4235150
BLAST score	183
E value	9.0e-99
Match length	183
% identity	100

NCBI Description	Arabidopsis thaliana chromosome I BAC T25B24 genomic sequence, complete sequence
Seq. No.	136859
Seq. ID	ARABL1-028-Q1-B1-H4
Method	BLASTN
NCBI GI	g3212846
BLAST score	347
E value	0.0e+00
Match length	350
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	136860
Seq. ID	ARABL1-029-Q1-B1-B1
Method	BLASTN
NCBI GI	g2924652
BLAST score	29
E value	7.0e-07
Match length	211
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9L2, complete sequence [Arabidopsis thaliana]
Seq. No.	136861
Seq. ID	ARABL1-029-Q1-B1-C1
Method	BLASTX
NCBI GI	g4490736
BLAST score	365
E value	2.0e-35
Match length	69
% identity	57
NCBI Description	(AL035708) putative protein [Arabidopsis thaliana]
Seq. No.	136862
Seq. ID	ARABL1-029-Q1-B1-C5
Method	BLASTN
NCBI GI	g3859658
BLAST score	166
E value	2.0e-88
Match length	327
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1 (ESSAII project)
Seq. No.	136863
Seq. ID	ARABL1-029-Q1-B1-D3
Method	BLASTX
NCBI GI	g2507281
BLAST score	408
E value	3.0e-40
Match length	74
% identity	100
NCBI Description	GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi_1668706_emb_CAA66048_ (X97380) atran2 [Arabidopsis thaliana]

Seq. No.	136864
Seq. ID	ARABL1-029-Q1-B1-F5
Method	BLASTN
NCBI GI	g4220645
BLAST score	150
E value	4.0e-79
Match length	206
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYA6, complete sequence [Arabidopsis thaliana]

Seq. No.	136865
Seq. ID	ARABL1-029-Q1-B1-F6
Method	BLASTN
NCBI GI	g4235150
BLAST score	72
E value	1.0e-32
Match length	177
% identity	94
NCBI Description	Arabidopsis thaliana chromosome I BAC T25B24 genomic sequence, complete sequence

Seq. No.	136866
Seq. ID	ARABL1-029-Q1-B1-G7
Method	BLASTN
NCBI GI	g2358139
BLAST score	75
E value	1.0e-34
Match length	100
% identity	81
NCBI Description	Arabidopsis thaliana chromosome 1 YAC yUP8H12 complete sequence [Arabidopsis thaliana]

Seq. No.	136867
Seq. ID	ARABL1-03-Q1-B1-D11
Method	BLASTX
NCBI GI	g2244999
BLAST score	626
E value	1.0e-65
Match length	121
% identity	100
NCBI Description	(Z97341) similarity to phaseolin G-box binding protein PG2 [Arabidopsis thaliana]

Seq. No.	136868
Seq. ID	ARABL1-03-Q1-B1-D12
Method	BLASTN
NCBI GI	g3169169
BLAST score	90
E value	1.0e-43
Match length	90
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F21P24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136869
Seq. ID	ARABL1-03-Q1-B1-D9

Method	BLASTX
NCBI GI	g1181533
BLAST score	348
E value	5.0e-33
Match length	106
% identity	62
NCBI Description	(L41245) thionin [Arabidopsis thaliana] >gi_1586834_prf__2204399B thionin [Arabidopsis thaliana]

Seq. No.	136870
Seq. ID	ARABL1-03-Q1-B1-E7
Method	BLASTN
NCBI GI	g4220635
BLAST score	137
E value	4.0e-71
Match length	291
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDB19, complete sequence [Arabidopsis thaliana]

Seq. No.	136871
Seq. ID	ARABL1-03-Q1-B1-F3
Method	BLASTX
NCBI GI	g1363492
BLAST score	279
E value	4.0e-25
Match length	78
% identity	63
NCBI Description	outer envelope membrane protein OEP75 precursor - garden pea >gi_576507 (L36858) outer membrane protein [Pisum sativum] >gi_633607_emb_CAA58720_ (X83767) chloroplastic outer envelope membrane protein (OEP75) [Pisum sativum]

Seq. No.	136872
Seq. ID	ARABL1-03-Q1-B1-F9
Method	BLASTN
NCBI GI	g4589439
BLAST score	279
E value	1.0e-156
Match length	279
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQM1, complete sequence

Seq. No.	136873
Seq. ID	ARABL1-03-Q1-B1-H1
Method	BLASTX
NCBI GI	g3901294
BLAST score	248
E value	3.0e-21
Match length	95
% identity	56
NCBI Description	(AF089711) rpp8 [Arabidopsis thaliana]

Seq. No.	136874
Seq. ID	ARABL1-030-Q1-B1-B3
Method	BLASTN

NCBI GI	g3985958
BLAST score	129
E value	2.0e-66
Match length	257
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZN1, complete sequence [Arabidopsis thaliana]

Seq. No.	136875
Seq. ID	ARABL1-030-Q1-B1-B6
Method	BLASTN
NCBI GI	g4115930
BLAST score	123
E value	4.0e-63
Match length	127
% identity	99
NCBI Description	Arabidopsis thaliana BAC T4B21

Seq. No.	136876
Seq. ID	ARABL1-030-Q1-B1-C6
Method	BLASTN
NCBI GI	g4519197
BLAST score	66
E value	3.0e-29
Match length	106
% identity	64
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MTC11, complete sequence

Seq. No.	136877
Seq. ID	ARABL1-030-Q1-B1-D4
Method	BLASTX
NCBI GI	g2252840
BLAST score	254
E value	3.0e-22
Match length	68
% identity	69
NCBI Description	(AF013293) contains regions of similarity to Haemophilus influenzae permease (SP:P38767) [Arabidopsis thaliana]

Seq. No.	136878
Seq. ID	ARABL1-030-Q1-B1-H8
Method	BLASTN
NCBI GI	g4581103
BLAST score	75
E value	3.0e-34
Match length	135
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC T24I21 genomic sequence, complete sequence

Seq. No.	136879
Seq. ID	ARABL1-031-Q1-B1-A11
Method	BLASTX
NCBI GI	g3935145
BLAST score	181
E value	9.0e-14

Match length	66
% identity	55
NCBI Description	(AC005106) T25N20.9 [Arabidopsis thaliana]

Seq. No.	136880
Seq. ID	ARABL1-031-Q1-B1-C1
Method	BLASTN
NCBI GI	g3869063
BLAST score	55
E value	2.0e-22
Match length	190
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K17O22, complete sequence [Arabidopsis thaliana]

Seq. No.	136881
Seq. ID	ARABL1-031-Q1-B1-E8
Method	BLASTX
NCBI GI	g2398531
BLAST score	450
E value	7.0e-45
Match length	99
% identity	87
NCBI Description	(Y13726) Transcription factor [Arabidopsis thaliana]

Seq. No.	136882
Seq. ID	ARABL1-031-Q1-B1-F6
Method	BLASTX
NCBI GI	g2342690
BLAST score	413
E value	1.0e-40
Match length	102
% identity	73
NCBI Description	(AC000106) Similar to Homo copine I (gb_U83246). [Arabidopsis thaliana]

Seq. No.	136883
Seq. ID	ARABL1-031-Q1-B1-G5
Method	BLASTX
NCBI GI	g2500430
BLAST score	675
E value	3.0e-71
Match length	130
% identity	100
NCBI Description	40S RIBOSOMAL PROTEIN S16

Seq. No.	136884
Seq. ID	ARABL1-031-Q1-E1-A7
Method	BLASTX
NCBI GI	g1408471
BLAST score	351
E value	2.0e-33
Match length	71
% identity	97
NCBI Description	(U48938) actin depolymerizing factor 1 [Arabidopsis thaliana] >gi_3851707 (AF102173) actin depolymerizing factor 1 [Arabidopsis thaliana]

Seq. No.	136885
Seq. ID	ARABL1-031-Q1-E1-A8
Method	BLASTN
NCBI GI	g1061039
BLAST score	193
E value	1.0e-104
Match length	213
% identity	98
NCBI Description	A.thaliana mRNA for sterol-C-methyltransferase

Seq. No.	136886
Seq. ID	ARABL1-031-Q1-E1-B12
Method	BLASTX
NCBI GI	g548484
BLAST score	355
E value	4.0e-34
Match length	80
% identity	82
NCBI Description	PROSTAGLANDIN G/H SYNTHASE 2 PRECURSOR (CYCLOOXYGENASE -2) (COX-2) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE 2) (PROSTAGLANDIN H2 SYNTHASE 2) (PGH SYNTHASE 2) (PGHS-2) (PHS II) >gi_543442_pir__JC2030 prostaglandin-endoperoxide synthase (EC 1.14.99.1)-2 - rat >gi_414813 (L25925) cyclooxygenase-2 [Rattus norvegicus] >gi_516872 (U04300) mitogen inducible cyclooxygenase [Rattus norvegicus] >gi_743591_prf__2013181A growth factor-inducible cyclooxygenase [Rattus norvegicus]

Seq. No.	136887
Seq. ID	ARABL1-031-Q1-E1-D4
Method	BLASTN
NCBI GI	g1469227
BLAST score	45
E value	4.0e-16
Match length	64
% identity	94
NCBI Description	B.oleracea mRNA for hypothetical protein

Seq. No.	136888
Seq. ID	ARABL1-031-Q1-E1-F2
Method	BLASTN
NCBI GI	g3445196
BLAST score	332
E value	0.0e+00
Match length	332
% identity	84
NCBI Description	Arabidopsis thaliana chromosome II BAC T20K9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136889
Seq. ID	ARABL1-031-Q1-E1-G9
Method	BLASTX
NCBI GI	g2143942
BLAST score	186
E value	2.0e-14
Match length	33

% identity	100
NCBI Description	prostaglandin G/H synthase 1 - rat (fragment)

Seq. No.	136890
Seq. ID	ARABL1-032-Q1-B1-B12
Method	BLASTX
NCBI GI	g2129773
BLAST score	378
E value	2.0e-36
Match length	70
% identity	94
NCBI Description	xyloglucan endotransglycosylase-related protein XTR3 - Arabidopsis thaliana (fragment) >gi_1244752 (U43485) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana]

Seq. No.	136891
Seq. ID	ARABL1-032-Q1-B1-C8
Method	BLASTN
NCBI GI	g2351065
BLAST score	87
E value	2.0e-41
Match length	203
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHF15, complete sequence [Arabidopsis thaliana]

Seq. No.	136892
Seq. ID	ARABL1-032-Q1-B1-C9
Method	BLASTX
NCBI GI	g1495259
BLAST score	171
E value	2.0e-12
Match length	55
% identity	56
NCBI Description	(X97826) orf04 [Arabidopsis thaliana]

Seq. No.	136893
Seq. ID	ARABL1-032-Q1-B1-D4
Method	BLASTN
NCBI GI	g4467131
BLAST score	180
E value	5.0e-97
Match length	180
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20M13 (ESSA project)

Seq. No.	136894
Seq. ID	ARABL1-032-Q1-B1-D6
Method	BLASTN
NCBI GI	g2828180
BLAST score	81
E value	4.0e-38
Match length	121
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MDK4, complete sequence [Arabidopsis thaliana]

Seq. No.	136895
Seq. ID	ARABL1-032-Q1-B1-E3
Method	BLASTN
NCBI GI	g2244788
BLAST score	176
E value	1.0e-94
Match length	176
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	136896
Seq. ID	ARABL1-032-Q1-B1-F1
Method	BLASTN
NCBI GI	g3063690
BLAST score	172
E value	5.0e-92
Match length	294
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11 (ESSAII project)

Seq. No.	136897
Seq. ID	ARABL1-032-Q1-B1-G5
Method	BLASTX
NCBI GI	g134976
BLAST score	97
E value	8.0e-04
Match length	88
% identity	83
NCBI Description	GLUCOSE TRANSPORTER (SUGAR CARRIER) >gi_81619_pir__S12042 glucose transport protein STP1 - Arabidopsis thaliana >gi_16520_emb_CAA39037_ (X55350) glucose transporter [Arabidopsis thaliana]

Seq. No.	136898
Seq. ID	ARABL1-032-Q1-B1-H10
Method	BLASTN
NCBI GI	g2618601
BLAST score	273
E value	1.0e-152
Match length	273
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	136899
Seq. ID	ARABL1-032-Q1-B1-H4
Method	BLASTN
NCBI GI	g2995989
BLAST score	59
E value	6.0e-25
Match length	95
% identity	91
NCBI Description	Arabidopsis thaliana dormancy-associated protein (DRM1)

mRNA, complete cds

Seq. No.	136900
Seq. ID	ARABL1-032-Q1-E1-A6
Method	BLASTN
NCBI GI	g12139
BLAST score	39
E value	7.0e-13
Match length	76
% identity	87
NCBI Description	Pea plastid genes rps2, atpI, atpH, atpF, atpA, trnR and trnG coding for ribosomal protein S2, one CF(1) and three CF(O) subunits of ATP synthase and tRNA-Arg and tRNA-Gly

Seq. No.	136901
Seq. ID	ARABL1-032-Q1-E1-B3
Method	BLASTN
NCBI GI	g2323343
BLAST score	227
E value	1.0e-125
Match length	300
% identity	92
NCBI Description	Arabidopsis thaliana alpha-glucosidase 1 (Aglu1) gene, complete cds

Seq. No.	136902
Seq. ID	ARABL1-032-Q1-E1-B9
Method	BLASTX
NCBI GI	g3355465
BLAST score	230
E value	1.0e-19
Match length	66
% identity	68
NCBI Description	(AC004218) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No.	136903
Seq. ID	ARABL1-032-Q1-E1-E3
Method	BLASTN
NCBI GI	g2244788
BLAST score	174
E value	2.0e-93
Match length	186
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	136904
Seq. ID	ARABL1-032-Q1-E1-G3
Method	BLASTN
NCBI GI	g4567300
BLAST score	230
E value	1.0e-126
Match length	255
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II P1 MHK10 genomic sequence, complete sequence

Seq. No.	136905
Seq. ID	ARABL1-033-Q1-B1-A10
Method	BLASTX
NCBI GI	g3478637
BLAST score	196
E value	2.0e-15
Match length	81
% identity	44
NCBI Description	(AC005546) R29425_1 [Homo sapiens]

Seq. No.	136906
Seq. ID	ARABL1-033-Q1-B1-A12
Method	BLASTN
NCBI GI	g16375
BLAST score	54
E value	4.0e-22
Match length	54
% identity	100
NCBI Description	A.thaliana gene (LHCP AB 140) for chlorophyll a/b binding protein

Seq. No.	136907
Seq. ID	ARABL1-033-Q1-B1-A9
Method	BLASTN
NCBI GI	g2264317
BLAST score	138
E value	8.0e-72
Match length	239
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUG13, complete sequence [Arabidopsis thaliana]

Seq. No.	136908
Seq. ID	ARABL1-033-Q1-B1-B10
Method	BLASTX
NCBI GI	g4510345
BLAST score	339
E value	3.0e-32
Match length	76
% identity	79
NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]

Seq. No.	136909
Seq. ID	ARABL1-033-Q1-B1-B2
Method	BLASTN
NCBI GI	g4733953
BLAST score	96
E value	3.0e-47
Match length	96
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC F13O11 genomic sequence, complete sequence

Seq. No.	136910
Seq. ID	ARABL1-033-Q1-B1-B3
Method	BLASTX

NCBI GI	g4102703
BLAST score	504
E value	3.0e-51
Match length	99
% identity	100
NCBI Description	(AF015274) ribulose-5-phosphate-3-epimerase [Arabidopsis thaliana]

Seq. No.	136911
Seq. ID	ARABL1-033-Q1-B1-B7
Method	BLASTN
NCBI GI	g4249393
BLAST score	306
E value	1.0e-172
Match length	306
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T9J23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136912
Seq. ID	ARABL1-033-Q1-B1-C3
Method	BLASTX
NCBI GI	g4263697
BLAST score	502
E value	4.0e-51
Match length	99
% identity	99
NCBI Description	(AC006223) putative ribosomal protein L27 [Arabidopsis thaliana]

Seq. No.	136913
Seq. ID	ARABL1-033-Q1-B1-D9
Method	BLASTN
NCBI GI	g4757405
BLAST score	128
E value	7.0e-66
Match length	248
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOJ10, complete sequence

Seq. No.	136914
Seq. ID	ARABL1-033-Q1-B1-E10
Method	BLASTX
NCBI GI	g131398
BLAST score	348
E value	3.0e-33
Match length	71
% identity	100
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400

come from this gene. [Arabidopsis

Seq. No.	136915
Seq. ID	ARABL1-033-Q1-B1-E7
Method	BLASTN
NCBI GI	g1354271
BLAST score	20
E value	1.8e-01
Match length	220
% identity	98
NCBI Description	Arabidopsis thaliana aspartic proteinase mRNA, partial cds

Seq. No.	136916
Seq. ID	ARABL1-033-Q1-B1-F10
Method	BLASTX
NCBI GI	g4240120
BLAST score	395
E value	8.0e-39
Match length	74
% identity	100
NCBI Description	(AB007801) cytochrome b5 [Arabidopsis thaliana]

Seq. No.	136917
Seq. ID	ARABL1-033-Q1-B1-F6
Method	BLASTX
NCBI GI	g2119846
BLAST score	681
E value	6.0e-72
Match length	129
% identity	99
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	136918
Seq. ID	ARABL1-033-Q1-B1-F9
Method	BLASTN
NCBI GI	g2244788
BLAST score	104
E value	2.0e-51
Match length	250
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	136919
Seq. ID	ARABL1-033-Q1-B1-G10
Method	BLASTX
NCBI GI	g3885511
BLAST score	233
E value	8.0e-20
Match length	65
% identity	74

NCBI Description	(AF084200) similar to PSI-K subunit of photosystem I from barley [Medicago sativa]
Seq. No.	136920
Seq. ID	ARABL1-033-Q1-B1-G2
Method	BLASTX
NCBI GI	g2264373
BLAST score	617
E value	2.0e-64
Match length	114
% identity	100
NCBI Description	(AC002354) putative NAM/no apical meristem protein [Arabidopsis thaliana]
Seq. No.	136921
Seq. ID	ARABL1-033-Q1-B1-G5
Method	BLASTX
NCBI GI	g3123188
BLAST score	583
E value	2.0e-60
Match length	111
% identity	96
NCBI Description	CATALASE 3 >gi_2347178 (U43147) catalase 3 [Arabidopsis thaliana] >gi_2511726 (AF021937) catalase 3 [Arabidopsis thaliana]
Seq. No.	136922
Seq. ID	ARABL1-033-Q1-B1-G7
Method	BLASTN
NCBI GI	g4662609
BLAST score	81
E value	6.0e-38
Match length	133
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10A5, complete sequence
Seq. No.	136923
Seq. ID	ARABL1-033-Q1-B1-H9
Method	BLASTX
NCBI GI	g3152581
BLAST score	365
E value	3.0e-35
Match length	82
% identity	83
NCBI Description	(AC002986) Similar to E. coli sulfurtransferase (rhodanese) gb_AE00338. ESTs gb_T03984, gb_T03983 and gb_W43228 come from this gene. [Arabidopsis thaliana]
Seq. No.	136924
Seq. ID	ARABL1-033-Q1-E1-A9
Method	BLASTN
NCBI GI	g2264317
BLAST score	99
E value	7.0e-49
Match length	119
% identity	96

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUG13, complete sequence [Arabidopsis thaliana]
Seq. No.	136925
Seq. ID	ARABL1-033-Q1-E1-B3
Method	BLASTN
NCBI GI	g4102702
BLAST score	331
E value	0.0e+00
Match length	331
% identity	100
NCBI Description	Arabidopsis thaliana ribulose-5-phosphate-3-epimerase mRNA, complete cds
Seq. No.	136926
Seq. ID	ARABL1-033-Q1-E1-C9
Method	BLASTN
NCBI GI	g555975
BLAST score	99
E value	8.0e-49
Match length	135
% identity	93
NCBI Description	Arabidopsis thaliana metallothionein-like protein (AtMT-K) mRNA, complete cds
Seq. No.	136927
Seq. ID	ARABL1-033-Q1-E1-D4
Method	BLASTN
NCBI GI	g2828182
BLAST score	241
E value	1.0e-133
Match length	241
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOJ9, complete sequence [Arabidopsis thaliana]
Seq. No.	136928
Seq. ID	ARABL1-033-Q1-E1-E1
Method	BLASTN
NCBI GI	g4584339
BLAST score	181
E value	1.0e-97
Match length	206
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T23A1 genomic sequence, complete sequence
Seq. No.	136929
Seq. ID	ARABL1-033-Q1-E1-E8
Method	BLASTX
NCBI GI	g132102
BLAST score	506
E value	2.0e-51
Match length	89
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR (RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	136930
Seq. ID	ARABL1-033-Q1-E1-G2
Method	BLASTN
NCBI GI	g2264367
BLAST score	346
E value	0.0e+00
Match length	346
% identity	100
NCBI Description	Arabidopsis thaliana BAC F6P23 from chromosome IV, top arm, complete sequence [Arabidopsis thaliana]

Seq. No.	136931
Seq. ID	ARABL1-033-Q1-E1-G7
Method	BLASTN
NCBI GI	g4662609
BLAST score	72
E value	1.0e-32
Match length	125
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10A5, complete sequence

Seq. No.	136932
Seq. ID	ARABL1-033-Q1-E1-H9
Method	BLASTX
NCBI GI	g3152581
BLAST score	174
E value	1.0e-12
Match length	42
% identity	83
NCBI Description	(AC002986) Similar to E. coli sulfurtransferase (rhodanese) gb_AE00338. ESTs gb_T03984, gb_T03983 and gb_W43228 come from this gene. [Arabidopsis thaliana]

Seq. No.	136933
Seq. ID	ARABL1-034-Q1-B1-A10
Method	BLASTN
NCBI GI	g4753195
BLAST score	78
E value	4.0e-36
Match length	198
% identity	96
NCBI Description	Arabidopsis thaliana BAC F15A18 from chromosome V near 68.5 cM, complete sequence

Seq. No.	136934
Seq. ID	ARABL1-034-Q1-B1-A2
Method	BLASTX
NCBI GI	g861155
BLAST score	274
E value	2.0e-24
Match length	77

% identity	61
NCBI Description	(Z35162) beta-fructofuranosidase; cell wall invertase I; fructosidase [Vicia faba]

Seq. No.	136935
Seq. ID	ARABL1-034-Q1-B1-A3
Method	BLASTX
NCBI GI	g2493144
BLAST score	404
E value	1.0e-39
Match length	95
% identity	57
NCBI Description	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-ATPASE 16 KD PROTEOLIPID SUBUNIT) >gi_2118221_pir__S60132 H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P2) - Arabidopsis thaliana >gi_926937 (L44585) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]

Seq. No.	136936
Seq. ID	ARABL1-034-Q1-B1-B11
Method	BLASTN
NCBI GI	g166810
BLAST score	190
E value	1.0e-103
Match length	194
% identity	99
NCBI Description	Arabidopsis thaliana Columbia protein kinase mRNA, complete cds

Seq. No.	136937
Seq. ID	ARABL1-034-Q1-B1-C10
Method	BLASTN
NCBI GI	g3805839
BLAST score	104
E value	2.0e-51
Match length	224
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4B14 (ESSAII project)

Seq. No.	136938
Seq. ID	ARABL1-034-Q1-B1-C5
Method	BLASTX
NCBI GI	g2129773
BLAST score	518
E value	6.0e-53
Match length	113
% identity	87
NCBI Description	xyloglucan endotransglycosylase-related protein XTR3 - Arabidopsis thaliana (fragment) >gi_1244752 (U43485) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana]

Seq. No.	136939
Seq. ID	ARABL1-034-Q1-B1-C7
Method	BLASTX

NCBI GI	g4755189
BLAST score	300
E value	2.0e-27
Match length	119
% identity	66
NCBI Description	(AC007018) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	136940
Seq. ID	ARABL1-034-Q1-B1-D10
Method	BLASTX
NCBI GI	g3298536
BLAST score	415
E value	4.0e-41
Match length	82
% identity	100
NCBI Description	(AC004681) unknown protein [Arabidopsis thaliana]

Seq. No.	136941
Seq. ID	ARABL1-034-Q1-B1-D11
Method	BLASTX
NCBI GI	g1076678
BLAST score	388
E value	5.0e-38
Match length	78
% identity	100
NCBI Description	ubiquitin / ribosomal protein S27a - potato (fragment)

Seq. No.	136942
Seq. ID	ARABL1-034-Q1-B1-D8
Method	BLASTX
NCBI GI	g3766248
BLAST score	203
E value	6.0e-16
Match length	57
% identity	67
NCBI Description	(Y18227) blue copper binding-like protein [Arabidopsis thaliana]

Seq. No.	136943
Seq. ID	ARABL1-034-Q1-B1-E11
Method	BLASTX
NCBI GI	g2827546
BLAST score	287
E value	4.0e-26
Match length	77
% identity	65
NCBI Description	(AL021635) cytochrome P450 like protein [Arabidopsis thaliana]

Seq. No.	136944
Seq. ID	ARABL1-034-Q1-B1-E8
Method	BLASTX
NCBI GI	g2129550
BLAST score	618
E value	1.0e-64
Match length	121
% identity	69

NCBI Description	calcium-dependent protein kinase (EC 2.7.1.-) CDPK6 - Arabidopsis thaliana >gi_2129554_pir__S71901 calcium-dependent protein kinase 6 - Arabidopsis thaliana >gi_836940 (U20623) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_836944 (U20625) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_4454034_emb_CAA23031.1_ (AL035394) calcium-dependent protein kinase (CDPK6) [Arabidopsis thaliana]

Seq. No.	136945
Seq. ID	ARABL1-034-Q1-B1-E9
Method	BLASTN
NCBI GI	g4741959
BLAST score	213
E value	1.0e-116
Match length	243
% identity	97
NCBI Description	Arabidopsis thaliana Lhcb6 protein (Lhcb6) mRNA, complete cds

Seq. No.	136946
Seq. ID	ARABL1-034-Q1-B1-F1
Method	BLASTN
NCBI GI	g2618599
BLAST score	347
E value	0.0e+00
Match length	347
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBD2, complete sequence [Arabidopsis thaliana]

Seq. No.	136947
Seq. ID	ARABL1-034-Q1-B1-F2
Method	BLASTX
NCBI GI	g4559384
BLAST score	436
E value	2.0e-43
Match length	115
% identity	83
NCBI Description	(AC006526) unknown protein [Arabidopsis thaliana]

Seq. No.	136948
Seq. ID	ARABL1-034-Q1-B1-G10
Method	BLASTN
NCBI GI	g4309719
BLAST score	244
E value	1.0e-135
Match length	248
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T30D6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	136949
Seq. ID	ARABL1-034-Q1-B1-G11
Method	BLASTX
NCBI GI	g124372
BLAST score	360

E value	1.0e-34
Match length	68
% identity	100
NCBI Description	ACETOLACTATE SYNTHASE PRECURSOR (ACETOHYDROXY-ACID SYNTHASE) (ALS) >gi_68240_pir__YCMU acetolactate synthase (EC 4.1.3.18) precursor - Arabidopsis thaliana >gi_226221_prf__1501386B acetolactate synthase [Arabidopsis thaliana]

Seq. No.	136950
Seq. ID	ARABL1-034-Q1-B1-G6
Method	BLASTN
NCBI GI	g4006885
BLAST score	100
E value	6.0e-49
Match length	336
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	136951
Seq. ID	ARABL1-034-Q1-B1-H10
Method	BLASTX
NCBI GI	g2497886
BLAST score	197
E value	1.0e-15
Match length	39
% identity	100
NCBI Description	METALLOTHIONEIN-LIKE PROTEIN 2B (MT-2B) >gi_1361999_pir__S57862 metallothionein 2b - Arabidopsis thaliana >gi_1086463 (U11256) metallothionein [Arabidopsis thaliana]

Seq. No.	136952
Seq. ID	ARABL1-034-Q1-B1-H11
Method	BLASTX
NCBI GI	g464986
BLAST score	258
E value	9.0e-23
Match length	48
% identity	100
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi_421857_pir__S32674 ubiquitin--protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating enzyme E2 [Arabidopsis thaliana] >gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein ligase UBC9 [Arabidopsis thaliana]

Seq. No.	136953
Seq. ID	ARABL1-034-Q1-B1-H9
Method	BLASTX
NCBI GI	g4185505

BLAST score	248
E value	1.0e-21
Match length	61
% identity	80
NCBI Description	(AF101038) nonspecific lipid-transfer protein precursor [Brassica napus]

Seq. No.	136954
Seq. ID	ARABL1-034-Q1-E1-F6
Method	BLASTX
NCBI GI	g4755190
BLAST score	242
E value	1.0e-20
Match length	60
% identity	73
NCBI Description	(AC007018) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	136955
Seq. ID	ARABL1-035-Q1-B1-A2
Method	BLASTN
NCBI GI	g3128142
BLAST score	252
E value	1.0e-140
Match length	272
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQN23, complete sequence [Arabidopsis thaliana]

Seq. No.	136956
Seq. ID	ARABL1-035-Q1-B1-B1
Method	BLASTN
NCBI GI	g4159706
BLAST score	82
E value	6.0e-39
Match length	82
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGL6, complete sequence

Seq. No.	136957
Seq. ID	ARABL1-035-Q1-B1-B2
Method	BLASTX
NCBI GI	g4455214
BLAST score	92
E value	5.0e-42
Match length	109
% identity	98
NCBI Description	(AL035440) putative dihydrolipoamide succinyltransferase [Arabidopsis thaliana]

Seq. No.	136958
Seq. ID	ARABL1-035-Q1-B1-B3
Method	BLASTX
NCBI GI	g131398
BLAST score	440
E value	8.0e-44
Match length	105

% identity	86
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No.	136959
Seq. ID	ARABL1-035-Q1-B1-B5
Method	BLASTX
NCBI GI	g4584548
BLAST score	648
E value	4.0e-68
Match length	120
% identity	100
NCBI Description	(AL049608) putative protein [Arabidopsis thaliana]

Seq. No.	136960
Seq. ID	ARABL1-035-Q1-B1-B6
Method	BLASTX
NCBI GI	g4335734
BLAST score	96
E value	2.0e-03
Match length	53
% identity	25
NCBI Description	(AC006248) putative calmodulin [Arabidopsis thaliana]

Seq. No.	136961
Seq. ID	ARABL1-035-Q1-B1-C10
Method	BLASTX
NCBI GI	g1710530
BLAST score	592
E value	1.0e-61
Match length	110
% identity	96
NCBI Description	60S RIBOSOMAL PROTEIN L27A >gi_2129719_pir__S71256 ribosomal protein L27a - Arabidopsis thaliana >gi_1107487_emb_CAA63025_ (X91959) 60S ribosomal protein L27a [Arabidopsis thaliana]

Seq. No.	136962
Seq. ID	ARABL1-035-Q1-B1-E1
Method	BLASTN
NCBI GI	g1688071
BLAST score	66
E value	3.0e-29
Match length	106
% identity	91
NCBI Description	Arabidopsis thaliana biotin holocarboxylase synthetase mRNA, complete cds

Seq. No.	136963
Seq. ID	ARABL1-035-Q1-B1-E12

Method	BLASTX
NCBI GI	g2894596
BLAST score	311
E value	4.0e-29
Match length	62
% identity	100
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	136964
Seq. ID	ARABL1-035-Q1-B1-E6
Method	BLASTN
NCBI GI	g3449327
BLAST score	190
E value	1.0e-103
Match length	217
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCA23, complete sequence [Arabidopsis thaliana]

Seq. No.	136965
Seq. ID	ARABL1-035-Q1-B1-F1
Method	BLASTX
NCBI GI	g4580460
BLAST score	372
E value	7.0e-36
Match length	89
% identity	83
NCBI Description	(AC006081) putative 26S Protease Subunit 4 [Arabidopsis thaliana]

Seq. No.	136966
Seq. ID	ARABL1-035-Q1-B1-F2
Method	BLASTX
NCBI GI	g4678259
BLAST score	391
E value	4.0e-38
Match length	101
% identity	74
NCBI Description	(AL049657) putative protein [Arabidopsis thaliana]

Seq. No.	136967
Seq. ID	ARABL1-035-Q1-B1-G8
Method	BLASTX
NCBI GI	g1071912
BLAST score	227
E value	7.0e-19
Match length	45
% identity	100
NCBI Description	cysteine synthase (EC 4.2.99.8) cpACS1 - Arabidopsis thaliana >gi_572517_emb_CAA57344_ (X81698) cysteine synthase [Arabidopsis thaliana]

Seq. No.	136968
Seq. ID	ARABL1-035-Q1-E1-A11
Method	BLASTN
NCBI GI	g4193383
BLAST score	111

E value	1.0e-55
Match length	115
% identity	99
NCBI Description	Arabidopsis thaliana ribosomal protein S27 (ARS27A) gene, complete cds

Seq. No.	136969
Seq. ID	ARABL1-035-Q1-E1-B1
Method	BLASTN
NCBI GI	g4159706
BLAST score	82
E value	6.0e-39
Match length	82
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGL6, complete sequence

Seq. No.	136970
Seq. ID	ARABL1-035-Q1-E1-D4
Method	BLASTN
NCBI GI	g4757392
BLAST score	251
E value	1.0e-139
Match length	251
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K14A17, complete sequence

Seq. No.	136971
Seq. ID	ARABL1-035-Q1-E1-E12
Method	BLASTX
NCBI GI	g2894596
BLAST score	311
E value	4.0e-29
Match length	62
% identity	100
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	136972
Seq. ID	ARABL1-035-Q1-E1-E6
Method	BLASTN
NCBI GI	g3449327
BLAST score	190
E value	1.0e-103
Match length	217
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCA23, complete sequence [Arabidopsis thaliana]

Seq. No.	136973
Seq. ID	ARABL1-035-Q1-E1-G3
Method	BLASTN
NCBI GI	g2815404
BLAST score	134
E value	2.0e-69
Match length	238
% identity	90

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMG4, complete sequence [Arabidopsis thaliana]
Seq. No.	136974
Seq. ID	ARABL1-036-Q1-B1-A3
Method	BLASTN
NCBI GI	g3128135
BLAST score	80
E value	5.0e-37
Match length	348
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E1, complete sequence [Arabidopsis thaliana]
Seq. No.	136975
Seq. ID	ARABL1-036-Q1-B1-A5
Method	BLASTX
NCBI GI	g16374
BLAST score	161
E value	2.0e-11
Match length	29
% identity	100
NCBI Description	(X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.	136976
Seq. ID	ARABL1-036-Q1-B1-B1
Method	BLASTX
NCBI GI	g3688175
BLAST score	451
E value	5.0e-45
Match length	107
% identity	81
NCBI Description	(AL031804) gamma-VPE (vacuolar processing enzyme) [Arabidopsis thaliana]
Seq. No.	136977
Seq. ID	ARABL1-036-Q1-B1-B11
Method	BLASTN
NCBI GI	g4335744
BLAST score	73
E value	8.0e-33
Match length	197
% identity	84
NCBI Description	Arabidopsis thaliana chromosome II BAC T4M8 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	136978
Seq. ID	ARABL1-036-Q1-B1-B3
Method	BLASTN
NCBI GI	g4691223
BLAST score	102
E value	2.0e-50
Match length	203
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15 (ESSA project)

Seq. No.	136979
Seq. ID	ARABL1-036-Q1-B1-B7
Method	BLASTX
NCBI GI	g2160142
BLAST score	405
E value	1.0e-39
Match length	104
% identity	80
NCBI Description	(AC000375) Strong similarity to Arabidopsis APR2 (gb_U56921). [Arabidopsis thaliana] >gi_2738758 (AF016283) 5'-adenylylsulfate reductase [Arabidopsis thaliana]

Seq. No.	136980
Seq. ID	ARABL1-036-Q1-B1-B8
Method	BLASTN
NCBI GI	g3250673
BLAST score	187
E value	1.0e-101
Match length	378
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T16H5 (ESSAII project)

Seq. No.	136981
Seq. ID	ARABL1-036-Q1-B1-C7
Method	BLASTX
NCBI GI	g1929056
BLAST score	293
E value	2.0e-26
Match length	99
% identity	54
NCBI Description	(Y12090) putative 3,4-dihydroxy-2-butanone kinase [Lycopersicon esculentum]

Seq. No.	136982
Seq. ID	ARABL1-036-Q1-B1-E5
Method	BLASTN
NCBI GI	g3763944
BLAST score	170
E value	5.0e-91
Match length	170
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28A23 (ESSAII project)

Seq. No.	136983
Seq. ID	ARABL1-036-Q1-B1-F11
Method	BLASTN
NCBI GI	g2864607
BLAST score	23
E value	2.0e-03
Match length	67
% identity	89
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6 (ESSAII project)

Seq. No.	136984
Seq. ID	ARABL1-036-Q1-B1-G10
Method	BLASTX
NCBI GI	g2398679
BLAST score	313
E value	5.0e-29
Match length	66
% identity	89
NCBI Description	(Y14797) 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase [Morinda citrifolia]

Seq. No.	136985
Seq. ID	ARABL1-036-Q1-B1-G12
Method	BLASTX
NCBI GI	g3885892
BLAST score	532
E value	1.0e-54
Match length	112
% identity	88
NCBI Description	(AF093634) photosystem-1 F subunit precursor [Oryza sativa]

Seq. No.	136986
Seq. ID	ARABL1-036-Q1-B1-H6
Method	BLASTN
NCBI GI	g2358139
BLAST score	144
E value	3.0e-75
Match length	401
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 YAC yUP8H12 complete sequence [Arabidopsis thaliana]

Seq. No.	136987
Seq. ID	ARABL1-036-Q1-B1-H8
Method	BLASTX
NCBI GI	g2338712
BLAST score	262
E value	8.0e-23
Match length	69
% identity	74
NCBI Description	(AF013959) metallothionein-like protein [Arabidopsis thaliana]

Seq. No.	136988
Seq. ID	ARABL1-036-Q1-E1-A5
Method	BLASTX
NCBI GI	g16374
BLAST score	161
E value	2.0e-11
Match length	29
% identity	100
NCBI Description	(X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	136989
Seq. ID	ARABL1-036-Q1-E1-B3
Method	BLASTN

NCBI GI	g4691223
BLAST score	207
E value	1.0e-113
Match length	391
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15 (ESSA project)

Seq. No.	136990
Seq. ID	ARABL1-036-Q1-E1-B8
Method	BLASTN
NCBI GI	g3250673
BLAST score	303
E value	1.0e-170
Match length	350
% identity	56
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T16H5 (ESSAII project)

Seq. No.	136991
Seq. ID	ARABL1-036-Q1-E1-C6
Method	BLASTN
NCBI GI	g4204948
BLAST score	182
E value	7.0e-98
Match length	189
% identity	99
NCBI Description	Arabidopsis thaliana serine/threonine protein phosphatase 2A-4 catalytic subunit gene, complete cds

Seq. No.	136992
Seq. ID	ARABL1-036-Q1-E1-E5
Method	BLASTN
NCBI GI	g3763944
BLAST score	170
E value	5.0e-91
Match length	170
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28A23 (ESSAII project)

Seq. No.	136993
Seq. ID	ARABL1-036-Q1-E1-F6
Method	BLASTN
NCBI GI	g3702735
BLAST score	322
E value	0.0e+00
Match length	343
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQL5, complete sequence [Arabidopsis thaliana]

Seq. No.	136994
Seq. ID	ARABL1-036-Q1-E1-H3
Method	BLASTN
NCBI GI	g4538949
BLAST score	99

E value	2.0e-48
Match length	270
% identity	85
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F24G24 (ESSA project)

Seq. No.	136995
Seq. ID	ARABL1-037-Q1-B1-A12
Method	BLASTN
NCBI GI	g2564050
BLAST score	120
E value	2.0e-61
Match length	132
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUA22, complete sequence [Arabidopsis thaliana]

Seq. No.	136996
Seq. ID	ARABL1-037-Q1-B1-A7
Method	BLASTN
NCBI GI	g4662609
BLAST score	190
E value	1.0e-103
Match length	211
% identity	97
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10A5, complete sequence

Seq. No.	136997
Seq. ID	ARABL1-037-Q1-B1-A8
Method	BLASTX
NCBI GI	g2809232
BLAST score	476
E value	5.0e-48
Match length	110
% identity	81
NCBI Description	(AC002560) F21B7.1 [Arabidopsis thaliana]

Seq. No.	136998
Seq. ID	ARABL1-037-Q1-B1-B7
Method	BLASTN
NCBI GI	g4567300
BLAST score	68
E value	1.0e-30
Match length	68
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II P1 MHK10 genomic sequence, complete sequence

Seq. No.	136999
Seq. ID	ARABL1-037-Q1-B1-C5
Method	BLASTN
NCBI GI	g16375
BLAST score	65
E value	1.0e-28
Match length	65
% identity	100

NCBI Description	A.thaliana gene (LHCP AB 140) for chlorophyll a/b binding protein
Seq. No.	137000
Seq. ID	ARABL1-037-Q1-B1-D10
Method	BLASTN
NCBI GI	g4159706
BLAST score	149
E value	1.0e-78
Match length	149
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGL6, complete sequence
Seq. No.	137001
Seq. ID	ARABL1-037-Q1-B1-E1
Method	BLASTX
NCBI GI	g115785
BLAST score	272
E value	3.0e-24
Match length	51
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-2) (LHCP) >gi_82380_pir__S04028 chlorophyll a/b-binding protein 2 precursor - barley >gi_18943_emb_CAA31232_ (X12735) LHC precursor protein (AA -34 to 230) [Hordeum vulgare]
Seq. No.	137002
Seq. ID	ARABL1-037-Q1-B1-F9
Method	BLASTN
NCBI GI	g4538949
BLAST score	156
E value	9.0e-83
Match length	156
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F24G24 (ESSA project)
Seq. No.	137003
Seq. ID	ARABL1-037-Q1-B1-G12
Method	BLASTN
NCBI GI	g2623294
BLAST score	91
E value	3.0e-44
Match length	99
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T20B5 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	137004
Seq. ID	ARABL1-037-Q1-B1-G6
Method	BLASTN
NCBI GI	g3241924
BLAST score	79
E value	2.0e-36
Match length	205

% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNC6, complete sequence [Arabidopsis thaliana]

Seq. No.	137005
Seq. ID	ARABL1-037-Q1-B1-H10
Method	BLASTX
NCBI GI	g2829920
BLAST score	170
E value	1.0e-12
Match length	35
% identity	100
NCBI Description	(AC002291) Similar to 'MADS box' transcription factors [Arabidopsis thaliana]

Seq. No.	137006
Seq. ID	ARABL1-037-Q1-E1-B12
Method	BLASTX
NCBI GI	g1769849
BLAST score	290
E value	2.0e-26
Match length	55
% identity	100
NCBI Description	(Z75663) chlorophyll a/b binding protein [Apium graveolens]

Seq. No.	137007
Seq. ID	ARABL1-037-Q1-E1-B7
Method	BLASTN
NCBI GI	g4567300
BLAST score	68
E value	1.0e-30
Match length	68
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II P1 MHK10 genomic sequence, complete sequence

Seq. No.	137008
Seq. ID	ARABL1-037-Q1-E1-C11
Method	BLASTN
NCBI GI	g886427
BLAST score	86
E value	7.0e-41
Match length	178
% identity	87
NCBI Description	A.thaliana mRNA for zeta-crystallin homologue

Seq. No.	137009
Seq. ID	ARABL1-037-Q1-E1-C5
Method	BLASTN
NCBI GI	g16375
BLAST score	53
E value	2.0e-21
Match length	65
% identity	95
NCBI Description	A.thaliana gene (LHCP AB 140) for chlorophyll a/b binding protein

Seq. No.	137010
Seq. ID	ARABL1-037-Q1-E1-D10
Method	BLASTN
NCBI GI	g4159706
BLAST score	144
E value	1.0e-75
Match length	152
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGL6, complete sequence

Seq. No.	137011
Seq. ID	ARABL1-037-Q1-E1-E6
Method	BLASTN
NCBI GI	g4063730
BLAST score	358
E value	0.0e+00
Match length	358
% identity	100
NCBI Description	Arabidopsis thaliana BAC F21J6 from chromosome V, containing KNAT3 and mapping near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	137012
Seq. ID	ARABL1-038-Q1-B1-A11
Method	BLASTX
NCBI GI	g3738261
BLAST score	211
E value	4.0e-17
Match length	100
% identity	56
NCBI Description	(AB018412) chloroplast phosphoglycerate kinase [Populus nigra]

Seq. No.	137013
Seq. ID	ARABL1-038-Q1-B1-A12
Method	BLASTX
NCBI GI	g3286693
BLAST score	547
E value	2.0e-56
Match length	104
% identity	100
NCBI Description	(Y15433) 33 kDa polypeptide of oxygen-evolving complex (OEC) in photosystem II [Arabidopsis thaliana]

Seq. No.	137014
Seq. ID	ARABL1-038-Q1-B1-B7
Method	BLASTX
NCBI GI	g2493144
BLAST score	404
E value	1.0e-39
Match length	95
% identity	57
NCBI Description	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-ATPASE 16 KD PROTEOLIPID SUBUNIT) >gi_2118221_pir__S60132 H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P2) - Arabidopsis thaliana >gi_926937 (L44585)

vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]

Seq. No.	137015
Seq. ID	ARABL1-038-Q1-B1-B9
Method	BLASTX
NCBI GI	g3287862
BLAST score	465
E value	8.0e-47
Match length	85
% identity	100
NCBI Description	PUTATIVE TRYPSIN INHIBITOR T01O24.27 PRECURSOR >gi_2289007 (AC002335) trypsin inhibitor 2 precursor isolog [Arabidopsis thaliana]

Seq. No.	137016
Seq. ID	ARABL1-038-Q1-B1-D10
Method	BLASTN
NCBI GI	g4757403
BLAST score	40
E value	3.0e-13
Match length	114
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJL12, complete sequence

Seq. No.	137017
Seq. ID	ARABL1-038-Q1-B1-D3
Method	BLASTX
NCBI GI	g2315463
BLAST score	235
E value	8.0e-20
Match length	98
% identity	50
NCBI Description	(AF016449) similar to enzymes that act through an ATP dependent binding of AMP; most similar to CoA ligases [Caenorhabditis elegans]

Seq. No.	137018
Seq. ID	ARABL1-038-Q1-B1-E11
Method	BLASTN
NCBI GI	g4335744
BLAST score	71
E value	1.0e-31
Match length	167
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC T4M8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137019
Seq. ID	ARABL1-038-Q1-B1-F11
Method	BLASTX
NCBI GI	g2146733
BLAST score	364
E value	6.0e-35
Match length	82
% identity	79

NCBI Description	GAST1 protein homolog (clone GASA1) - Arabidopsis thaliana
Seq. No.	137020
Seq. ID	ARABL1-038-Q1-B1-F12
Method	BLASTN
NCBI GI	g3522932
BLAST score	272
E value	1.0e-151
Match length	304
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	137021
Seq. ID	ARABL1-038-Q1-B1-F7
Method	BLASTX
NCBI GI	g3033397
BLAST score	261
E value	7.0e-23
Match length	51
% identity	100
NCBI Description	(AC004238) unknown protein [Arabidopsis thaliana]
Seq. No.	137022
Seq. ID	ARABL1-038-Q1-B1-G10
Method	BLASTN
NCBI GI	g2924651
BLAST score	159
E value	3.0e-84
Match length	313
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana]
Seq. No.	137023
Seq. ID	ARABL1-038-Q1-B1-G11
Method	BLASTX
NCBI GI	g464987
BLAST score	456
E value	9.0e-46
Match length	84
% identity	100
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10) >gi_421858_pir__S32672 ubiquitin--protein ligase (EC 6.3.2.19) UBC10 - Arabidopsis thaliana >gi_297878_emb_CAA78715_ (Z14991) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_349213 (L00640) ubiquitin conjugating enzyme [Arabidopsis thaliana]
Seq. No.	137024
Seq. ID	ARABL1-038-Q1-B1-G2
Method	BLASTX
NCBI GI	g3402685
BLAST score	625
E value	2.0e-65
Match length	123

% identity	99
NCBI Description	(AC004697) unknown protein [Arabidopsis thaliana]

Seq. No.	137025
Seq. ID	ARABL1-038-Q1-B1-G4
Method	BLASTX
NCBI GI	g2119848
BLAST score	336
E value	6.0e-32
Match length	70
% identity	93
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B1 - Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128229 (AC004077) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	137026
Seq. ID	ARABL1-038-Q1-B1-G6
Method	BLASTN
NCBI GI	g3869075
BLAST score	370
E value	0.0e+00
Match length	382
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence [Arabidopsis thaliana]

Seq. No.	137027
Seq. ID	ARABL1-038-Q1-B1-H11
Method	BLASTX
NCBI GI	g2507587
BLAST score	284
E value	1.0e-25
Match length	57
% identity	88
NCBI Description	METALLOTHIONEIN-LIKE PROTEIN 2A (MT-2A) (MT-K) (MT-1G) >gi_1361998_pir__S57861 metallothionein 2a - Arabidopsis thaliana >gi_555976 (U15108) metallothionein-like protein [Arabidopsis thaliana] >gi_1580892_prf__2116236A metallothionein 1 [Arabidopsis thaliana]

Seq. No.	137028
Seq. ID	ARABL1-038-Q1-E1-A9
Method	BLASTX
NCBI GI	g131398
BLAST score	258
E value	2.0e-22
Match length	81
% identity	69
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana]

>gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No.	137029
Seq. ID	ARABL1-038-Q1-E1-B10
Method	BLASTX
NCBI GI	g2119846
BLAST score	323
E value	3.0e-30
Match length	62
% identity	100
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	137030
Seq. ID	ARABL1-038-Q1-E1-B7
Method	BLASTX
NCBI GI	g1200116
BLAST score	168
E value	7.0e-12
Match length	50
% identity	76
NCBI Description	(X95752) c subunit of V-type ATPase [Nicotiana tabacum]

Seq. No.	137031
Seq. ID	ARABL1-038-Q1-E1-D11
Method	BLASTN
NCBI GI	g2618603
BLAST score	114
E value	2.0e-57
Match length	242
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSL3, complete sequence [Arabidopsis thaliana]

Seq. No.	137032
Seq. ID	ARABL1-038-Q1-E1-D3
Method	BLASTN
NCBI GI	g3046855
BLAST score	170
E value	1.0e-90
Match length	385
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSL1, complete sequence [Arabidopsis thaliana]

Seq. No.	137033
Seq. ID	ARABL1-038-Q1-E1-D9
Method	BLASTX

NCBI GI	g2213597
BLAST score	191
E value	1.0e-14
Match length	48
% identity	79
NCBI Description	(AC000348) T7N9.17 [Arabidopsis thaliana]

Seq. No.	137034
Seq. ID	ARABL1-038-Q1-E1-F8
Method	BLASTN
NCBI GI	g16375
BLAST score	146
E value	1.0e-76
Match length	146
% identity	100
NCBI Description	A.thaliana gene (LHCP AB 140) for chlorophyll a/b binding protein

Seq. No.	137035
Seq. ID	ARABL1-038-Q1-E1-G10
Method	BLASTX
NCBI GI	g2435518
BLAST score	223
E value	2.0e-18
Match length	42
% identity	86
NCBI Description	(AF024504) contains similarity to C3HC4-type zinc fingers [Arabidopsis thaliana]

Seq. No.	137036
Seq. ID	ARABL1-038-Q1-E1-G11
Method	BLASTX
NCBI GI	g464987
BLAST score	198
E value	2.0e-15
Match length	36
% identity	97
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10) >gi_421858_pir__S32672 ubiquitin--protein ligase (EC 6.3.2.19) UBC10 - Arabidopsis thaliana >gi_297878_emb_CAA78715_ (Z14991) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_349213 (L00640) ubiquitin conjugating enzyme [Arabidopsis thaliana]

Seq. No.	137037
Seq. ID	ARABL1-038-Q1-E1-G2
Method	BLASTN
NCBI GI	g3402671
BLAST score	325
E value	0.0e+00
Match length	325
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T16B24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137038

Seq. ID	ARABL1-038-Q1-E1-G6
Method	BLASTN
NCBI GI	g3869075
BLAST score	116
E value	1.0e-58
Match length	136
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence [Arabidopsis thaliana]

Seq. No.	137039
Seq. ID	ARABL1-038-Q1-E1-G8
Method	BLASTN
NCBI GI	g3337347
BLAST score	139
E value	1.0e-72
Match length	143
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC F13P17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137040
Seq. ID	ARABL1-038-Q1-E1-H10
Method	BLASTX
NCBI GI	g643469
BLAST score	238
E value	4.0e-20
Match length	59
% identity	73
NCBI Description	(U19886) unknown [Lycopersicon esculentum]

Seq. No.	137041
Seq. ID	ARABL1-038-Q1-E1-H7
Method	BLASTX
NCBI GI	g99696
BLAST score	299
E value	3.0e-27
Match length	60
% identity	98
NCBI Description	glutamate--ammonia ligase (EC 6.3.1.2) precursor, chloroplast (clone lambdaAtgsl1) - Arabidopsis thaliana >gi_240070_bbs_69728 (S69727) light-regulated glutamine synthetase isoenzyme [Arabidopsis thaliana, Peptide, 430 aa] [Arabidopsis thaliana] >gi_228453_prf__1804333A Gln synthetase [Arabidopsis thaliana]

Seq. No.	137042
Seq. ID	ARABL1-039-Q1-B1-A7
Method	BLASTX
NCBI GI	g2651297
BLAST score	329
E value	1.0e-30
Match length	84
% identity	75
NCBI Description	(AC002336) putative expansin [Arabidopsis thaliana]

Seq. No. 137043

Seq. ID	ARABL1-039-Q1-B1-B1
Method	BLASTX
NCBI GI	g4678226
BLAST score	511
E value	5.0e-52
Match length	119
% identity	88
NCBI Description	(AC007135) putative 40S ribosomal protein S14 [Arabidopsis thaliana]

Seq. No.	137044
Seq. ID	ARABL1-039-Q1-B1-B3
Method	BLASTX
NCBI GI	g4741952
BLAST score	265
E value	9.0e-24
Match length	50
% identity	100
NCBI Description	(AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No.	137045
Seq. ID	ARABL1-039-Q1-B1-B7
Method	BLASTX
NCBI GI	g4584110
BLAST score	320
E value	1.0e-29
Match length	121
% identity	51
NCBI Description	(AJ133639) SAH7 protein [Arabidopsis thaliana]

Seq. No.	137046
Seq. ID	ARABL1-039-Q1-B1-C8
Method	BLASTX
NCBI GI	g399298
BLAST score	217
E value	1.0e-17
Match length	66
% identity	70
NCBI Description	STRESS-INDUCED KIN2 PROTEIN (COLD-INDUCED COR6.6 PROTEIN) >gi_1084343_pir__S22529 cold-regulated protein kin2 - Arabidopsis thaliana >gi_16230_emb_CAA38894_ (X55053) cold regulated [Arabidopsis thaliana]

Seq. No.	137047
Seq. ID	ARABL1-039-Q1-B1-D2
Method	BLASTN
NCBI GI	g4803835
BLAST score	322
E value	0.0e+00
Match length	322
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for a dynamin-like protein ADL3, complete cds

Seq. No.	137048
Seq. ID	ARABL1-039-Q1-B1-E1
Method	BLASTN

NCBI GI	g4586241
BLAST score	110
E value	2.0e-55
Match length	110
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T20K18 (ESSA project)

Seq. No.	137049
Seq. ID	ARABL1-039-Q1-B1-E10
Method	BLASTX
NCBI GI	g1076302
BLAST score	529
E value	4.0e-54
Match length	108
% identity	100
NCBI Description	cold-regulated protein cor15a precursor - Arabidopsis thaliana >gi_413922_emb_CAA45499_ (X64138) cor15 [Arabidopsis thaliana] >gi_507149 (U01377) cor15a [Arabidopsis thaliana] >gi_4559337_gb_AAD22999.1_AC007087_18 (AC007087) cold-regulated protein cor15a precursor [Arabidopsis thaliana] >gi_444330_prf__1906379A cor15 gene [Arabidopsis thaliana]

Seq. No.	137050
Seq. ID	ARABL1-039-Q1-B1-E9
Method	BLASTN
NCBI GI	g3063438
BLAST score	60
E value	5.0e-26
Match length	60
% identity	100
NCBI Description	Complete sequence of Arabidopsis F22013, complete sequence [Arabidopsis thaliana]

Seq. No.	137051
Seq. ID	ARABL1-039-Q1-B1-F2
Method	BLASTX
NCBI GI	g2497886
BLAST score	300
E value	3.0e-27
Match length	54
% identity	100
NCBI Description	METALLOTHIONEIN-LIKE PROTEIN 2B (MT-2B) >gi_1361999_pir__S57862 metallothionein 2b - Arabidopsis thaliana >gi_1086463 (U11256) metallothionein [Arabidopsis thaliana]

Seq. No.	137052
Seq. ID	ARABL1-039-Q1-B1-F4
Method	BLASTN
NCBI GI	g4218109
BLAST score	211
E value	1.0e-115
Match length	275
% identity	94

NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F16A16 (ESSAII project)
Seq. No.	137053
Seq. ID	ARABL1-039-Q1-B1-F7
Method	BLASTN
NCBI GI	g2351069
BLAST score	275
E value	1.0e-153
Match length	393
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSH12, complete sequence [Arabidopsis thaliana]
Seq. No.	137054
Seq. ID	ARABL1-039-Q1-B1-G10
Method	BLASTN
NCBI GI	g4115352
BLAST score	317
E value	1.0e-178
Match length	317
% identity	79
NCBI Description	Arabidopsis thaliana chromosome II BAC T15J14 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	137055
Seq. ID	ARABL1-039-Q1-B1-H1
Method	BLASTN
NCBI GI	g4584841
BLAST score	64
E value	1.0e-27
Match length	289
% identity	66
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T23E23, complete sequence
Seq. No.	137056
Seq. ID	ARABL1-039-Q1-B1-H2
Method	BLASTN
NCBI GI	g3860243
BLAST score	69
E value	9.0e-31
Match length	194
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC F15K20 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	137057
Seq. ID	ARABL1-039-Q1-E1-A9
Method	BLASTX
NCBI GI	g541858
BLAST score	361
E value	2.0e-34
Match length	62
% identity	100
NCBI Description	endoxyloglucan transferase - Arabidopsis thaliana >gi_469484_dbj_BAA03921_ (D16454) endo-xyloglucan

transferase [Arabidopsis thaliana] >gi_4063757 (AC005561) endo-xyloglucan transferase [Arabidopsis thaliana]

Seq. No.	137058
Seq. ID	ARABL1-039-Q1-E1-B12
Method	BLASTX
NCBI GI	g3176874
BLAST score	170
E value	4.0e-12
Match length	45
% identity	76
NCBI Description	(AF065639) cucumisin-like serine protease [Arabidopsis thaliana]

Seq. No.	137059
Seq. ID	ARABL1-039-Q1-E1-B3
Method	BLASTX
NCBI GI	g4741952
BLAST score	255
E value	1.0e-22
Match length	50
% identity	96
NCBI Description	(AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No.	137060
Seq. ID	ARABL1-039-Q1-E1-C11
Method	BLASTX
NCBI GI	g3540181
BLAST score	204
E value	4.0e-16
Match length	70
% identity	56
NCBI Description	(AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No.	137061
Seq. ID	ARABL1-039-Q1-E1-C4
Method	BLASTN
NCBI GI	g4589421
BLAST score	72
E value	8.0e-33
Match length	112
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K5K13, complete sequence

Seq. No.	137062
Seq. ID	ARABL1-039-Q1-E1-D4
Method	BLASTX
NCBI GI	g1370186
BLAST score	190
E value	2.0e-14
Match length	40
% identity	88
NCBI Description	(Z73942) RAB7C [Lotus japonicus]

Seq. No.	137063
Seq. ID	ARABL1-039-Q1-E1-D6

Method	BLASTN
NCBI GI	g2462930
BLAST score	79
E value	2.0e-36
Match length	100
% identity	100
NCBI Description	dArabidopsis thaliana mRNA for UDP-glucose:sterol glucosyltransferase

Seq. No.	137064
Seq. ID	ARABL1-039-Q1-E1-E1
Method	BLASTN
NCBI GI	g4586241
BLAST score	110
E value	2.0e-55
Match length	110
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T20K18 (ESSA project)

Seq. No.	137065
Seq. ID	ARABL1-039-Q1-E1-E9
Method	BLASTN
NCBI GI	g3063438
BLAST score	60
E value	5.0e-26
Match length	60
% identity	100
NCBI Description	Complete sequence of Arabidopsis F22O13, complete sequence [Arabidopsis thaliana]

Seq. No.	137066
Seq. ID	ARABL1-039-Q1-E1-F7
Method	BLASTN
NCBI GI	g2351069
BLAST score	152
E value	2.0e-80
Match length	164
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSH12, complete sequence [Arabidopsis thaliana]

Seq. No.	137067
Seq. ID	ARABL1-04-Q1-B1-B2
Method	BLASTX
NCBI GI	g4741952
BLAST score	646
E value	8.0e-68
Match length	122
% identity	75
NCBI Description	(AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No.	137068
Seq. ID	ARABL1-04-Q1-B1-B6
Method	BLASTX
NCBI GI	g4662642
BLAST score	668

E value	2.0e-70
Match length	128
% identity	100
NCBI Description	(AC006429) hypothetical protein [Arabidopsis thaliana]

Seq. No.	137069
Seq. ID	ARABL1-04-Q1-B1-B8
Method	BLASTX
NCBI GI	g464986
BLAST score	558
E value	2.0e-57
Match length	104
% identity	99
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi_421857_pir__S32674 ubiquitin--protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating enzyme E2 [Arabidopsis thaliana] >gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein ligase UBC9 [Arabidopsis thaliana]

Seq. No.	137070
Seq. ID	ARABL1-04-Q1-B1-C3
Method	BLASTX
NCBI GI	g3170230
BLAST score	462
E value	3.0e-46
Match length	134
% identity	66
NCBI Description	(AF041848) fructose-6-phosphate 2-kinase /fructose-2,6-bisphosphatase [Spinacia oleracea]

Seq. No.	137071
Seq. ID	ARABL1-04-Q1-B1-C8
Method	BLASTX
NCBI GI	g1709534
BLAST score	590
E value	3.0e-61
Match length	133
% identity	89
NCBI Description	DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE A (P5CS A) [CONTAINS: GLUTAMATE 5-KINASE (GAMMA-GLUTAMYL KINASE) (GK); GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMIALDE... >gi_2129572_pir__S66637 delta-1-pyrroline-5-carboxylate synthetase - Arabidopsis thaliana >gi_829100_emb_CAA60740_ (X87330) pyrroline-5-carboxylate synthetase [Arabidopsis thaliana] >gi_870866_emb_CAA60446_ (X86777) pyrroline-5-carboxylate synthetase A [Arabidopsis thaliana] >gi_1041248_emb_CAA61593_ (X89414) pyrroline-5-carboxylate synthase [Arabidopsis thaliana] >gi_2642162 (AC003000) delta-1-pyrroline 5-carboxylase synthetase, P5C1

[Arabidopsis thaliana]

Seq. No.	137072
Seq. ID	ARABL1-04-Q1-B1-D1
Method	BLASTN
NCBI GI	g3335331
BLAST score	327
E value	0.0e+00
Match length	327
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8F5 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137073
Seq. ID	ARABL1-04-Q1-B1-D5
Method	BLASTX
NCBI GI	g4469022
BLAST score	427
E value	2.0e-42
Match length	86
% identity	98
NCBI Description	(AL035602) cytochrome P450-like protein [Arabidopsis thaliana]

Seq. No.	137074
Seq. ID	ARABL1-04-Q1-B1-D6
Method	BLASTX
NCBI GI	g430947
BLAST score	541
E value	2.0e-55
Match length	133
% identity	80
NCBI Description	(U01103) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	137075
Seq. ID	ARABL1-04-Q1-B1-E8
Method	BLASTX
NCBI GI	g2127972
BLAST score	159
E value	9.0e-11
Match length	54
% identity	50
NCBI Description	HIT protein homolog - Methanococcus jannaschii

Seq. No.	137076
Seq. ID	ARABL1-04-Q1-B1-F1
Method	BLASTX
NCBI GI	g3068713
BLAST score	505
E value	3.0e-51
Match length	131
% identity	81
NCBI Description	(AF049236) unknown [Arabidopsis thaliana]

Seq. No.	137077
Seq. ID	ARABL1-04-Q1-B1-G1

Method	BLASTN
NCBI GI	g4572664
BLAST score	128
E value	9.0e-66
Match length	249
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC F25P17 genomic sequence, complete sequence

Seq. No.	137078
Seq. ID	ARABL1-04-Q1-B1-G3
Method	BLASTN
NCBI GI	g3152602
BLAST score	135
E value	5.0e-70
Match length	135
% identity	50
NCBI Description	Arabidopsis thaliana chromosome II BAC F27L4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137079
Seq. ID	ARABL1-04-Q1-B1-G5
Method	BLASTX
NCBI GI	g4678261
BLAST score	463
E value	2.0e-46
Match length	94
% identity	100
NCBI Description	(AL049657) putative proteasome regulatory subunit [Arabidopsis thaliana]

Seq. No.	137080
Seq. ID	ARABL1-04-Q1-B1-H6
Method	BLASTN
NCBI GI	g2656028
BLAST score	219
E value	1.0e-120
Match length	324
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNF13

Seq. No.	137081
Seq. ID	ARABL1-040-Q1-B1-A11
Method	BLASTX
NCBI GI	g4185599
BLAST score	153
E value	5.0e-10
Match length	107
% identity	37
NCBI Description	(AB010708) Anthocyanin 5-aromatic acyltransferase [Gentiana triflora]

Seq. No.	137082
Seq. ID	ARABL1-040-Q1-B1-A2
Method	BLASTX
NCBI GI	g543751

BLAST score	164
E value	7.0e-12
Match length	31
% identity	100
NCBI Description	1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE (ACC OXIDASE) (ETHYLENE-FORMING ENZYME) (EFE) >gi_541861_pir__JT0755 ethylene-forming enzyme - Arabidopsis thaliana >gi_16254_emb_CAA47251_ (X66719) ethylene-forming enzyme [Arabidopsis thaliana]

Seq. No.	137083
Seq. ID	ARABL1-040-Q1-B1-D7
Method	BLASTN
NCBI GI	g4662628
BLAST score	106
E value	2.0e-52
Match length	210
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC F27O10 genomic sequence, complete sequence

Seq. No.	137084
Seq. ID	ARABL1-040-Q1-B1-D9
Method	BLASTX
NCBI GI	g4585882
BLAST score	482
E value	1.0e-48
Match length	92
% identity	100
NCBI Description	(AC005850) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	137085
Seq. ID	ARABL1-040-Q1-B1-E11
Method	BLASTX
NCBI GI	g115783
BLAST score	479
E value	2.0e-48
Match length	90
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	137086
Seq. ID	ARABL1-040-Q1-B1-E8
Method	BLASTX
NCBI GI	g3335372
BLAST score	256
E value	4.0e-22
Match length	112
% identity	45
NCBI Description	(AC003028) putative SRG1 protein [Arabidopsis thaliana]

Seq. No.	137087
Seq. ID	ARABL1-040-Q1-B1-G9

Method	BLASTN
NCBI GI	g3241923
BLAST score	158
E value	6.0e-84
Match length	158
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMN10, complete sequence [Arabidopsis thaliana]

Seq. No.	137088
Seq. ID	ARABL1-040-Q1-B1-H10
Method	BLASTX
NCBI GI	g2760606
BLAST score	432
E value	9.0e-43
Match length	109
% identity	72
NCBI Description	(AB001568) phospholipid hydroperoxide glutathione peroxidase-like protein [Arabidopsis thaliana] >gi_3004869 (AF030132) glutathione peroxidase; ATGP1 [Arabidopsis thaliana] >gi_4539451_emb_CAB39931.1_ (AL049500) phospholipid hydroperoxide glutathione peroxidase [Arabidopsis thaliana]

Seq. No.	137089
Seq. ID	ARABL1-040-Q1-E1-C12
Method	BLASTN
NCBI GI	g2088638
BLAST score	389
E value	0.0e+00
Match length	389
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T28M21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137090
Seq. ID	ARABL1-040-Q1-E1-D5
Method	BLASTN
NCBI GI	g2584827
BLAST score	92
E value	3.0e-44
Match length	293
% identity	97
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F12F1 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137091
Seq. ID	ARABL1-040-Q1-E1-E10
Method	BLASTN
NCBI GI	g3063690
BLAST score	164
E value	3.0e-87
Match length	196
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11 (ESSAII project)

Seq. No.	137092
Seq. ID	ARABL1-040-Q1-E1-F12
Method	BLASTN
NCBI GI	g1707006
BLAST score	113
E value	4.0e-57
Match length	157
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC T1B8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137093
Seq. ID	ARABL1-040-Q1-E1-F4
Method	BLASTX
NCBI GI	g131398
BLAST score	283
E value	2.0e-25
Match length	65
% identity	85
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No.	137094
Seq. ID	ARABL1-040-Q1-E1-G3
Method	BLASTN
NCBI GI	g3241927
BLAST score	200
E value	1.0e-108
Match length	309
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTE17, complete sequence [Arabidopsis thaliana]

Seq. No.	137095
Seq. ID	ARABL1-040-Q1-E1-G9
Method	BLASTN
NCBI GI	g3241923
BLAST score	158
E value	6.0e-84
Match length	158
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMN10, complete sequence [Arabidopsis thaliana]

Seq. No.	137096
Seq. ID	ARABL1-040-Q1-E1-H1
Method	BLASTN
NCBI GI	g2618599
BLAST score	310
E value	1.0e-174

Match length	310
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBD2, complete sequence [Arabidopsis thaliana]

Seq. No.	137097
Seq. ID	ARABL1-041-Q1-B1-A10
Method	BLASTX
NCBI GI	g2244904
BLAST score	476
E value	6.0e-48
Match length	117
% identity	90
NCBI Description	(Z97339) similar to hypothetical protein C02F5.7 - Caenorha [Arabidopsis thaliana]

Seq. No.	137098
Seq. ID	ARABL1-041-Q1-B1-B9
Method	BLASTN
NCBI GI	g4191760
BLAST score	86
E value	4.0e-41
Match length	130
% identity	92
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17F8, complete sequence [Arabidopsis thaliana]

Seq. No.	137099
Seq. ID	ARABL1-041-Q1-B1-C7
Method	BLASTN
NCBI GI	g4220640
BLAST score	344
E value	0.0e+00
Match length	344
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPE11, complete sequence [Arabidopsis thaliana]

Seq. No.	137100
Seq. ID	ARABL1-041-Q1-B1-C8
Method	BLASTN
NCBI GI	g3522932
BLAST score	44
E value	2.0e-15
Match length	99
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137101
Seq. ID	ARABL1-041-Q1-B1-E9
Method	BLASTN
NCBI GI	g4262221
BLAST score	226
E value	1.0e-124
Match length	229
% identity	100

NCBI Description	Arabidopsis thaliana chromosome II BAC F10A8 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	137102
Seq. ID	ARABL1-041-Q1-B1-F4
Method	BLASTX
NCBI GI	g2338712
BLAST score	243
E value	1.0e-20
Match length	46
% identity	98
NCBI Description	(AF013959) metallothionein-like protein [Arabidopsis thaliana]
Seq. No.	137103
Seq. ID	ARABL1-041-Q1-B1-G4
Method	BLASTX
NCBI GI	g1922242
BLAST score	199
E value	2.0e-15
Match length	36
% identity	100
NCBI Description	(Y10084) hypothetical protein [Arabidopsis thaliana]
Seq. No.	137104
Seq. ID	ARABL1-041-Q1-B1-G5
Method	BLASTN
NCBI GI	g2749918
BLAST score	100
E value	2.0e-49
Match length	121
% identity	94
NCBI Description	Arabidopsis thaliana chromosome I BAC F3I6 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	137105
Seq. ID	ARABL1-041-Q1-B1-G7
Method	BLASTX
NCBI GI	g4584540
BLAST score	427
E value	3.0e-42
Match length	106
% identity	84
NCBI Description	(AL049608) putative protein [Arabidopsis thaliana]
Seq. No.	137106
Seq. ID	ARABL1-041-Q1-B1-H5
Method	BLASTX
NCBI GI	g3169287
BLAST score	640
E value	3.0e-67
Match length	128
% identity	99
NCBI Description	(AF050673) vacuolar H+-ATPase catalytic subunit [Gossypium hirsutum]
Seq. No.	137107

Seq. ID	ARABL1-041-Q1-B1-H7
Method	BLASTN
NCBI GI	g2281648
BLAST score	165
E value	1.0e-87
Match length	165
% identity	100
NCBI Description	Arabidopsis thaliana AP2 domain containing protein RAP2.12 mRNA, partial cds

Seq. No.	137108
Seq. ID	ARABL1-041-Q1-B1-H9
Method	BLASTX
NCBI GI	g586145
BLAST score	149
E value	1.0e-09
Match length	99
% identity	40
NCBI Description	UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT PRECURSOR (RIESKE IRON-SULFUR PROTEIN) (RISP) >gi_488848_emb_CAA55894_ (X79332) Rieske iron sulphur protein [Solanum tuberosum]

Seq. No.	137109
Seq. ID	ARABL1-041-Q1-E1-A12
Method	BLASTN
NCBI GI	g2264304
BLAST score	325
E value	0.0e+00
Match length	333
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBG8, complete sequence [Arabidopsis thaliana]

Seq. No.	137110
Seq. ID	ARABL1-041-Q1-E1-B7
Method	BLASTX
NCBI GI	g3123296
BLAST score	219
E value	6.0e-18
Match length	43
% identity	100
NCBI Description	CALMODULIN-RELATED PROTEIN 3, TOUCH-INDUCED >gi_598067 (L34546) calmodulin-related protein [Arabidopsis thaliana]

Seq. No.	137111
Seq. ID	ARABL1-041-Q1-E1-C10
Method	BLASTN
NCBI GI	g2098816
BLAST score	176
E value	2.0e-94
Match length	350
% identity	100
NCBI Description	Arabidopsis thaliana BAC F19G10, complete sequence

Seq. No.	137112
Seq. ID	ARABL1-041-Q1-E1-C9

Method	BLASTN
NCBI GI	g2347177
BLAST score	45
E value	3.0e-16
Match length	153
% identity	82
NCBI Description	Arabidopsis thaliana catalase 3 (CAT3) gene, complete cds

Seq. No.	137113
Seq. ID	ARABL1-041-Q1-E1-D11
Method	BLASTN
NCBI GI	g2264305
BLAST score	266
E value	1.0e-148
Match length	373
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK23, complete sequence [Arabidopsis thaliana]

Seq. No.	137114
Seq. ID	ARABL1-041-Q1-E1-E1
Method	BLASTX
NCBI GI	g2398679
BLAST score	411
E value	2.0e-40
Match length	84
% identity	92
NCBI Description	(Y14797) 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase [Morinda citrifolia]

Seq. No.	137115
Seq. ID	ARABL1-041-Q1-E1-E3
Method	BLASTX
NCBI GI	g3123188
BLAST score	252
E value	1.0e-21
Match length	51
% identity	94
NCBI Description	CATALASE 3 >gi_2347178 (U43147) catalase 3 [Arabidopsis thaliana] >gi_2511726 (AF021937) catalase 3 [Arabidopsis thaliana]

Seq. No.	137116
Seq. ID	ARABL1-041-Q1-E1-E9
Method	BLASTN
NCBI GI	g4262221
BLAST score	217
E value	1.0e-119
Match length	229
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137117
Seq. ID	ARABL1-041-Q1-E1-G5
Method	BLASTN
NCBI GI	g2749918

BLAST score	100
E value	2.0e-49
Match length	121
% identity	94
NCBI Description	Arabidopsis thaliana chromosome I BAC F3I6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137118
Seq. ID	ARABL1-041-Q1-E1-H7
Method	BLASTN
NCBI GI	g2281648
BLAST score	351
E value	0.0e+00
Match length	351
% identity	100
NCBI Description	Arabidopsis thaliana AP2 domain containing protein RAP2.12 mRNA, partial cds

Seq. No.	137119
Seq. ID	ARABL1-042-Q1-B1-A10
Method	BLASTX
NCBI GI	g1170089
BLAST score	224
E value	6.0e-19
Match length	46
% identity	100
NCBI Description	GLUTATHIONE S-TRANSFERASE ERD13 (CLASS PHI) >gi_481822_pir__S39542 probable glutathione transferase (EC 2.5.1.18) (clone ERD13) - Arabidopsis thaliana >gi_497789_dbj_BAA04554_ (D17673) glutathione S-transferase [Arabidopsis thaliana] >gi_3201614 (AC004669) glutathione S-transferase [Arabidopsis thaliana]

Seq. No.	137120
Seq. ID	ARABL1-042-Q1-B1-A9
Method	BLASTX
NCBI GI	g3121825
BLAST score	245
E value	7.0e-21
Match length	93
% identity	56
NCBI Description	2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) >gi_1498247_emb_CAA63910_ (X94219) bas1 protein [Spinacia oleracea]

Seq. No.	137121
Seq. ID	ARABL1-042-Q1-B1-B10
Method	BLASTX
NCBI GI	g3367576
BLAST score	523
E value	2.0e-53
Match length	126
% identity	75
NCBI Description	(AL031135) NAM / CUC2 -like protein [Arabidopsis thaliana]

Seq. No.	137122
Seq. ID	ARABL1-042-Q1-B1-B11

Method	BLASTN
NCBI GI	g4220638
BLAST score	384
E value	0.0e+00
Match length	387
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIF21, complete sequence [Arabidopsis thaliana]

Seq. No.	137123
Seq. ID	ARABL1-042-Q1-B1-C9
Method	BLASTX
NCBI GI	g2119848
BLAST score	273
E value	2.0e-24
Match length	66
% identity	76
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B1 - Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128229 (AC004077) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	137124
Seq. ID	ARABL1-042-Q1-B1-E12
Method	BLASTX
NCBI GI	g4583542
BLAST score	477
E value	4.0e-48
Match length	126
% identity	83
NCBI Description	(Y16847) 16 kDa polypeptide of oxygen-evolving complex [Arabidopsis thaliana]

Seq. No.	137125
Seq. ID	ARABL1-042-Q1-B1-E3
Method	BLASTN
NCBI GI	g2673901
BLAST score	142
E value	2.0e-74
Match length	142
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T24P15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137126
Seq. ID	ARABL1-042-Q1-B1-G4
Method	BLASTX
NCBI GI	g3242075
BLAST score	144
E value	3.0e-09
Match length	31
% identity	90
NCBI Description	(Z97059) S-adenosyl-L-homocysteine hydrolase [Arabidopsis

thaliana]

Seq. No.	137127
Seq. ID	ARABL1-042-Q1-E1-C11
Method	BLASTN
NCBI GI	g2959729
BLAST score	62
E value	2.0e-26
Match length	160
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for GATA transcription factor

Seq. No.	137128
Seq. ID	ARABL1-042-Q1-E1-D6
Method	BLASTN
NCBI GI	g4220640
BLAST score	158
E value	8.0e-84
Match length	210
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPE11, complete sequence [Arabidopsis thaliana]

Seq. No.	137129
Seq. ID	ARABL1-042-Q1-E1-E2
Method	BLASTX
NCBI GI	g115767
BLAST score	330
E value	6.0e-31
Match length	63
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	137130
Seq. ID	ARABL1-042-Q1-E1-E3
Method	BLASTN
NCBI GI	g2673901
BLAST score	142
E value	2.0e-74
Match length	142
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T24P15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137131
Seq. ID	ARABL1-042-Q1-E1-F6
Method	BLASTN
NCBI GI	g297877
BLAST score	200
E value	1.0e-109
Match length	221

% identity	97
NCBI Description	A.thaliana UBC10 mRNA for ubiquitin conjugating enzyme homolog >gi_349212_gb_L00640_ATHUBCC Arabidopsis thaliana ubiquitin conjugating enzyme mRNA, complete cds

Seq. No.	137132
Seq. ID	ARABL1-042-Q1-E1-G2
Method	BLASTN
NCBI GI	g499161
BLAST score	58
E value	2.0e-24
Match length	141
% identity	84
NCBI Description	A.thaliana mRNA Athb-6

Seq. No.	137133
Seq. ID	ARABL1-042-Q1-E1-H12
Method	BLASTN
NCBI GI	g3449327
BLAST score	296
E value	1.0e-166
Match length	296
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCA23, complete sequence [Arabidopsis thaliana]

Seq. No.	137134
Seq. ID	ARABL1-043-Q1-B1-A6
Method	BLASTX
NCBI GI	g2828293
BLAST score	226
E value	2.0e-48
Match length	95
% identity	94
NCBI Description	(AL021687) putative protein [Arabidopsis thaliana]

Seq. No.	137135
Seq. ID	ARABL1-043-Q1-B1-A8
Method	BLASTN
NCBI GI	g16300
BLAST score	34
E value	7.0e-10
Match length	169
% identity	95
NCBI Description	A.thaliana mRNA for glycine rich protein >gi_166836_gb_L00648_ATHRBPA Arabidopsis thaliana RNA-binding protein mRNA, complete cds

Seq. No.	137136
Seq. ID	ARABL1-043-Q1-B1-B10
Method	BLASTX
NCBI GI	g2894601
BLAST score	336
E value	8.0e-32
Match length	79
% identity	76
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

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Seq. No.	137137
Seq. ID	ARABL1-043-Q1-B1-B8
Method	BLASTX
NCBI GI	g3128177
BLAST score	632
E value	3.0e-66
Match length	126
% identity	100
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	137138
Seq. ID	ARABL1-043-Q1-B1-C2
Method	BLASTX
NCBI GI	g4522006
BLAST score	375
E value	2.0e-36
Match length	77
% identity	99
NCBI Description	(AC007069) hypothetical protein [Arabidopsis thaliana]

Seq. No.	137139
Seq. ID	ARABL1-043-Q1-B1-C3
Method	BLASTN
NCBI GI	g3169169
BLAST score	355
E value	0.0e+00
Match length	359
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F21P24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137140
Seq. ID	ARABL1-043-Q1-B1-C4
Method	BLASTN
NCBI GI	g4589439
BLAST score	96
E value	9.0e-47
Match length	169
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQM1, complete sequence

Seq. No.	137141
Seq. ID	ARABL1-043-Q1-B1-C5
Method	BLASTX
NCBI GI	g2795809
BLAST score	542
E value	1.0e-55
Match length	123
% identity	79
NCBI Description	(AC003674) putative expansin [Arabidopsis thaliana]

Seq. No.	137142
Seq. ID	ARABL1-043-Q1-B1-E10
Method	BLASTX
NCBI GI	g4038352

BLAST score	346
E value	1.0e-32
Match length	124
% identity	54
NCBI Description	(AF098951) breast cancer resistance protein [Homo sapiens]

Seq. No.	137143
Seq. ID	ARABL1-043-Q1-B1-E9
Method	BLASTX
NCBI GI	g3287693
BLAST score	670
E value	1.0e-70
Match length	125
% identity	100
NCBI Description	(AC003979) Similar to LIM17 gene product gb_1653769 from the genome of Synechocystis sp. gb_D90916. [Arabidopsis thaliana]

Seq. No.	137144
Seq. ID	ARABL1-043-Q1-B1-G12
Method	BLASTN
NCBI GI	g4325340
BLAST score	223
E value	1.0e-122
Match length	338
% identity	99
NCBI Description	Arabidopsis thaliana BAC T1J1

Seq. No.	137145
Seq. ID	ARABL1-043-Q1-B1-G4
Method	BLASTN
NCBI GI	g3985952
BLAST score	249
E value	1.0e-138
Match length	286
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MRC8, complete sequence [Arabidopsis thaliana]

Seq. No.	137146
Seq. ID	ARABL1-043-Q1-E1-A6
Method	BLASTN
NCBI GI	g2828278
BLAST score	138
E value	9.0e-72
Match length	254
% identity	89
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16 (ESSAII project)

Seq. No.	137147
Seq. ID	ARABL1-043-Q1-E1-A8
Method	BLASTN
NCBI GI	g166656
BLAST score	129
E value	1.0e-66
Match length	184

% identity	94
NCBI Description	Arabidopsis thaliana Ccr2 mRNA, partial ORF

Seq. No.	137148
Seq. ID	ARABL1-043-Q1-E1-B2
Method	BLASTN
NCBI GI	g3702728
BLAST score	166
E value	2.0e-88
Match length	299
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M13, complete sequence [Arabidopsis thaliana]

Seq. No.	137149
Seq. ID	ARABL1-043-Q1-E1-B7
Method	BLASTX
NCBI GI	g2507587
BLAST score	235
E value	1.0e-19
Match length	41
% identity	100
NCBI Description	METALLOTHIONEIN-LIKE PROTEIN 2A (MT-2A) (MT-K) (MT-1G) >gi_1361998_pir__S57861 metallothionein 2a - Arabidopsis thaliana >gi_555976 (U15108) metallothionein-like protein [Arabidopsis thaliana] >gi_1580892_prf__2116236A metallothionein 1 [Arabidopsis thaliana]

Seq. No.	137150
Seq. ID	ARABL1-043-Q1-E1-C3
Method	BLASTN
NCBI GI	g2642427
BLAST score	109
E value	2.0e-54
Match length	216
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T20D16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137151
Seq. ID	ARABL1-043-Q1-E1-C6
Method	BLASTN
NCBI GI	g3169169
BLAST score	96
E value	6.0e-47
Match length	152
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC F21P24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137152
Seq. ID	ARABL1-043-Q1-E1-D3
Method	BLASTN
NCBI GI	g2832358
BLAST score	52
E value	9.0e-21
Match length	108

% identity	87
NCBI Description	Arabidopsis thaliana mRNA for HMG beta1 protein
Seq. No.	137153
Seq. ID	ARABL1-044-Q1-B1-A6
Method	BLASTN
NCBI GI	g3445196
BLAST score	44
E value	2.0e-15
Match length	191
% identity	82
NCBI Description	Arabidopsis thaliana chromosome II BAC T20K9 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	137154
Seq. ID	ARABL1-044-Q1-B1-B1
Method	BLASTX
NCBI GI	g115783
BLAST score	512
E value	3.0e-52
Match length	96
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]
Seq. No.	137155
Seq. ID	ARABL1-044-Q1-B1-B4
Method	BLASTN
NCBI GI	g4589415
BLAST score	119
E value	2.0e-60
Match length	179
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K14A3, complete sequence
Seq. No.	137156
Seq. ID	ARABL1-044-Q1-B1-C11
Method	BLASTX
NCBI GI	g2598589
BLAST score	219
E value	8.0e-18
Match length	73
% identity	56
NCBI Description	(Y15367) MtN19 [Medicago truncatula]
Seq. No.	137157
Seq. ID	ARABL1-044-Q1-B1-C2
Method	BLASTN
NCBI GI	g3005688
BLAST score	215
E value	1.0e-117
Match length	362
% identity	100
NCBI Description	Arabidopsis thaliana AT4 mRNA sequence

Seq. No.	137158
Seq. ID	ARABL1-044-Q1-B1-C8
Method	BLASTN
NCBI GI	g2760164
BLAST score	398
E value	0.0e+00
Match length	398
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18P6, complete sequence [Arabidopsis thaliana]

Seq. No.	137159
Seq. ID	ARABL1-044-Q1-B1-D8
Method	BLASTN
NCBI GI	g4455229
BLAST score	252
E value	1.0e-139
Match length	380
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F13M23 (ESSAII project)

Seq. No.	137160
Seq. ID	ARABL1-044-Q1-B1-D9
Method	BLASTX
NCBI GI	g4468999
BLAST score	108
E value	8.0e-05
Match length	97
% identity	20
NCBI Description	(Z97342) unnamed protein product [Arabidopsis thaliana]

Seq. No.	137161
Seq. ID	ARABL1-044-Q1-B1-G2
Method	BLASTX
NCBI GI	g2828292
BLAST score	492
E value	8.0e-50
Match length	92
% identity	100
NCBI Description	(AL021687) neoxanthin cleavage enzyme-like protein [Arabidopsis thaliana]

Seq. No.	137162
Seq. ID	ARABL1-044-Q1-B1-G8
Method	BLASTX
NCBI GI	g4544374
BLAST score	201
E value	6.0e-16
Match length	54
% identity	74
NCBI Description	(AC006920) unknown protein [Arabidopsis thaliana]

Seq. No.	137163
Seq. ID	ARABL1-044-Q1-B1-H5
Method	BLASTX

NCBI GI	g4583542
BLAST score	495
E value	4.0e-50
Match length	130
% identity	83
NCBI Description	(Y16847) 16 kDa polypeptide of oxygen-evolving complex [Arabidopsis thaliana]

Seq. No.	137164
Seq. ID	ARABL1-044-Q1-B1-H7
Method	BLASTX
NCBI GI	g2281631
BLAST score	591
E value	2.0e-61
Match length	110
% identity	100
NCBI Description	(AF003096) AP2 domain containing protein RAP2.3 [Arabidopsis thaliana]

Seq. No.	137165
Seq. ID	ARABL1-044-Q1-E1-A12
Method	BLASTX
NCBI GI	g3582341
BLAST score	220
E value	5.0e-18
Match length	85
% identity	60
NCBI Description	(AC005496) putative flavonol 3-o-glucosyltransferase [Arabidopsis thaliana]

Seq. No.	137166
Seq. ID	ARABL1-044-Q1-E1-D5
Method	BLASTX
NCBI GI	g3763923
BLAST score	233
E value	1.0e-19
Match length	50
% identity	90
NCBI Description	(AC004450) hypothetical protein [Arabidopsis thaliana]

Seq. No.	137167
Seq. ID	ARABL1-044-Q1-E1-D8
Method	BLASTN
NCBI GI	g4678258
BLAST score	245
E value	1.0e-135
Match length	339
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I7 (ESSA project)

Seq. No.	137168
Seq. ID	ARABL1-044-Q1-E1-E10
Method	BLASTN
NCBI GI	g2760316
BLAST score	85
E value	3.0e-40

Match length	117
% identity	93
NCBI Description	The sequence of BAC F1N21 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	137169
Seq. ID	ARABL1-044-Q1-E1-E11
Method	BLASTN
NCBI GI	g1708776
BLAST score	335
E value	0.0e+00
Match length	355
% identity	99
NCBI Description	A.thaliana mRNA for potassium channel

Seq. No.	137170
Seq. ID	ARABL1-044-Q1-E1-E2
Method	BLASTN
NCBI GI	g2760167
BLAST score	193
E value	1.0e-105
Match length	193
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCO15, complete sequence [Arabidopsis thaliana]

Seq. No.	137171
Seq. ID	ARABL1-044-Q1-E1-E6
Method	BLASTN
NCBI GI	g2780191
BLAST score	167
E value	3.0e-89
Match length	207
% identity	95
NCBI Description	Arabidopsis thaliana nap gene

Seq. No.	137172
Seq. ID	ARABL1-044-Q1-E1-F2
Method	BLASTN
NCBI GI	g4559344
BLAST score	178
E value	8.0e-96
Match length	182
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F27C12 genomic sequence, complete sequence

Seq. No.	137173
Seq. ID	ARABL1-044-Q1-E1-G8
Method	BLASTX
NCBI GI	g4544374
BLAST score	247
E value	1.0e-21
Match length	49
% identity	92
NCBI Description	(AC006920) unknown protein [Arabidopsis thaliana]

Seq. No.	137174
Seq. ID	ARABL1-045-Q1-B1-A8
Method	BLASTX
NCBI GI	g4586256
BLAST score	552
E value	8.0e-57
Match length	127
% identity	86
NCBI Description	(AL049640) probable photosystem I chain XI precursor [Arabidopsis thaliana]

Seq. No.	137175
Seq. ID	ARABL1-045-Q1-B1-B1
Method	BLASTX
NCBI GI	g1769905
BLAST score	437
E value	2.0e-43
Match length	123
% identity	69
NCBI Description	(X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC) [Arabidopsis thaliana]

Seq. No.	137176
Seq. ID	ARABL1-045-Q1-B1-B10
Method	BLASTN
NCBI GI	g2760316
BLAST score	380
E value	0.0e+00
Match length	384
% identity	100
NCBI Description	The sequence of BAC F1N21 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	137177
Seq. ID	ARABL1-045-Q1-B1-B6
Method	BLASTX
NCBI GI	g2119846
BLAST score	637
E value	8.0e-67
Match length	122
% identity	99
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B2 - Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	137178
Seq. ID	ARABL1-045-Q1-B1-C5
Method	BLASTN
NCBI GI	g3098611
BLAST score	306
E value	1.0e-172
Match length	360
% identity	97

NCBI Description	Arabidopsis thaliana senescence associated gene (SAG20) mRNA, partial cds
Seq. No.	137179
Seq. ID	ARABL1-045-Q1-B1-C6
Method	BLASTN
NCBI GI	g3098611
BLAST score	113
E value	7.0e-57
Match length	197
% identity	91
NCBI Description	Arabidopsis thaliana senescence associated gene (SAG20) mRNA, partial cds
Seq. No.	137180
Seq. ID	ARABL1-045-Q1-B1-D1
Method	BLASTX
NCBI GI	g3766248
BLAST score	440
E value	1.0e-43
Match length	102
% identity	81
NCBI Description	(Y18227) blue copper binding-like protein [Arabidopsis thaliana]
Seq. No.	137181
Seq. ID	ARABL1-045-Q1-B1-D3
Method	BLASTN
NCBI GI	g3766106
BLAST score	25
E value	2.0e-04
Match length	181
% identity	69
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F9K20 sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	137182
Seq. ID	ARABL1-045-Q1-B1-D9
Method	BLASTN
NCBI GI	g397481
BLAST score	26
E value	6.0e-05
Match length	275
% identity	95
NCBI Description	A.thaliana hsc70 mRNA for heat shock cognate protein
Seq. No.	137183
Seq. ID	ARABL1-045-Q1-B1-E11
Method	BLASTX
NCBI GI	g1890352
BLAST score	678
E value	1.0e-71
Match length	126
% identity	60
NCBI Description	(X91398) transcription factor L2 [Arabidopsis thaliana]
Seq. No.	137184

Seq. ID	ARABL1-045-Q1-B1-E7
Method	BLASTX
NCBI GI	g4490323
BLAST score	536
E value	6.0e-55
Match length	132
% identity	83
NCBI Description	(AJ131464) nitrate transporter [Arabidopsis thaliana]

Seq. No.	137185
Seq. ID	ARABL1-045-Q1-B1-E8
Method	BLASTX
NCBI GI	g4585977
BLAST score	379
E value	1.0e-36
Match length	82
% identity	78
NCBI Description	(AC005287) Unknown protein [Arabidopsis thaliana]

Seq. No.	137186
Seq. ID	ARABL1-045-Q1-B1-G3
Method	BLASTX
NCBI GI	g4455318
BLAST score	290
E value	3.0e-26
Match length	117
% identity	50
NCBI Description	(AL035528) glycine hydroxymethyltransferase-like protein [Arabidopsis thaliana]

Seq. No.	137187
Seq. ID	ARABL1-045-Q1-B1-H12
Method	BLASTX
NCBI GI	g4688596
BLAST score	463
E value	2.0e-46
Match length	104
% identity	86
NCBI Description	(AJ005682) inositol 1,4,5-trisphosphate 5-phosphatase [Arabidopsis thaliana]

Seq. No.	137188
Seq. ID	ARABL1-045-Q1-E1-A5
Method	BLASTN
NCBI GI	g4220510
BLAST score	216
E value	1.0e-118
Match length	240
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18 (ESSAII project)

Seq. No.	137189
Seq. ID	ARABL1-045-Q1-E1-B9
Method	BLASTN
NCBI GI	g4519183
BLAST score	117

E value	1.0e-59
Match length	121
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15C23, complete sequence

Seq. No.	137190
Seq. ID	ARABL1-046-Q1-B1-A10
Method	BLASTX
NCBI GI	g2464914
BLAST score	272
E value	5.0e-24
Match length	106
% identity	55
NCBI Description	(Z99708) hypothetical protein [Arabidopsis thaliana]

Seq. No.	137191
Seq. ID	ARABL1-046-Q1-B1-B12
Method	BLASTN
NCBI GI	g3641835
BLAST score	173
E value	7.0e-93
Match length	173
% identity	81
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T4L20 (ESSAII project)

Seq. No.	137192
Seq. ID	ARABL1-046-Q1-B1-C12
Method	BLASTX
NCBI GI	g125576
BLAST score	394
E value	2.0e-38
Match length	100
% identity	81
NCBI Description	PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE) (PRK) >gi_99744_pir__S16583 phosphoribulokinase (EC 2.7.1.19) precursor - Arabidopsis thaliana >gi_16441_emb_CAA41155_ (X58149) Ribulose-5-phosphate kinase [Arabidopsis thaliana]

Seq. No.	137193
Seq. ID	ARABL1-046-Q1-B1-C8
Method	BLASTX
NCBI GI	g4091810
BLAST score	647
E value	5.0e-68
Match length	127
% identity	98
NCBI Description	(AF053345) fatty acid elongase 3-ketoacyl-CoA synthase 1 [Arabidopsis thaliana]

Seq. No.	137194
Seq. ID	ARABL1-046-Q1-B1-G8
Method	BLASTX
NCBI GI	g1769905
BLAST score	437

E value	2.0e-43
Match length	123
% identity	69
NCBI Description	(X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC) [Arabidopsis thaliana]

Seq. No.	137195
Seq. ID	ARABL1-046-Q1-B1-H1
Method	BLASTX
NCBI GI	g4512684
BLAST score	453
E value	3.0e-45
Match length	99
% identity	92
NCBI Description	(AC006931) unknown protein [Arabidopsis thaliana] >gi_4559324_gb_AAD22986.1_AC007087_5 (AC007087) unknown protein [Arabidopsis thaliana]

Seq. No.	137196
Seq. ID	ARABL1-046-Q1-B1-H5
Method	BLASTN
NCBI GI	g4056476
BLAST score	68
E value	2.0e-30
Match length	108
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC F3G5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137197
Seq. ID	ARABL1-046-Q1-E1-D11
Method	BLASTN
NCBI GI	g2924733
BLAST score	272
E value	1.0e-151
Match length	308
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]

Seq. No.	137198
Seq. ID	ARABL1-046-Q1-E1-H9
Method	BLASTX
NCBI GI	g115385
BLAST score	233
E value	1.0e-19
Match length	44
% identity	98
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	137199
Seq. ID	ARABL1-047-Q1-B1-A1
Method	BLASTX
NCBI GI	g2738248
BLAST score	297

E value	2.0e-27
Match length	78
% identity	79
NCBI Description	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No.	137200
Seq. ID	ARABL1-047-Q1-B1-A12
Method	BLASTN
NCBI GI	g4263753
BLAST score	257
E value	1.0e-143
Match length	261
% identity	100
NCBI Description	Arabidopsis thaliana chromosome V map near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	137201
Seq. ID	ARABL1-047-Q1-B1-A5
Method	BLASTN
NCBI GI	g4757414
BLAST score	40
E value	2.0e-13
Match length	44
% identity	62
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYF24, complete sequence

Seq. No.	137202
Seq. ID	ARABL1-047-Q1-B1-A6
Method	BLASTX
NCBI GI	g2119848
BLAST score	249
E value	9.0e-22
Match length	47
% identity	100
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B1 - Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128229 (AC004077) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	137203
Seq. ID	ARABL1-047-Q1-B1-A8
Method	BLASTX
NCBI GI	g2119848
BLAST score	259
E value	6.0e-23
Match length	49
% identity	100
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B1 - Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128229 (AC004077) putative

	photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.	137204
Seq. ID	ARABL1-047-Q1-B1-B1
Method	BLASTX
NCBI GI	g132090
BLAST score	322
E value	3.0e-30
Match length	62
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1B PRECURSOR (RUBISCO SMALL SUBUNIT 1B) >gi_68062_pir__RKMUB1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B1 precursor - Arabidopsis thaliana >gi_16193_emb_CAA32700_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]
Seq. No.	137205
Seq. ID	ARABL1-047-Q1-B1-B11
Method	BLASTN
NCBI GI	g4689466
BLAST score	55
E value	7.0e-23
Match length	80
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T23O15 genomic sequence, complete sequence
Seq. No.	137206
Seq. ID	ARABL1-047-Q1-B1-B12
Method	BLASTN
NCBI GI	g3075383
BLAST score	137
E value	3.0e-71
Match length	246
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T1D16 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	137207
Seq. ID	ARABL1-047-Q1-B1-B4
Method	BLASTX
NCBI GI	g3914917
BLAST score	204
E value	2.0e-16
Match length	39
% identity	100
NCBI Description	40S RIBOSOMAL PROTEIN S3A
Seq. No.	137208
Seq. ID	ARABL1-047-Q1-B1-B7
Method	BLASTX
NCBI GI	g4586256
BLAST score	268

E value	6.0e-24
Match length	73
% identity	75
NCBI Description	(AL049640) probable photosystem I chain XI precursor [Arabidopsis thaliana]

Seq. No.	137209
Seq. ID	ARABL1-047-Q1-B1-B9
Method	BLASTX
NCBI GI	g1086263
BLAST score	234
E value	7.0e-20
Match length	84
% identity	58
NCBI Description	TMV resistance protein N - tobacco (Nicotiana glutinosa) >gi_558887 (U15605) N [Nicotiana glutinosa]

Seq. No.	137210
Seq. ID	ARABL1-047-Q1-B1-C11
Method	BLASTN
NCBI GI	g4589427
BLAST score	261
E value	1.0e-145
Match length	261
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFG13, complete sequence

Seq. No.	137211
Seq. ID	ARABL1-047-Q1-B1-C12
Method	BLASTN
NCBI GI	g2924655
BLAST score	214
E value	1.0e-117
Match length	263
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKD10, complete sequence [Arabidopsis thaliana]

Seq. No.	137212
Seq. ID	ARABL1-047-Q1-B1-C2
Method	BLASTX
NCBI GI	g3355468
BLAST score	222
E value	1.0e-18
Match length	64
% identity	77
NCBI Description	(AC004218) putative ribosomal protein L35 [Arabidopsis thaliana]

Seq. No.	137213
Seq. ID	ARABL1-047-Q1-B1-D2
Method	BLASTN
NCBI GI	g4741959
BLAST score	172
E value	4.0e-92
Match length	202

09604705.100600

% identity	96
NCBI Description	Arabidopsis thaliana Lhcb6 protein (Lhcb6) mRNA, complete cds

Seq. No.	137214
Seq. ID	ARABL1-047-Q1-B1-D3
Method	BLASTN
NCBI GI	g2760170
BLAST score	97
E value	2.0e-47
Match length	202
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIO24, complete sequence [Arabidopsis thaliana]

Seq. No.	137215
Seq. ID	ARABL1-047-Q1-B1-E1
Method	BLASTX
NCBI GI	g115767
BLAST score	405
E value	5.0e-40
Match length	79
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	137216
Seq. ID	ARABL1-047-Q1-B1-E3
Method	BLASTX
NCBI GI	g3063472
BLAST score	307
E value	2.0e-28
Match length	59
% identity	100
NCBI Description	(AC003981) F22O13.34 [Arabidopsis thaliana]

Seq. No.	137217
Seq. ID	ARABL1-047-Q1-B1-E4
Method	BLASTX
NCBI GI	g421826
BLAST score	261
E value	4.0e-23
Match length	73
% identity	67
NCBI Description	chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis thaliana]

Seq. No.	137218
Seq. ID	ARABL1-047-Q1-B1-E6
Method	BLASTN
NCBI GI	g259446

BLAST score	204
E value	1.0e-111
Match length	208
% identity	72
NCBI Description	glycine-rich protein {clone atGRP-3} [Arabidopsis thaliana, C24, mRNA, 680 nt]

Seq. No.	137219
Seq. ID	ARABL1-047-Q1-B1-E9
Method	BLASTX
NCBI GI	g2129672
BLAST score	202
E value	4.0e-16
Match length	61
% identity	69
NCBI Description	photosystem II reaction center protein, 6.1K - Arabidopsis thaliana >gi_950023_emb_CAA62296_ (X90769) component of 6.1 kDa polypeptide of photosystem II reaction center [Arabidopsis thaliana]

Seq. No.	137220
Seq. ID	ARABL1-047-Q1-B1-F11
Method	BLASTN
NCBI GI	g4584841
BLAST score	170
E value	7.0e-91
Match length	259
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T23E23, complete sequence

Seq. No.	137221
Seq. ID	ARABL1-047-Q1-B1-F2
Method	BLASTN
NCBI GI	g2618601
BLAST score	240
E value	1.0e-132
Match length	240
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	137222
Seq. ID	ARABL1-047-Q1-B1-F6
Method	BLASTX
NCBI GI	g2338712
BLAST score	268
E value	6.0e-24
Match length	50
% identity	100
NCBI Description	(AF013959) metallothionein-like protein [Arabidopsis thaliana]

Seq. No.	137223
Seq. ID	ARABL1-047-Q1-B1-G1
Method	BLASTX
NCBI GI	g729479

BLAST score	243
E value	5.0e-21
Match length	71
% identity	66
NCBI Description	FERREDOXIN--NADP REDUCTASE PRECURSOR (FNR) >gi_551131 (U14956) ferredoxin NADP+ reductase precursor [Vicia faba]

Seq. No.	137224
Seq. ID	ARABL1-047-Q1-B1-G10
Method	BLASTX
NCBI GI	g16374
BLAST score	447
E value	7.0e-45
Match length	86
% identity	100
NCBI Description	(X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	137225
Seq. ID	ARABL1-047-Q1-B1-G11
Method	BLASTX
NCBI GI	g132939
BLAST score	338
E value	4.0e-32
Match length	73
% identity	88
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi_81657_pir__JQ0771 ribosomal protein L3 (ARP1) - Arabidopsis thaliana >gi_166858 (M32654) ribosomal protein [Arabidopsis thaliana]

Seq. No.	137226
Seq. ID	ARABL1-047-Q1-B1-G12
Method	BLASTX
NCBI GI	g3337367
BLAST score	237
E value	3.0e-20
Match length	86
% identity	60
NCBI Description	(AC004481) hypothetical protein [Arabidopsis thaliana]

Seq. No.	137227
Seq. ID	ARABL1-047-Q1-B1-G2
Method	BLASTN
NCBI GI	g3763915
BLAST score	52
E value	2.0e-20
Match length	76
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC F14B2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137228
Seq. ID	ARABL1-047-Q1-B1-G3
Method	BLASTX
NCBI GI	g1399349
BLAST score	205
E value	1.0e-16

Match length	59
% identity	75
NCBI Description	(U43412) 3'-phosphoadenosine 5'-phosphosulfate reductase [Arabidopsis thaliana]

Seq. No.	137229
Seq. ID	ARABL1-047-Q1-B1-G4
Method	BLASTN
NCBI GI	g1399348
BLAST score	112
E value	2.0e-56
Match length	136
% identity	96
NCBI Description	Arabidopsis thaliana 3'-phosphoadenosine 5'-phosphosulfate reductase mRNA, complete cds

Seq. No.	137230
Seq. ID	ARABL1-047-Q1-B1-G6
Method	BLASTX
NCBI GI	g549010
BLAST score	370
E value	5.0e-36
Match length	75
% identity	100
NCBI Description	EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1 (ERF1) (OMNIPOTENT SUPPRESSOR PROTEIN 1 HOMOLOG) (SUP1 HOMOLOG) >gi_322554_pir__S31328 omnipotent suppressor protein SUP1 homolog (clone G18) - Arabidopsis thaliana >gi_16514_emb_CAA49172_ (X69375) similar to yeast omnipotent suppressor protein SUP1 (SUP45) [Arabidopsis thaliana] >gi_1402882_emb_CAA66813_ (X98130) eukaryotic early release factor subunit 1-like protein [Arabidopsis thaliana] >gi_1495249_emb_CAA66118_ (X97486) eRF1-3 [Arabidopsis thaliana]

Seq. No.	137231
Seq. ID	ARABL1-047-Q1-B1-G7
Method	BLASTX
NCBI GI	g115783
BLAST score	258
E value	8.0e-23
Match length	52
% identity	96
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	137232
Seq. ID	ARABL1-047-Q1-B1-H11
Method	BLASTX
NCBI GI	g541858
BLAST score	459
E value	3.0e-46
Match length	85
% identity	100
NCBI Description	endoxyloglucan transferase - Arabidopsis thaliana

>gi_469484_dbj_BAA03921_ (D16454) endo-xyloglucan transferase [Arabidopsis thaliana] >gi_4063757 (AC005561) endo-xyloglucan transferase [Arabidopsis thaliana]

Seq. No.	137233
Seq. ID	ARABL1-047-Q1-B1-H2
Method	BLASTN
NCBI GI	g4757414
BLAST score	242
E value	1.0e-134
Match length	242
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYF24, complete sequence

Seq. No.	137234
Seq. ID	ARABL1-047-Q1-B1-H4
Method	BLASTN
NCBI GI	g2696018
BLAST score	134
E value	2.0e-69
Match length	243
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC9, complete sequence [Arabidopsis thaliana]

Seq. No.	137235
Seq. ID	ARABL1-047-Q1-B1-H6
Method	BLASTX
NCBI GI	g2160158
BLAST score	254
E value	2.0e-22
Match length	50
% identity	100
NCBI Description	(AC000132) Similar to elongation factor 1-gamma (gb_EF1G_XENLA). ESTs gb_T20564,gb_T45940,gb_T04527 come from this gene. [Arabidopsis thaliana]

Seq. No.	137236
Seq. ID	ARABL1-047-Q1-B1-H8
Method	BLASTX
NCBI GI	g4585882
BLAST score	165
E value	7.0e-12
Match length	34
% identity	100
NCBI Description	(AC005850) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	137237
Seq. ID	ARABL1-047-Q1-E1-A12
Method	BLASTN
NCBI GI	g4063735
BLAST score	104
E value	2.0e-51
Match length	211
% identity	76

NCBI Description	Arabidopsis thaliana BAC F18G18 from chromosome V near 60.5 cM, complete sequence [Arabidopsis thaliana]
Seq. No.	137238
Seq. ID	ARABL1-047-Q1-E1-B11
Method	BLASTN
NCBI GI	g4689466
BLAST score	25
E value	6.0e-05
Match length	80
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T23O15 genomic sequence, complete sequence
Seq. No.	137239
Seq. ID	ARABL1-047-Q1-E1-C7
Method	BLASTN
NCBI GI	g2760166
BLAST score	262
E value	1.0e-146
Match length	262
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK20, complete sequence [Arabidopsis thaliana]
Seq. No.	137240
Seq. ID	ARABL1-047-Q1-E1-G6
Method	BLASTX
NCBI GI	g322525
BLAST score	370
E value	4.0e-36
Match length	75
% identity	100
NCBI Description	omnipotent suppressor protein SUP1 homolog (clone A18) - Arabidopsis thaliana (fragment) >gi_16512_emb_CAA49171_ (X69374) similar to yeast omnipotent suppressor protein SUP1 (SUP45); ORF [Arabidopsis thaliana]
Seq. No.	137241
Seq. ID	ARABL1-047-Q1-E1-H2
Method	BLASTN
NCBI GI	g4757414
BLAST score	246
E value	1.0e-136
Match length	280
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYF24, complete sequence
Seq. No.	137242
Seq. ID	ARABL1-047-Q1-E1-H4
Method	BLASTN
NCBI GI	g2696018
BLAST score	242
E value	1.0e-134
Match length	327
% identity	100

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC9, complete sequence [Arabidopsis thaliana]
Seq. No.	137243
Seq. ID	ARABL1-05-Q1-B1-A3
Method	BLASTN
NCBI GI	g2749918
BLAST score	119
E value	9.0e-61
Match length	140
% identity	95
NCBI Description	Arabidopsis thaliana chromosome I BAC F3I6 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	137244
Seq. ID	ARABL1-05-Q1-B1-A4
Method	BLASTN
NCBI GI	g3335331
BLAST score	132
E value	2.0e-68
Match length	153
% identity	94
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8F5 sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	137245
Seq. ID	ARABL1-05-Q1-B1-B2
Method	BLASTX
NCBI GI	g586079
BLAST score	516
E value	8.0e-53
Match length	103
% identity	100
NCBI Description	TUBULIN GAMMA-1 CHAIN >gi_460089 (U02069) g1-tubulin [Arabidopsis thaliana]
Seq. No.	137246
Seq. ID	ARABL1-05-Q1-B1-B3
Method	BLASTN
NCBI GI	g3193282
BLAST score	118
E value	7.0e-60
Match length	225
% identity	86
NCBI Description	Arabidopsis thaliana BAC T14P8
Seq. No.	137247
Seq. ID	ARABL1-05-Q1-B1-C12
Method	BLASTX
NCBI GI	g4335724
BLAST score	527
E value	4.0e-54
Match length	93
% identity	100
NCBI Description	(AC006248) putative RING-H2 finger protein [Arabidopsis thaliana]

Seq. No.	137248
Seq. ID	ARABL1-05-Q1-B1-C6
Method	BLASTN
NCBI GI	g3873174
BLAST score	381
E value	0.0e+00
Match length	384
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14N23, complete sequence [Arabidopsis thaliana]

Seq. No.	137249
Seq. ID	ARABL1-05-Q1-B1-D7
Method	BLASTX
NCBI GI	g4741952
BLAST score	265
E value	9.0e-24
Match length	50
% identity	100
NCBI Description	(AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No.	137250
Seq. ID	ARABL1-05-Q1-B1-E5
Method	BLASTX
NCBI GI	g2275217
BLAST score	379
E value	3.0e-41
Match length	112
% identity	82
NCBI Description	(AC002337) chloroplast protein CP12 isolog [Arabidopsis thaliana]

Seq. No.	137251
Seq. ID	ARABL1-05-Q1-B1-E9
Method	BLASTX
NCBI GI	g3021266
BLAST score	303
E value	9.0e-28
Match length	95
% identity	60
NCBI Description	(AL022347) serine/threonine kinase - like protein [Arabidopsis thaliana] >gi_3292840_emb_CAA19830_ (AL031018) serine/threonine kinase - like protein [Arabidopsis thaliana]

Seq. No.	137252
Seq. ID	ARABL1-05-Q1-B1-F10
Method	BLASTX
NCBI GI	g602076
BLAST score	500
E value	8.0e-51
Match length	101
% identity	23
NCBI Description	(X77456) pentameric polyubiquitin [Nicotiana tabacum]

Seq. No.	137253
Seq. ID	ARABL1-05-Q1-B1-F4

Method	BLASTN
NCBI GI	g4538895
BLAST score	176
E value	2.0e-94
Match length	334
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17A8 (ESSA project)

Seq. No.	137254
Seq. ID	ARABL1-05-Q1-B1-F6
Method	BLASTN
NCBI GI	g4741184
BLAST score	304
E value	1.0e-171
Match length	304
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone T23J7 (ESSA project)

Seq. No.	137255
Seq. ID	ARABL1-05-Q1-B1-F8
Method	BLASTN
NCBI GI	g2618602
BLAST score	289
E value	1.0e-162
Match length	329
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	137256
Seq. ID	ARABL1-05-Q1-B1-H9
Method	BLASTN
NCBI GI	g3327922
BLAST score	195
E value	1.0e-106
Match length	195
% identity	72
NCBI Description	Arabidopsis thaliana chromosome II BAC T31E10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137257
Seq. ID	ARABL1-06-Q1-B1-A6
Method	BLASTX
NCBI GI	g2827714
BLAST score	258
E value	2.0e-22
Match length	112
% identity	4
NCBI Description	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	137258
Seq. ID	ARABL1-06-Q1-B1-C3
Method	BLASTX
NCBI GI	g1173245

BLAST score	273
E value	2.0e-24
Match length	69
% identity	74
NCBI Description	40S RIBOSOMAL PROTEIN RP10 >gi_2130267_pir__S62431 hypothetical protein SPAC13G6.02c - fission yeast (Schizosaccharomyces pombe) >gi_1008987_emb_CAA91095_ (Z54308) 40S ribosomal protein subunit [Schizosaccharomyces pombe]

Seq. No.	137259
Seq. ID	ARABL1-06-Q1-B1-E1
Method	BLASTN
NCBI GI	g4581161
BLAST score	129
E value	2.0e-66
Match length	319
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T20G20 genomic sequence, complete sequence

Seq. No.	137260
Seq. ID	ARABL1-06-Q1-B1-F3
Method	BLASTX
NCBI GI	g1345594
BLAST score	409
E value	4.0e-40
Match length	85
% identity	98
NCBI Description	14-3-3-LIKE PROTEIN GF14 KAPPA >gi_1022780 (U36447) GF14 Kappa isoform [Arabidopsis thaliana]

Seq. No.	137261
Seq. ID	ARABL1-06-Q1-B1-F6
Method	BLASTN
NCBI GI	g16300
BLAST score	169
E value	2.0e-90
Match length	227
% identity	97
NCBI Description	A.thaliana mRNA for glycine rich protein >gi_166836_gb_L00648_ATHRBPA Arabidopsis thaliana RNA-binding protein mRNA, complete cds

Seq. No.	137262
Seq. ID	ARABL1-06-Q1-B1-G2
Method	BLASTN
NCBI GI	g2828180
BLAST score	361
E value	0.0e+00
Match length	364
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDK4, complete sequence [Arabidopsis thaliana]

Seq. No.	137263
Seq. ID	ARABL1-06-Q1-B1-G3

Method	BLASTX
NCBI GI	g4586256
BLAST score	422
E value	8.0e-42
Match length	102
% identity	82
NCBI Description	(AL049640) probable photosystem I chain XI precursor [Arabidopsis thaliana]

Seq. No.	137264
Seq. ID	ARABL1-06-Q1-B1-G7
Method	BLASTN
NCBI GI	g2696018
BLAST score	191
E value	1.0e-103
Match length	191
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC9, complete sequence [Arabidopsis thaliana]

Seq. No.	137265
Seq. ID	ARABL1-07-Q1-B1-A2
Method	BLASTN
NCBI GI	g16375
BLAST score	67
E value	2.0e-29
Match length	143
% identity	97
NCBI Description	A.thaliana gene (LHCP AB 140) for chlorophyll a/b binding protein

Seq. No.	137266
Seq. ID	ARABL1-07-Q1-B1-G11
Method	BLASTN
NCBI GI	g2853071
BLAST score	132
E value	4.0e-68
Match length	295
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F24J7 (ESSA project)

Seq. No.	137267
Seq. ID	ARABL1-07-Q1-B1-G3
Method	BLASTX
NCBI GI	g131398
BLAST score	434
E value	4.0e-43
Match length	105
% identity	85
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520,

gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No.	137268
Seq. ID	ARABL1-08-Q1-B1-A6
Method	BLASTX
NCBI GI	g3287696
BLAST score	420
E value	1.0e-41
Match length	90
% identity	92
NCBI Description	(AC003979) Strong similarity to phosphoribosylanthranilate transferase gb_D86180 from Pisum sativum. This ORF may be part of a larger gene that lies in the overlapping region. [Arabidopsis thaliana]

Seq. No.	137269
Seq. ID	ARABL1-08-Q1-B1-C2
Method	BLASTN
NCBI GI	g4584841
BLAST score	130
E value	6.0e-67
Match length	291
% identity	39
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T23E23, complete sequence

Seq. No.	137270
Seq. ID	ARABL1-08-Q1-B1-C9
Method	BLASTN
NCBI GI	g2738247
BLAST score	100
E value	2.0e-49
Match length	144
% identity	92
NCBI Description	Arabidopsis thaliana cobalamin-independent methionine synthase (ATCIMS) mRNA, complete cds

Seq. No.	137271
Seq. ID	ARABL1-08-Q1-B1-D6
Method	BLASTN
NCBI GI	g4589410
BLAST score	128
E value	5.0e-66
Match length	164
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F2O15, complete sequence

Seq. No.	137272
Seq. ID	ARABL1-08-Q1-B1-D9
Method	BLASTN
NCBI GI	g4567300
BLAST score	138
E value	5.0e-72
Match length	159
% identity	96

NCBI Description	Arabidopsis thaliana chromosome II P1 MHK10 genomic sequence, complete sequence
Seq. No.	137273
Seq. ID	ARABL1-08-Q1-B1-E5
Method	BLASTX
NCBI GI	g3128205
BLAST score	345
E value	1.0e-32
Match length	87
% identity	83
NCBI Description	(AC004077) putative pyruvate dehydrogenase complex E1 beta subunit [Arabidopsis thaliana]
Seq. No.	137274
Seq. ID	ARABL1-08-Q1-B1-F2
Method	BLASTX
NCBI GI	g2119848
BLAST score	94
E value	8.0e-21
Match length	53
% identity	79
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B1 - Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128229 (AC004077) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.	137275
Seq. ID	ARABL1-08-Q1-B1-F9
Method	BLASTX
NCBI GI	g2338712
BLAST score	262
E value	7.0e-23
Match length	69
% identity	74
NCBI Description	(AF013959) metallothionein-like protein [Arabidopsis thaliana]
Seq. No.	137276
Seq. ID	ARABL1-08-Q1-B1-G8
Method	BLASTX
NCBI GI	g464621
BLAST score	196
E value	2.0e-15
Match length	47
% identity	79
NCBI Description	60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__S28586 ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16 [Mesembryanthemum crystallinum]
Seq. No.	137277
Seq. ID	ARABL1-08-Q1-B1-H10

Method	BLASTN
NCBI GI	g2583106
BLAST score	94
E value	1.0e-45
Match length	189
% identity	61
NCBI Description	Arabidopsis thaliana chromosome II BAC F4L23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137278
Seq. ID	ARABL1-16-Q1-B1-E12
Method	BLASTX
NCBI GI	g16374
BLAST score	355
E value	7.0e-34
Match length	68
% identity	100
NCBI Description	(X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	137279
Seq. ID	ARABL1-16-Q1-B1-E9
Method	BLASTX
NCBI GI	g1943945
BLAST score	159
E value	6.0e-11
Match length	42
% identity	69
NCBI Description	(U85780) Spinacia oleracea Spinach choline monooxygenase TRANSLATE of cmo1117.gcg from: 57 to: 1376 [Spinacia oleracea]

Seq. No.	137280
Seq. ID	ARABL1-16-Q1-B1-F12
Method	BLASTN
NCBI GI	g11802
BLAST score	189
E value	1.0e-102
Match length	341
% identity	90
NCBI Description	Tobacco chloropast DNA homologous to ribosomal protein S12 gene

Seq. No.	137281
Seq. ID	ARABL1-16-Q1-B1-G9
Method	BLASTN
NCBI GI	g2351061
BLAST score	53
E value	6.0e-21
Match length	334
% identity	63
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAF19, complete sequence [Arabidopsis thaliana]

Seq. No.	137282
Seq. ID	ARABL1-17-Q1-B1-A12
Method	BLASTN

NCBI GI	g4454585
BLAST score	187
E value	1.0e-101
Match length	350
% identity	100
NCBI Description	Arabidopsis thaliana BAC T13D4 from chromosome IV near 21.5 cM, complete sequence

Seq. No.	137283
Seq. ID	ARABL1-17-Q1-B1-E10
Method	BLASTN
NCBI GI	g3176695
BLAST score	238
E value	1.0e-131
Match length	281
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC F14J9 genomic sequence contains phyA marker, complete sequence [Arabidopsis thaliana]

Seq. No.	137284
Seq. ID	ARABL1-18-Q1-B1-D11
Method	BLASTN
NCBI GI	g2252823
BLAST score	23
E value	4.0e-03
Match length	257
% identity	91
NCBI Description	Arabidopsis thaliana BAC IG005I10

Seq. No.	137285
Seq. ID	ARABL1-18-Q1-B1-G3
Method	BLASTX
NCBI GI	g421826
BLAST score	197
E value	2.0e-15
Match length	92
% identity	64
NCBI Description	chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis thaliana]

Seq. No.	137286
Seq. ID	ARABL1-18-Q1-B1-H12
Method	BLASTX
NCBI GI	g2894574
BLAST score	502
E value	4.0e-51
Match length	95
% identity	100
NCBI Description	(AL021890) peroxidase prxr1 [Arabidopsis thaliana] >gi_2961341_emb_CAA18099.1_ (AL022140) peroxidase prxr1 [Arabidopsis thaliana]

Seq. No.	137287
Seq. ID	ARABLI-04-Q1-B1-D12
Method	BLASTN

NCBI GI	g2435510
BLAST score	208
E value	1.0e-113
Match length	323
% identity	100
NCBI Description	Arabidopsis thaliana BAC TM017A05

Seq. No.	137288
Seq. ID	ARABLI-06-Q1-B1-A12
Method	BLASTX
NCBI GI	g2809232
BLAST score	530
E value	2.0e-54
Match length	114
% identity	88
NCBI Description	(AC002560) F21B7.1 [Arabidopsis thaliana]

Seq. No.	137289
Seq. ID	ARABLI-06-Q1-B1-C12
Method	BLASTX
NCBI GI	g2317913
BLAST score	541
E value	2.0e-55
Match length	106
% identity	100
NCBI Description	(U89959) cathepsin B-like cysteine proteinase [Arabidopsis thaliana]

Seq. No.	137290
Seq. ID	ARABLI-06-Q1-B1-D10
Method	BLASTX
NCBI GI	g4262236
BLAST score	383
E value	4.0e-37
Match length	110
% identity	75
NCBI Description	(AC006200) putative ribose 5-phosphate isomerase [Arabidopsis thaliana]

Seq. No.	137291
Seq. ID	ARABLI-06-Q1-B1-E9
Method	BLASTX
NCBI GI	g4587527
BLAST score	287
E value	7.0e-26
Match length	106
% identity	52
NCBI Description	(AC007060) Strong similarity to F19I3.2 gi_3033375 putative berberine bridge enzyme from Arabidopsis thaliana BAC gb_AC004238

Seq. No.	137292
Seq. ID	ARABLI-09-Q1-B1-A10
Method	BLASTX
NCBI GI	g3123327
BLAST score	223
E value	2.0e-18

Match length	63
% identity	97
NCBI Description	(AJ005927) squalene epoxidase homologue [Arabidopsis thaliana]

Seq. No.	137293
Seq. ID	ARABLI-09-Q1-B1-B1
Method	BLASTN
NCBI GI	g1871173
BLAST score	56
E value	1.0e-23
Match length	56
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T06D20 genomic sequence, complete sequence

Seq. No.	137294
Seq. ID	ARABLI-09-Q1-B1-D12
Method	BLASTX
NCBI GI	g3738316
BLAST score	343
E value	2.0e-32
Match length	80
% identity	80
NCBI Description	(AC005170) unknown protein [Arabidopsis thaliana]

Seq. No.	137295
Seq. ID	ARABLI-09-Q1-B1-D3
Method	BLASTX
NCBI GI	g135406
BLAST score	406
E value	7.0e-40
Match length	76
% identity	99
NCBI Description	TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi_99768_pir__A32712 tubulin alpha-5 chain - Arabidopsis thaliana >gi_166912 (M17189) alpha-tubulin [Arabidopsis thaliana] >gi_166918 (M84698) alpha-5 tubulin [Arabidopsis thaliana]

Seq. No.	137296
Seq. ID	ARABLI-09-Q1-B1-D5
Method	BLASTN
NCBI GI	g457715
BLAST score	225
E value	1.0e-123
Match length	333
% identity	99
NCBI Description	A.thaliana CXc750 gene

Seq. No.	137297
Seq. ID	ARABLI-09-Q1-B1-F2
Method	BLASTX
NCBI GI	g3386569
BLAST score	251
E value	1.0e-21
Match length	48
% identity	96

NCBI Description	(AF079590) photosystem II type II chlorophyll a/b binding protein [Sorghum bicolor]
Seq. No.	137298
Seq. ID	ARABLI-09-Q1-B1-G1
Method	BLASTN
NCBI GI	g4572664
BLAST score	80
E value	3.0e-37
Match length	253
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F25P17 genomic sequence, complete sequence
Seq. No.	137299
Seq. ID	ARABLI-09-Q1-B1-G4
Method	BLASTN
NCBI GI	g2894557
BLAST score	91
E value	3.0e-44
Match length	91
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T8O5 (ESSAII project)
Seq. No.	137300
Seq. ID	ARABLI-09-Q1-B1-H2
Method	BLASTN
NCBI GI	g4454447
BLAST score	218
E value	1.0e-119
Match length	322
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	137301
Seq. ID	ARABLI-10-Q1-B1-B2
Method	BLASTN
NCBI GI	g3492855
BLAST score	46
E value	7.0e-17
Match length	130
% identity	90
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F20N2, complete sequence [Arabidopsis thaliana]
Seq. No.	137302
Seq. ID	ARABLI-10-Q1-B1-C3
Method	BLASTX
NCBI GI	g4741954
BLAST score	618
E value	1.0e-64
Match length	129
% identity	91
NCBI Description	(AF134127) Lhcb4.2 protein [Arabidopsis thaliana]

Seq. No.	137303
Seq. ID	ARABLI-10-Q1-B1-C7
Method	BLASTX
NCBI GI	g1170089
BLAST score	661
E value	1.0e-69
Match length	130
% identity	100
NCBI Description	GLUTATHIONE S-TRANSFERASE ERD13 (CLASS PHI) >gi_481822_pir__S39542 probable glutathione transferase (EC 2.5.1.18) (clone ERD13) - Arabidopsis thaliana >gi_497789_dbj_BAA04554_ (D17673) glutathione S-transferase [Arabidopsis thaliana] >gi_3201614 (AC004669) glutathione S-transferase [Arabidopsis thaliana]

Seq. No.	137304
Seq. ID	ARABLI-10-Q1-B1-D10
Method	BLASTX
NCBI GI	g4512689
BLAST score	155
E value	2.0e-10
Match length	82
% identity	41
NCBI Description	(AC006931) hypothetical protein [Arabidopsis thaliana]

Seq. No.	137305
Seq. ID	ARABLI-10-Q1-B1-D9
Method	BLASTX
NCBI GI	g1351271
BLAST score	518
E value	5.0e-53
Match length	111
% identity	87
NCBI Description	TRIOSEPHOSPHATE ISOMERASE CHLOROPLAST PRECURSOR (TIM) >gi_1084309_pir__S52032 triose-phosphate isomerase (EC 5.3.1.1) precursor, chloroplast - spinach >gi_806312 (L36387) triosephosphate isomerase, chloroplast isozyme [Spinacia oleracea]

Seq. No.	137306
Seq. ID	ARABLI-10-Q1-B1-E5
Method	BLASTX
NCBI GI	g4454481
BLAST score	523
E value	2.0e-53
Match length	122
% identity	84
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana] >gi_4512647_gb_AAD21702.1_ (AC007048) unknown protein [Arabidopsis thaliana]

Seq. No.	137307
Seq. ID	ARABLI-10-Q1-B1-F11
Method	BLASTX
NCBI GI	g115767
BLAST score	166
E value	4.0e-12

Match length	30
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	137308
Seq. ID	ARABLI-10-Q1-B1-F7
Method	BLASTN
NCBI GI	g3176701
BLAST score	173
E value	1.0e-92
Match length	250
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T20K24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137309
Seq. ID	ARABLI-10-Q1-B1-G2
Method	BLASTX
NCBI GI	g4741952
BLAST score	279
E value	2.0e-25
Match length	53
% identity	100
NCBI Description	(AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No.	137310
Seq. ID	ARABLI-10-Q1-B1-G5
Method	BLASTN
NCBI GI	g3688798
BLAST score	61
E value	2.0e-26
Match length	61
% identity	100
NCBI Description	Arabidopsis thaliana gamma tonoplast intrinsic protein 2 (TIP2) mRNA, complete cds

Seq. No.	137311
Seq. ID	ARABLI-10-Q1-B1-H11
Method	BLASTN
NCBI GI	g4262221
BLAST score	176
E value	2.0e-94
Match length	338
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137312
Seq. ID	ARABLI-11-Q1-B1-B4
Method	BLASTX
NCBI GI	g444790

BLAST score	530
E value	3.0e-54
Match length	122
% identity	88
NCBI Description	nucleotide translocator [Arabidopsis thaliana]

Seq. No.	137313
Seq. ID	ARABLI-11-Q1-B1-B5
Method	BLASTX
NCBI GI	g2853084
BLAST score	206
E value	3.0e-16
Match length	68
% identity	54
NCBI Description	(AL021768) putative protein [Arabidopsis thaliana]

Seq. No.	137314
Seq. ID	ARABLI-11-Q1-B1-B6
Method	BLASTX
NCBI GI	g4580393
BLAST score	263
E value	6.0e-23
Match length	111
% identity	50
NCBI Description	(AC007171) hypothetical protein [Arabidopsis thaliana]

Seq. No.	137315
Seq. ID	ARABLI-11-Q1-B1-D7
Method	BLASTX
NCBI GI	g1076345
BLAST score	129
E value	2.0e-07
Match length	71
% identity	9
NCBI Description	cold acclimation protein lti30 - Arabidopsis thaliana (fragment)

Seq. No.	137316
Seq. ID	ARABLI-11-Q1-B1-E7
Method	BLASTN
NCBI GI	g4454587
BLAST score	346
E value	0.0e+00
Match length	362
% identity	99
NCBI Description	Arabidopsis thaliana BAC F21A20 from chromosome V near 61 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	137317
Seq. ID	ARABLI-12-Q1-B1-A3
Method	BLASTN
NCBI GI	g3366536
BLAST score	342
E value	0.0e+00
Match length	342
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T25N20,

complete sequence [Arabidopsis thaliana]

Seq. No.	137318
Seq. ID	ARABLI-12-Q1-B1-B11
Method	BLASTN
NCBI GI	g3901293
BLAST score	182
E value	3.0e-98
Match length	190
% identity	99
NCBI Description	Arabidopsis thaliana rpp8 gene, complete cds

Seq. No.	137319
Seq. ID	ARABLI-12-Q1-B1-B2
Method	BLASTN
NCBI GI	g870791
BLAST score	60
E value	2.0e-25
Match length	111
% identity	95
NCBI Description	Arabidopsis thaliana polyubiquitin (ubq10) mRNA, complete cds

Seq. No.	137320
Seq. ID	ARABLI-12-Q1-B1-B8
Method	BLASTN
NCBI GI	g4581161
BLAST score	347
E value	0.0e+00
Match length	354
% identity	65
NCBI Description	Arabidopsis thaliana chromosome II BAC T20G20 genomic sequence, complete sequence

Seq. No.	137321
Seq. ID	ARABLI-12-Q1-B1-C4
Method	BLASTN
NCBI GI	g4159704
BLAST score	201
E value	1.0e-109
Match length	343
% identity	66
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MCB17, complete sequence

Seq. No.	137322
Seq. ID	ARABLI-12-Q1-B1-D8
Method	BLASTX
NCBI GI	g3420008
BLAST score	233
E value	2.0e-19
Match length	113
% identity	39
NCBI Description	(AF000307) steroid sulfotransferase 3 [Brassica napus]

Seq. No.	137323
Seq. ID	ARABLI-12-Q1-B1-E5

Method	BLASTX
NCBI GI	g2244949
BLAST score	200
E value	2.0e-15
Match length	104
% identity	45
NCBI Description	(Z97339) similarity to ORF - Lilium longiflorum [Arabidopsis thaliana]

Seq. No.	137324
Seq. ID	ARABLI-12-Q1-B1-G1
Method	BLASTX
NCBI GI	g2894574
BLAST score	529
E value	3.0e-54
Match length	110
% identity	100
NCBI Description	(AL021890) peroxidase prxr1 [Arabidopsis thaliana] >gi_2961341_emb_CAA18099.1_ (AL022140) peroxidase prxr1 [Arabidopsis thaliana]

Seq. No.	137325
Seq. ID	ARABLI-13-Q1-B1-A2
Method	BLASTN
NCBI GI	g4581161
BLAST score	148
E value	5.0e-78
Match length	148
% identity	65
NCBI Description	Arabidopsis thaliana chromosome II BAC T20G20 genomic sequence, complete sequence

Seq. No.	137326
Seq. ID	ARABLI-13-Q1-B1-B7
Method	BLASTX
NCBI GI	g2842615
BLAST score	337
E value	1.0e-31
Match length	128
% identity	55
NCBI Description	ASPARTATE-SEMIALDEHYDE DEHYDROGENASE (ASA DEHYDROGENASE) >gi_1359593_emb_CAA66607_ (X97964) aspartate-semialdehyde dehydrogenase [Campylobacter jejuni]

Seq. No.	137327
Seq. ID	ARABLI-13-Q1-B1-B8
Method	BLASTX
NCBI GI	g2213592
BLAST score	264
E value	5.0e-23
Match length	110
% identity	26
NCBI Description	(AC000348) T7N9.12 [Arabidopsis thaliana]

Seq. No.	137328
Seq. ID	ARABLI-13-Q1-B1-E5
Method	BLASTN

NCBI GI	g2244788
BLAST score	315
E value	1.0e-177
Match length	336
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	137329
Seq. ID	ARABLI-13-Q1-B1-H4
Method	BLASTX
NCBI GI	g4741923
BLAST score	305
E value	7.0e-28
Match length	92
% identity	63
NCBI Description	(AF130849) PIT1 [Arabidopsis thaliana]

Seq. No.	137330
Seq. ID	ARABLI-14-Q1-B1-A2
Method	BLASTX
NCBI GI	g4587564
BLAST score	443
E value	3.0e-44
Match length	89
% identity	100
NCBI Description	(AC006550) Strong similarity to gb_X14017 photosystem I reaction centre subunit II precursor (psaD) from Spinacia oleracea. ESTs gb_R30423, gb_T42998, gb_Z18178, gb_T14133, gb_N65521, gb_T42498, gb_T41918, gb_N38024

Seq. No.	137331
Seq. ID	ARABLI-14-Q1-B1-B11
Method	BLASTN
NCBI GI	g4757662
BLAST score	279
E value	1.0e-156
Match length	392
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome I, complete sequence

Seq. No.	137332
Seq. ID	ARABLI-14-Q1-B1-C12
Method	BLASTX
NCBI GI	g2498731
BLAST score	373
E value	4.0e-36
Match length	83
% identity	84
NCBI Description	PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1 >gi_1362013_pir__S57611 zeta-crystallin homolog - Arabidopsis thaliana >gi_886428_emb_CAA89838_ (Z49768) zeta-crystallin homologue [Arabidopsis thaliana]

Seq. No.	137333
Seq. ID	ARABLI-14-Q1-B1-D8

Method	BLASTX
NCBI GI	g1175012
BLAST score	439
E value	1.0e-43
Match length	98
% identity	89
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 1C (TRANSMEMBRANE PROTEIN B) (TMP-B) >gi_396218_emb_CAA49155_ (X69294) transmembrane protein TMP-B [Arabidopsis thaliana]

Seq. No.	137334
Seq. ID	ARABLI-14-Q1-B1-E7
Method	BLASTX
NCBI GI	g4538963
BLAST score	492
E value	8.0e-50
Match length	94
% identity	72
NCBI Description	(AL049488) chlorophyll a/b-binding protein-like [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1 (AF134129) Lhcb5 protein [Arabidopsis thaliana]

Seq. No.	137335
Seq. ID	ARABLI-14-Q1-B1-F1
Method	BLASTX
NCBI GI	g4741940
BLAST score	467
E value	7.0e-47
Match length	85
% identity	61
NCBI Description	(AF134120) Lhca2 protein [Arabidopsis thaliana]

Seq. No.	137336
Seq. ID	ARABLI-14-Q1-B1-F10
Method	BLASTX
NCBI GI	g629511
BLAST score	440
E value	7.0e-44
Match length	90
% identity	100
NCBI Description	cold-regulated protein cor15b precursor - Arabidopsis thaliana >gi_4559338_gb_AAD23000.1_AC007087_19 (AC007087) cold-regulated protein cor15b precursor [Arabidopsis thaliana]

Seq. No.	137337
Seq. ID	ARABLI-14-Q1-B1-F11
Method	BLASTN
NCBI GI	g4581138
BLAST score	238
E value	1.0e-131
Match length	315
% identity	66
NCBI Description	Arabidopsis thaliana chromosome II BAC F1O11 genomic sequence, complete sequence

Seq. No.	137338

Seq. ID	ARABLI-14-Q1-B1-F9
Method	BLASTX
NCBI GI	g602076
BLAST score	500
E value	8.0e-51
Match length	101
% identity	23
NCBI Description	(X77456) pentameric polyubiquitin [Nicotiana tabacum]

Seq. No.	137339
Seq. ID	ARABLI-14-Q1-B1-H7
Method	BLASTN
NCBI GI	g3046850
BLAST score	198
E value	1.0e-107
Match length	397
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24G6, complete sequence [Arabidopsis thaliana]

Seq. No.	137340
Seq. ID	ARABLI-15-Q1-B1-A8
Method	BLASTX
NCBI GI	g3668080
BLAST score	365
E value	3.0e-35
Match length	88
% identity	78
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	137341
Seq. ID	ARABLI-15-Q1-B1-B11
Method	BLASTN
NCBI GI	g166679
BLAST score	119
E value	1.0e-60
Match length	166
% identity	99
NCBI Description	Arabidopsis thaliana negative regulator of the ethylene response pathway (CTR1) mRNA, complete cds. >gi_996469_gb_I14046_I14046 Sequence 1 from patent US 5444166 >gi_2087615_gb_I35764_I35764 Sequence 1 from patent US

Seq. No.	137342
Seq. ID	ARABLI-15-Q1-B1-C10
Method	BLASTX
NCBI GI	g2493144
BLAST score	331
E value	3.0e-31
Match length	82
% identity	52
NCBI Description	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-ATPASE 16 KD PROTEOLIPID SUBUNIT) >gi_2118221_pir__S60132 H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P2) - Arabidopsis thaliana >gi_926937 (L44585) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis

thaliana]

Seq. No.	137343
Seq. ID	ARABLI-15-Q1-B1-D1
Method	BLASTN
NCBI GI	g4206762
BLAST score	96
E value	1.0e-46
Match length	169
% identity	83
NCBI Description	Arabidopsis thaliana cell wall-plasma membrane linker protein homolog (CWLP) mRNA, complete cds

Seq. No.	137344
Seq. ID	ARABLI-15-Q1-B1-G2
Method	BLASTX
NCBI GI	g2982452
BLAST score	588
E value	4.0e-61
Match length	125
% identity	92
NCBI Description	(AL022223) receptor protein kinase-like protein [Arabidopsis thaliana]

Seq. No.	137345
Seq. ID	ARABLI-15-Q1-B1-G6
Method	BLASTX
NCBI GI	g115767
BLAST score	632
E value	3.0e-66
Match length	135
% identity	96
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	137346
Seq. ID	ARABLI-15-Q1-B1-G7
Method	BLASTN
NCBI GI	g4589433
BLAST score	287
E value	1.0e-160
Match length	287
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNI5, complete sequence

Seq. No.	137347
Seq. ID	ARABLI-15-Q1-B1-H8
Method	BLASTN
NCBI GI	g16260
BLAST score	345
E value	0.0e+00

Match length	360
% identity	99
NCBI Description	Arabisdopsis thaliana EF-1 alpha A1 gene for elongation factor 1-alpha

Seq. No.	137348
Seq. ID	ARABLI-16-Q1-B1-B7
Method	BLASTN
NCBI GI	g3128142
BLAST score	290
E value	1.0e-162
Match length	290
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQN23, complete sequence [Arabidopsis thaliana]

Seq. No.	137349
Seq. ID	ARABLI-16-Q1-B1-B8
Method	BLASTN
NCBI GI	g4581161
BLAST score	278
E value	1.0e-155
Match length	278
% identity	66
NCBI Description	Arabidopsis thaliana chromosome II BAC T20G20 genomic sequence, complete sequence

Seq. No.	137350
Seq. ID	ARABLI-16-Q1-B1-D6
Method	BLASTX
NCBI GI	g282865
BLAST score	490
E value	1.0e-49
Match length	108
% identity	86
NCBI Description	chlorophyll a/b-binding protein - Arabidopsis thaliana >gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding protein [Arabidopsis thaliana] >gi_166644 (M85150) chlorophyll a/b-binding protein [Arabidopsis thaliana] >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	137351
Seq. ID	ARABLI-16-Q1-B1-E3
Method	BLASTX
NCBI GI	g1495366
BLAST score	213
E value	3.0e-17
Match length	93
% identity	51
NCBI Description	(Z69370) nitrite transporter [Cucumis sativus]

Seq. No.	137352
Seq. ID	ARABLI-16-Q1-B1-E7
Method	BLASTN
NCBI GI	g4539290
BLAST score	356

E value	0.0e+00
Match length	416
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F14M19 (ESSA project)

Seq. No.	137353
Seq. ID	ARABLI-16-Q1-B1-F6
Method	BLASTX
NCBI GI	g2578823
BLAST score	289
E value	5.0e-26
Match length	56
% identity	98
NCBI Description	(AB000835) similar to YGR200c [Arabidopsis thaliana]

Seq. No.	137354
Seq. ID	ARABLI-16-Q1-B1-F8
Method	BLASTX
NCBI GI	g544424
BLAST score	240
E value	1.0e-20
Match length	47
% identity	100
NCBI Description	GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi_419755_pir__S30147 glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana >gi_16301_emb_CAA78711_ (Z14987) glycine rich protein [Arabidopsis thaliana] >gi_166837 (L00648) RNA-binding protein [Arabidopsis thaliana] >gi_4567224_gb_AAD23639.1_AC007119_5 (AC007119) glycine-rich RNA binding protein 7 [Arabidopsis thaliana]

Seq. No.	137355
Seq. ID	ARABLI-16-Q1-B1-G1
Method	BLASTX
NCBI GI	g1170555
BLAST score	187
E value	5.0e-14
Match length	88
% identity	51
NCBI Description	MYO-INOSITOL 4-O-METHYLTRANSFERASE >gi_282822_pir__S22696 methyltransferase - common ice plant >gi_167262 (M87340) myo-inositol O-methyl transferase [Mesembryanthemum crystallinum] >gi_1488237 (U63634) inositol methyltransferase [Mesembryanthemum crystallinum]

Seq. No.	137356
Seq. ID	ARABLI-17-Q1-B1-B7
Method	BLASTN
NCBI GI	g4510360
BLAST score	33
E value	5.0e-09
Match length	65
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC F11F19 genomic sequence, complete sequence

Seq. No.	137357
Seq. ID	ARABLI-17-Q1-B1-D3
Method	BLASTN
NCBI GI	g2828183
BLAST score	318
E value	1.0e-179
Match length	318
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPL12, complete sequence [Arabidopsis thaliana]

Seq. No.	137358
Seq. ID	ARABLI-17-Q1-B1-E8
Method	BLASTX
NCBI GI	g3600039
BLAST score	355
E value	5.0e-34
Match length	85
% identity	95
NCBI Description	(AF080119) similar to Schizosaccharomyces pombe isp4 protein (GB:D14061) [Arabidopsis thaliana]

Seq. No.	137359
Seq. ID	ARABLI-17-Q1-B1-G2
Method	BLASTX
NCBI GI	g115783
BLAST score	410
E value	2.0e-40
Match length	96
% identity	83
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	137360
Seq. ID	ARABLI-17-Q1-B1-G8
Method	BLASTN
NCBI GI	g3492855
BLAST score	89
E value	8.0e-43
Match length	132
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F20N2, complete sequence [Arabidopsis thaliana]

Seq. No.	137361
Seq. ID	ARABLI-17-Q1-B1-H2
Method	BLASTX
NCBI GI	g231700
BLAST score	240
E value	8.0e-21
Match length	47
% identity	100
NCBI Description	22 KD CALMODULIN-LIKE CALCIUM-BINDING PROTEIN (CABP-22) >gi_479694_pir__S35188 calmodulin-related protein (clone CaBP-22) - Arabidopsis thaliana >gi_16209_emb_CAA78124_

(Z12136) calcium binding protein [Arabidopsis thaliana] >gi_3402708 (AC004261) calcium binding protein [Arabidopsis thaliana]

Seq. No.	137362
Seq. ID	LIB146-001-Q1-E1-A1
Method	BLASTX
NCBI GI	g4559369
BLAST score	581
E value	2.0e-60
Match length	106
% identity	96
NCBI Description	(AC006585) putative Rieske iron-sulfur protein [Arabidopsis thaliana]

Seq. No.	137363
Seq. ID	LIB146-001-Q1-E1-A9
Method	BLASTX
NCBI GI	g4581108
BLAST score	534
E value	7.0e-55
Match length	105
% identity	100
NCBI Description	(AC005825) putative chloroplast outer membrane protein 86,also very similar to GTP-inding protein from pea (GB:L36857) [Arabidopsis thaliana]

Seq. No.	137364
Seq. ID	LIB146-001-Q1-E1-B6
Method	BLASTX
NCBI GI	g112741
BLAST score	530
E value	2.0e-54
Match length	99
% identity	99
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	137365
Seq. ID	LIB146-001-Q1-E1-B7
Method	BLASTX
NCBI GI	g1628583
BLAST score	545
E value	4.0e-56
Match length	105
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	137366
Seq. ID	LIB146-001-Q1-E1-C11

Method	BLASTX
NCBI GI	g2623306
BLAST score	332
E value	5.0e-31
Match length	84
% identity	76
NCBI Description	(AC002409) unknown protein [Arabidopsis thaliana]

Seq. No.	137367
Seq. ID	LIB146-001-Q1-E1-C5
Method	BLASTX
NCBI GI	g112737
BLAST score	456
E value	5.0e-50
Match length	130
% identity	72
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	137368
Seq. ID	LIB146-001-Q1-E1-D12
Method	BLASTX
NCBI GI	g4056489
BLAST score	303
E value	1.0e-27
Match length	129
% identity	60
NCBI Description	(AC005896) putative white protein [Arabidopsis thaliana]

Seq. No.	137369
Seq. ID	LIB146-001-Q1-E1-D2
Method	BLASTX
NCBI GI	g112739
BLAST score	421
E value	2.0e-41
Match length	120
% identity	71
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	137370
Seq. ID	LIB146-001-Q1-E1-D8
Method	BLASTN
NCBI GI	g4757399
BLAST score	38
E value	5.0e-12
Match length	346

% identity	28
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MEE13, complete sequence

Seq. No.	137371
Seq. ID	LIB146-001-Q1-E1-D9
Method	BLASTX
NCBI GI	g112682
BLAST score	538
E value	3.0e-55
Match length	115
% identity	88
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	137372
Seq. ID	LIB146-001-Q1-E1-E2
Method	BLASTX
NCBI GI	g1628583
BLAST score	545
E value	4.0e-56
Match length	105
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	137373
Seq. ID	LIB146-001-Q1-E1-E9
Method	BLASTX
NCBI GI	g4204299
BLAST score	706
E value	7.0e-75
Match length	133
% identity	100
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	137374
Seq. ID	LIB146-001-Q1-E1-F12
Method	BLASTN
NCBI GI	g2264304
BLAST score	280
E value	1.0e-156
Match length	310
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBG8, complete sequence [Arabidopsis thaliana]

Seq. No.	137375
Seq. ID	LIB146-001-Q1-E1-F3
Method	BLASTX
NCBI GI	g3075398
BLAST score	164

E value	2.0e-11
Match length	84
% identity	48
NCBI Description	(AC004484) unknown protein [Arabidopsis thaliana]

Seq. No.	137376
Seq. ID	LIB146-001-Q1-E1-F8
Method	BLASTX
NCBI GI	g3860247
BLAST score	506
E value	2.0e-51
Match length	102
% identity	90
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]

Seq. No.	137377
Seq. ID	LIB146-001-Q1-E1-H7
Method	BLASTX
NCBI GI	g3004546
BLAST score	175
E value	9.0e-13
Match length	61
% identity	62
NCBI Description	(AC003673) hypothetical protein [Arabidopsis thaliana] >gi_4185149 (AC005724) hypothetical protein [Arabidopsis thaliana]

Seq. No.	137378
Seq. ID	LIB146-001-Q1-E1-H9
Method	BLASTX
NCBI GI	g3269286
BLAST score	375
E value	4.0e-36
Match length	94
% identity	87
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.	137379
Seq. ID	LIB146-002-Q1-E1-A3
Method	BLASTN
NCBI GI	g3241917
BLAST score	316
E value	1.0e-178
Match length	324
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19B1, complete sequence [Arabidopsis thaliana]

Seq. No.	137380
Seq. ID	LIB146-002-Q1-E1-B10
Method	BLASTX
NCBI GI	g1628583
BLAST score	528
E value	4.0e-54
Match length	104
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	137381
Seq. ID	LIB146-002-Q1-E1-B2
Method	BLASTX
NCBI GI	g112741
BLAST score	581
E value	2.0e-60
Match length	110
% identity	97
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	137382
Seq. ID	LIB146-002-Q1-E1-C11
Method	BLASTX
NCBI GI	g266693
BLAST score	357
E value	5.0e-34
Match length	66
% identity	100
NCBI Description	OLEOSIN >gi_282875_pir__S22538 oleosin - Arabidopsis thaliana >gi_16405_emb_CAA44225_ (X62353) oleosin [Arabidopsis thaliana] >gi_4455257_emb_CAB36756.1_ (AL035523) oleosin, 18.5K [Arabidopsis thaliana]

Seq. No.	137383
Seq. ID	LIB146-002-Q1-E1-D12
Method	BLASTX
NCBI GI	g1628583
BLAST score	668
E value	2.0e-70
Match length	128
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	137384
Seq. ID	LIB146-002-Q1-E1-D7
Method	BLASTX
NCBI GI	g112737
BLAST score	501
E value	7.0e-51
Match length	124
% identity	79
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

	>gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]
Seq. No.	137385
Seq. ID	LIB146-002-Q1-E1-E1
Method	BLASTX
NCBI GI	g135858
BLAST score	316
E value	2.0e-29
Match length	53
% identity	100
NCBI Description	TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP) >gi_99760_pir__S22201 tonoplast intrinsic protein alpha - Arabidopsis thaliana >gi_16182_emb_CAA45114_ (X63551) tonoplast intrinsic protein: alpha-TIP(Ara) [Arabidopsis thaliana] >gi_166623 (M84343) tonoplast intrinsic protein [Arabidopsis thaliana] >gi_445128_prf__1908432A tonoplast intrinsic protein alpha [Arabidopsis thaliana]
Seq. No.	137386
Seq. ID	LIB146-002-Q1-E1-E11
Method	BLASTX
NCBI GI	g1628583
BLAST score	545
E value	4.0e-56
Match length	105
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.	137387
Seq. ID	LIB146-002-Q1-E1-E5
Method	BLASTX
NCBI GI	g1628583
BLAST score	493
E value	6.0e-50
Match length	129
% identity	77
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.	137388
Seq. ID	LIB146-002-Q1-E1-E6
Method	BLASTN
NCBI GI	g4454004
BLAST score	187
E value	1.0e-101
Match length	219
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F24A6 (ESSAII project)
Seq. No.	137389
Seq. ID	LIB146-002-Q1-E1-F4
Method	BLASTX

NCBI GI	g1628583
BLAST score	663
E value	7.0e-70
Match length	127
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	137390
Seq. ID	LIB146-002-Q1-E1-F9
Method	BLASTX
NCBI GI	g4455208
BLAST score	652
E value	1.0e-68
Match length	135
% identity	93
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	137391
Seq. ID	LIB146-002-Q1-E1-G11
Method	BLASTX
NCBI GI	g3882273
BLAST score	155
E value	2.0e-10
Match length	88
% identity	40
NCBI Description	(AB018319) KIAA0776 protein [Homo sapiens]

Seq. No.	137392
Seq. ID	LIB146-002-Q1-E1-G12
Method	BLASTX
NCBI GI	g1174864
BLAST score	525
E value	7.0e-54
Match length	99
% identity	100
NCBI Description	UBIQUINOL-CYTOCHROME-C REDUCTASE COMPLEX CORE PROTEIN I PRECURSOR >gi_1076200_pir__JX0300 ubiquinol--cytochrome-c reductase (EC 1.10.2.2) chain I precursor - Euglena gracilis mitochondrion >gi_464153_dbj_BAA04079_ (D16671) complex III subunit I precursor [Euglena gracilis]

Seq. No.	137393
Seq. ID	LIB146-002-Q1-E1-H2
Method	BLASTN
NCBI GI	g3046852
BLAST score	88
E value	4.0e-42
Match length	179
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQJ16, complete sequence [Arabidopsis thaliana]

Seq. No.	137394
Seq. ID	LIB146-003-Q1-E1-A6
Method	BLASTN

NCBI GI	g4220632
BLAST score	218
E value	1.0e-119
Match length	397
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K6M13, complete sequence [Arabidopsis thaliana]

Seq. No.	137395
Seq. ID	LIB146-003-Q1-E1-B10
Method	BLASTX
NCBI GI	g3820564
BLAST score	162
E value	4.0e-11
Match length	122
% identity	34
NCBI Description	(AF080002) ATP-dependent zinc metallopeptidase FtsH [Heliobacillus mobilis]

Seq. No.	137396
Seq. ID	LIB146-003-Q1-E1-C10
Method	BLASTX
NCBI GI	g3608412
BLAST score	304
E value	1.0e-27
Match length	137
% identity	50
NCBI Description	(AF079355) protein phosphatase-2c [Mesembryanthemum crystallinum]

Seq. No.	137397
Seq. ID	LIB146-003-Q1-E1-C3
Method	BLASTX
NCBI GI	g2982431
BLAST score	128
E value	4.0e-07
Match length	127
% identity	4
NCBI Description	(AL022224) leucine rich repeat-like protein [Arabidopsis thaliana]

Seq. No.	137398
Seq. ID	LIB146-003-Q1-E1-E2
Method	BLASTN
NCBI GI	g4006885
BLAST score	430
E value	0.0e+00
Match length	430
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	137399
Seq. ID	LIB146-003-Q1-E1-E6
Method	BLASTX
NCBI GI	g3075390
BLAST score	583

E value 2.0e-60
Match length 140
% identity 77
NCBI Description (AC004484) protein kinase ARSK1 [Arabidopsis thaliana]

Seq. No. 137400
Seq. ID LIB146-003-Q1-E1-F10
Method BLASTN
NCBI GI g2264305
BLAST score 34
E value 1.0e-09
Match length 78
% identity 86
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK23, complete sequence [Arabidopsis thaliana]

Seq. No. 137401
Seq. ID LIB146-003-Q1-E1-G8
Method BLASTN
NCBI GI g2182286
BLAST score 412
E value 0.0e+00
Match length 420
% identity 100
NCBI Description Sequence of BAC F20P5 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No. 137402
Seq. ID LIB146-003-Q1-E1-H8
Method BLASTN
NCBI GI g4589445
BLAST score 392
E value 0.0e+00
Match length 416
% identity 99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWL2, complete sequence

Seq. No. 137403
Seq. ID LIB146-004-Q1-E1-A7
Method BLASTN
NCBI GI g4454447
BLAST score 170
E value 9.0e-91
Match length 338
% identity 100
NCBI Description Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 137404
Seq. ID LIB146-004-Q1-E1-B4
Method BLASTN
NCBI GI g4558586
BLAST score 227
E value 1.0e-125
Match length 296
% identity 95

NCBI Description	Arabidopsis thaliana chromosome 1 BAC T5I8 sequence, complete sequence

Seq. No.	137405
Seq. ID	LIB146-004-Q1-E1-B9
Method	BLASTN
NCBI GI	g3135250
BLAST score	128
E value	1.0e-65
Match length	336
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC F27F23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137406
Seq. ID	LIB146-004-Q1-E1-C1
Method	BLASTN
NCBI GI	g4757414
BLAST score	167
E value	6.0e-89
Match length	219
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYF24, complete sequence

Seq. No.	137407
Seq. ID	LIB146-004-Q1-E1-C6
Method	BLASTX
NCBI GI	g1628583
BLAST score	490
E value	1.0e-49
Match length	93
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	137408
Seq. ID	LIB146-004-Q1-E1-D12
Method	BLASTX
NCBI GI	g3738315
BLAST score	217
E value	1.0e-17
Match length	118
% identity	47
NCBI Description	(AC005170) unknown protein [Arabidopsis thaliana]

Seq. No.	137409
Seq. ID	LIB146-004-Q1-E1-E5
Method	BLASTX
NCBI GI	g2586081
BLAST score	178
E value	4.0e-13
Match length	110
% identity	7
NCBI Description	(U72725) receptor kinase-like protein [Oryza longistaminata]

Seq. No.	137410
Seq. ID	LIB146-004-Q1-E1-F12
Method	BLASTX
NCBI GI	g1628583
BLAST score	263
E value	2.0e-23
Match length	53
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	137411
Seq. ID	LIB146-004-Q1-E1-G12
Method	BLASTN
NCBI GI	g4454585
BLAST score	53
E value	2.0e-21
Match length	92
% identity	96
NCBI Description	Arabidopsis thaliana BAC T13D4 from chromosome IV near 21.5 cM, complete sequence

Seq. No.	137412
Seq. ID	LIB146-004-Q1-E1-H1
Method	BLASTN
NCBI GI	g2494106
BLAST score	93
E value	7.0e-45
Match length	326
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137413
Seq. ID	LIB146-004-Q1-E1-H11
Method	BLASTX
NCBI GI	g3927836
BLAST score	233
E value	2.0e-19
Match length	70
% identity	66
NCBI Description	(AC005727) unknown protein [Arabidopsis thaliana]

Seq. No.	137414
Seq. ID	LIB146-004-Q1-E1-H9
Method	BLASTX
NCBI GI	g266693
BLAST score	581
E value	3.0e-60
Match length	137
% identity	86
NCBI Description	OLEOSIN >gi_282875_pir__S22538 oleosin - Arabidopsis thaliana >gi_16405_emb_CAA44225_ (X62353) oleosin [Arabidopsis thaliana] >gi_4455257_emb_CAB36756.1_ (AL035523) oleosin, 18.5K [Arabidopsis thaliana]

Seq. No.	137415
Seq. ID	LIB146-005-Q1-E1-A6
Method	BLASTX
NCBI GI	g1628583
BLAST score	654
E value	8.0e-69
Match length	127
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	137416
Seq. ID	LIB146-005-Q1-E1-B10
Method	BLASTN
NCBI GI	g4510338
BLAST score	211
E value	1.0e-115
Match length	399
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F2H17 genomic sequence, complete sequence

Seq. No.	137417
Seq. ID	LIB146-005-Q1-E1-C8
Method	BLASTX
NCBI GI	g4263543
BLAST score	610
E value	1.0e-63
Match length	129
% identity	88
NCBI Description	(AC006250) putative Athila retroelement ORF1 protein [Arabidopsis thaliana]

Seq. No.	137418
Seq. ID	LIB146-005-Q1-E1-D6
Method	BLASTX
NCBI GI	g4559391
BLAST score	471
E value	2.0e-47
Match length	89
% identity	100
NCBI Description	(AC006526) putative auxin response factor 1 [Arabidopsis thaliana]

Seq. No.	137419
Seq. ID	LIB146-005-Q1-E1-F11
Method	BLASTN
NCBI GI	g4586241
BLAST score	332
E value	0.0e+00
Match length	397
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T20K18 (ESSA project)

Seq. No.	137420
Seq. ID	LIB146-005-Q1-E1-F7
Method	BLASTX
NCBI GI	g112681
BLAST score	474
E value	1.0e-47
Match length	115
% identity	81
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	137421
Seq. ID	LIB146-005-Q1-E1-F9
Method	BLASTX
NCBI GI	g266693
BLAST score	493
E value	7.0e-50
Match length	119
% identity	84
NCBI Description	OLEOSIN >gi_282875_pir__S22538 oleosin - Arabidopsis thaliana >gi_16405_emb_CAA44225_ (X62353) oleosin [Arabidopsis thaliana] >gi_4455257_emb_CAB36756.1_ (AL035523) oleosin, 18.5K [Arabidopsis thaliana]

Seq. No.	137422
Seq. ID	LIB146-005-Q1-E1-G12
Method	BLASTN
NCBI GI	g4519193
BLAST score	299
E value	1.0e-167
Match length	363
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC11, complete sequence

Seq. No.	137423
Seq. ID	LIB146-005-Q1-E1-G8
Method	BLASTN
NCBI GI	g4467131
BLAST score	364
E value	0.0e+00
Match length	372
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20M13 (ESSA project)

Seq. No.	137424
Seq. ID	LIB146-005-Q1-E1-G9
Method	BLASTN
NCBI GI	g3510339
BLAST score	259
E value	1.0e-144
Match length	401
% identity	98

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K3K7, complete sequence [Arabidopsis thaliana]
Seq. No.	137425
Seq. ID	LIB146-005-Q1-E1-H6
Method	BLASTX
NCBI GI	g4103987
BLAST score	246
E value	5.0e-21
Match length	61
% identity	75
NCBI Description	(AF030516) 5,10-methylenetetrahydrofolate dehydrogenase-5,10-methenyltetrahydrofolate cyclohydrolase [Pisum sativum]
Seq. No.	137426
Seq. ID	LIB146-006-Q1-E1-A10
Method	BLASTX
NCBI GI	g4038045
BLAST score	268
E value	2.0e-23
Match length	96
% identity	59
NCBI Description	(AC005936) putative DNA-binding protein [Arabidopsis thaliana]
Seq. No.	137427
Seq. ID	LIB146-006-Q1-E1-A6
Method	BLASTX
NCBI GI	g4544399
BLAST score	367
E value	4.0e-35
Match length	106
% identity	65
NCBI Description	(AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]
Seq. No.	137428
Seq. ID	LIB146-006-Q1-E1-C11
Method	BLASTX
NCBI GI	g1628583
BLAST score	475
E value	4.0e-48
Match length	92
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.	137429
Seq. ID	LIB146-006-Q1-E1-C3
Method	BLASTX
NCBI GI	g4406051
BLAST score	236
E value	5.0e-20
Match length	93
% identity	59

NCBI Description	(AF067605) linalool synthase-like protein [Arabidopsis thaliana]
Seq. No.	137430
Seq. ID	LIB146-006-Q1-E1-C4
Method	BLASTN
NCBI GI	g4757414
BLAST score	340
E value	0.0e+00
Match length	340
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYF24, complete sequence
Seq. No.	137431
Seq. ID	LIB146-006-Q1-E1-C8
Method	BLASTN
NCBI GI	g3582315
BLAST score	181
E value	3.0e-97
Match length	343
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T27A16 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	137432
Seq. ID	LIB146-006-Q1-E1-D10
Method	BLASTX
NCBI GI	g1628583
BLAST score	540
E value	1.0e-55
Match length	105
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.	137433
Seq. ID	LIB146-006-Q1-E1-D12
Method	BLASTX
NCBI GI	g4567295
BLAST score	574
E value	2.0e-59
Match length	133
% identity	77
NCBI Description	(AC006918) putative pol polyprotein [Arabidopsis thaliana]
Seq. No.	137434
Seq. ID	LIB146-006-Q1-E1-D6
Method	BLASTX
NCBI GI	g2583120
BLAST score	550
E value	1.0e-56
Match length	130
% identity	86
NCBI Description	(AC002387) putative receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	137435
Seq. ID	LIB146-006-Q1-E1-D8
Method	BLASTX
NCBI GI	g3763936
BLAST score	643
E value	1.0e-67
Match length	122
% identity	100
NCBI Description	(AC004450) putative myb-related transcription factor [Arabidopsis thaliana]

Seq. No.	137436
Seq. ID	LIB146-006-Q1-E1-G12
Method	BLASTX
NCBI GI	g4467129
BLAST score	572
E value	3.0e-59
Match length	111
% identity	99
NCBI Description	(AL035538) calcium-dependent protein kinase-like protein [Arabidopsis thaliana]

Seq. No.	137437
Seq. ID	LIB146-006-Q1-E1-G6
Method	BLASTX
NCBI GI	g3176665
BLAST score	689
E value	7.0e-73
Match length	128
% identity	98
NCBI Description	(AC004393) T1F15.9 [Arabidopsis thaliana]

Seq. No.	137438
Seq. ID	LIB146-007-Q1-E1-A4
Method	BLASTN
NCBI GI	g3449322
BLAST score	112
E value	3.0e-56
Match length	302
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC17, complete sequence [Arabidopsis thaliana]

Seq. No.	137439
Seq. ID	LIB146-007-Q1-E1-B3
Method	BLASTN
NCBI GI	g3510342
BLAST score	35
E value	3.0e-10
Match length	87
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MGN6, complete sequence [Arabidopsis thaliana]

Seq. No.	137440
Seq. ID	LIB146-007-Q1-E1-B7

Method	BLASTX
NCBI GI	g1628583
BLAST score	249
E value	2.0e-21
Match length	48
% identity	98
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	137441
Seq. ID	LIB146-007-Q1-E1-C6
Method	BLASTX
NCBI GI	g4454027
BLAST score	178
E value	3.0e-13
Match length	63
% identity	62
NCBI Description	(AL035394) putative protein [Arabidopsis thaliana]

Seq. No.	137442
Seq. ID	LIB146-007-Q1-E1-G1
Method	BLASTN
NCBI GI	g4406752
BLAST score	314
E value	1.0e-176
Match length	339
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F19B11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137443
Seq. ID	LIB146-007-Q1-E1-G10
Method	BLASTX
NCBI GI	g112741
BLAST score	588
E value	4.0e-61
Match length	108
% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	137444
Seq. ID	LIB146-007-Q1-E1-G6
Method	BLASTX
NCBI GI	g1628583
BLAST score	541
E value	1.0e-55
Match length	104
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	137445
Seq. ID	LIB146-008-Q1-E1-B11
Method	BLASTX
NCBI GI	g4567296
BLAST score	341
E value	4.0e-32
Match length	94
% identity	73
NCBI Description	(AC006918) putative Athila retroelement ORF1 protein [Arabidopsis thaliana]

Seq. No.	137446
Seq. ID	LIB146-008-Q1-E1-C4
Method	BLASTN
NCBI GI	g4510360
BLAST score	281
E value	1.0e-157
Match length	325
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F11F19 genomic sequence, complete sequence

Seq. No.	137447
Seq. ID	LIB146-008-Q1-E1-D9
Method	BLASTX
NCBI GI	g1628583
BLAST score	489
E value	2.0e-49
Match length	127
% identity	77
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	137448
Seq. ID	LIB146-008-Q1-E1-E11
Method	BLASTX
NCBI GI	g4512651
BLAST score	289
E value	6.0e-26
Match length	128
% identity	45
NCBI Description	(AC007048) putative tyrosine transaminase [Arabidopsis thaliana]

Seq. No.	137449
Seq. ID	LIB146-008-Q1-E1-G4
Method	BLASTX
NCBI GI	g4567216
BLAST score	274
E value	2.0e-24
Match length	110
% identity	55
NCBI Description	(AC007113) hypothetical protein [Arabidopsis thaliana]

Seq. No.	137450
Seq. ID	LIB146-008-Q1-E1-G9
Method	BLASTX
NCBI GI	g112681
BLAST score	580
E value	5.0e-60
Match length	135
% identity	84
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	137451
Seq. ID	LIB146-008-Q1-E1-H10
Method	BLASTN
NCBI GI	g2924733
BLAST score	423
E value	0.0e+00
Match length	423
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]

Seq. No.	137452
Seq. ID	LIB146-008-Q1-E1-H3
Method	BLASTN
NCBI GI	g3449318
BLAST score	230
E value	1.0e-126
Match length	242
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLF18, complete sequence [Arabidopsis thaliana]

Seq. No.	137453
Seq. ID	LIB146-008-Q1-E1-H6
Method	BLASTX
NCBI GI	g4773887
BLAST score	363
E value	6.0e-35
Match length	90
% identity	87
NCBI Description	(AF076243) hypothetical protein [Arabidopsis thaliana]

Seq. No.	137454
Seq. ID	LIB146-009-Q1-E1-A5
Method	BLASTN
NCBI GI	g2924651
BLAST score	382
E value	0.0e+00
Match length	382
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana]

Seq. No.	137455
Seq. ID	LIB146-009-Q1-E1-C12
Method	BLASTN
NCBI GI	g3080406
BLAST score	19
E value	1.3e+00
Match length	103
% identity	90
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F23E12 (ESSA project)

Seq. No.	137456
Seq. ID	LIB146-009-Q1-E1-C6
Method	BLASTN
NCBI GI	g2656028
BLAST score	136
E value	2.0e-70
Match length	323
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNF13

Seq. No.	137457
Seq. ID	LIB146-009-Q1-E1-D12
Method	BLASTN
NCBI GI	g2264321
BLAST score	75
E value	5.0e-34
Match length	236
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXM12, complete sequence [Arabidopsis thaliana]

Seq. No.	137458
Seq. ID	LIB146-009-Q1-E1-F10
Method	BLASTN
NCBI GI	g2264319
BLAST score	268
E value	1.0e-149
Match length	341
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXA21, complete sequence [Arabidopsis thaliana]

Seq. No.	137459
Seq. ID	LIB146-009-Q1-E1-F4
Method	BLASTX
NCBI GI	g1628583
BLAST score	535
E value	5.0e-55
Match length	104
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	137460

Seq. ID	LIB146-009-Q1-E1-G1
Method	BLASTX
NCBI GI	g112741
BLAST score	483
E value	6.0e-49
Match length	91
% identity	99
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	137461
Seq. ID	LIB146-009-Q1-E1-G2
Method	BLASTN
NCBI GI	g2656031
BLAST score	356
E value	0.0e+00
Match length	364
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC20

Seq. No.	137462
Seq. ID	LIB146-009-Q1-E1-G3
Method	BLASTN
NCBI GI	g2264303
BLAST score	214
E value	1.0e-117
Match length	218
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBB18, complete sequence [Arabidopsis thaliana]

Seq. No.	137463
Seq. ID	LIB146-009-Q1-E1-G9
Method	BLASTN
NCBI GI	g4580365
BLAST score	188
E value	1.0e-101
Match length	235
% identity	94
NCBI Description	Arabidopsis thaliana chromosome I BAC F3F20 genomic sequence, complete sequence

Seq. No.	137464
Seq. ID	LIB146-009-Q1-E1-H7
Method	BLASTN
NCBI GI	g3292807
BLAST score	415
E value	0.0e+00
Match length	415
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F7H19

(ESSAII project)

Seq. No.	137465
Seq. ID	LIB146-010-Q1-E1-A1
Method	BLASTX
NCBI GI	g2494144
BLAST score	143
E value	2.0e-09
Match length	45
% identity	69
NCBI Description	(AC002329) predicted leucine-rich protein [Arabidopsis thaliana]

Seq. No.	137466
Seq. ID	LIB146-010-Q1-E1-A12
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	137467
Seq. ID	LIB146-010-Q1-E1-A5
Method	BLASTX
NCBI GI	g4510401
BLAST score	486
E value	4.0e-49
Match length	114
% identity	74
NCBI Description	(AC006587) putative general negative regulator of transcription [Arabidopsis thaliana]

Seq. No.	137468
Seq. ID	LIB146-010-Q1-E1-A8
Method	BLASTN
NCBI GI	g4757404
BLAST score	38
E value	6.0e-12
Match length	369
% identity	36
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLJ15, complete sequence

Seq. No.	137469
Seq. ID	LIB146-010-Q1-E1-B4
Method	BLASTN
NCBI GI	g3335331
BLAST score	366
E value	0.0e+00
Match length	370
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8F5 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137470
Seq. ID	LIB146-010-Q1-E1-C3
Method	BLASTX
NCBI GI	g2129659
BLAST score	337
E value	1.0e-31
Match length	66
% identity	97
NCBI Description	oleosin, isoform 21K - Arabidopsis thaliana >gi_725260 (L40954) oleosin [Arabidopsis thaliana]

Seq. No.	137471
Seq. ID	LIB146-010-Q1-E1-D2
Method	BLASTX
NCBI GI	g4033365
BLAST score	86
E value	1.0e-69
Match length	135
% identity	97
NCBI Description	(AJ223499) ATP sulfurylase [Brassica juncea]

Seq. No.	137472
Seq. ID	LIB146-010-Q1-E1-D3
Method	BLASTX
NCBI GI	g112741
BLAST score	618
E value	1.0e-64
Match length	114
% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	137473
Seq. ID	LIB146-010-Q1-E1-D7
Method	BLASTN
NCBI GI	g4757414
BLAST score	205
E value	1.0e-111
Match length	361
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYF24, complete sequence

Seq. No.	137474
Seq. ID	LIB146-010-Q1-E1-F11
Method	BLASTX
NCBI GI	g1628583
BLAST score	607
E value	3.0e-63
Match length	116
% identity	100

NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.	137475
Seq. ID	LIB146-010-Q1-E1-F3
Method	BLASTX
NCBI GI	g1628583
BLAST score	663
E value	7.0e-70
Match length	127
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.	137476
Seq. ID	LIB146-010-Q1-E1-G5
Method	BLASTX
NCBI GI	g3805763
BLAST score	149
E value	8.0e-10
Match length	83
% identity	45
NCBI Description	(AC005693) hypothetical protein [Arabidopsis thaliana]
Seq. No.	137477
Seq. ID	LIB146-011-Q1-E1-A12
Method	BLASTN
NCBI GI	g2828182
BLAST score	225
E value	1.0e-123
Match length	246
% identity	51
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOJ9, complete sequence [Arabidopsis thaliana]
Seq. No.	137478
Seq. ID	LIB146-011-Q1-E1-A3
Method	BLASTN
NCBI GI	g3510343
BLAST score	293
E value	1.0e-164
Match length	348
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJC20, complete sequence [Arabidopsis thaliana]
Seq. No.	137479
Seq. ID	LIB146-011-Q1-E1-A8
Method	BLASTN
NCBI GI	g4678315
BLAST score	285
E value	1.0e-159
Match length	363
% identity	49
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone T17F15

(ESSA project)

Seq. No.	137480
Seq. ID	LIB146-011-Q1-E1-A9
Method	BLASTX
NCBI GI	g1628583
BLAST score	545
E value	4.0e-56
Match length	105
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	137481
Seq. ID	LIB146-011-Q1-E1-B8
Method	BLASTN
NCBI GI	g4589445
BLAST score	128
E value	1.0e-65
Match length	345
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWL2, complete sequence

Seq. No.	137482
Seq. ID	LIB146-011-Q1-E1-D12
Method	BLASTX
NCBI GI	g4753655
BLAST score	312
E value	7.0e-29
Match length	88
% identity	77
NCBI Description	(AL049751) pectate lyase like protein [Arabidopsis thaliana]

Seq. No.	137483
Seq. ID	LIB146-011-Q1-E1-E7
Method	BLASTN
NCBI GI	g4584841
BLAST score	187
E value	1.0e-101
Match length	255
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T23E23, complete sequence

Seq. No.	137484
Seq. ID	LIB146-011-Q1-E1-F1
Method	BLASTX
NCBI GI	g3157930
BLAST score	583
E value	2.0e-60
Match length	109
% identity	99
NCBI Description	(AC002131) Strong similarity to amino-cyclopropane-carboxylic acid oxidase gb_L27664 from

Brassica napus. ESTs gb_Z48548 and gb_Z48549 come from this gene. [Arabidopsis thaliana]

Seq. No.	137485
Seq. ID	LIB146-011-Q1-E1-G4
Method	BLASTX
NCBI GI	g1628583
BLAST score	473
E value	7.0e-48
Match length	92
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	137486
Seq. ID	LIB146-011-Q1-E1-G7
Method	BLASTX
NCBI GI	g534982
BLAST score	192
E value	4.0e-15
Match length	79
% identity	53
NCBI Description	(X75898) phosphoglucomutase [Spinacia oleracea]

Seq. No.	137487
Seq. ID	LIB146-012-Q1-E1-A2
Method	BLASTX
NCBI GI	g1628583
BLAST score	541
E value	1.0e-55
Match length	104
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	137488
Seq. ID	LIB146-012-Q1-E1-C12
Method	BLASTN
NCBI GI	g2842474
BLAST score	158
E value	6.0e-84
Match length	162
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F2009 (ESSAII project)

Seq. No.	137489
Seq. ID	LIB146-012-Q1-E1-D1
Method	BLASTX
NCBI GI	g4678361
BLAST score	561
E value	5.0e-58
Match length	112
% identity	96
NCBI Description	(AL049659) cytochrome P450-like protein [Arabidopsis

thaliana]

Seq. No.	137490
Seq. ID	LIB146-012-Q1-E1-D9
Method	BLASTN
NCBI GI	g4432793
BLAST score	280
E value	1.0e-156
Match length	360
% identity	46
NCBI Description	Arabidopsis thaliana chromosome II BAC T19K21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137491
Seq. ID	LIB146-012-Q1-E1-E6
Method	BLASTN
NCBI GI	g16231
BLAST score	130
E value	3.0e-67
Match length	150
% identity	97
NCBI Description	Arabidopsis CRA1 gene for 12S seed storage protein >gi_166675_gb_M37247_ATHCRA1AA A.thaliana 12S storage protein CRA1 gene, exons 1-4

Seq. No.	137492
Seq. ID	LIB146-012-Q1-E1-F11
Method	BLASTN
NCBI GI	g3426033
BLAST score	233
E value	1.0e-128
Match length	257
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F12C20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137493
Seq. ID	LIB146-012-Q1-E1-F4
Method	BLASTN
NCBI GI	g3522932
BLAST score	242
E value	1.0e-133
Match length	331
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137494
Seq. ID	LIB146-012-Q1-E1-F8
Method	BLASTX
NCBI GI	g112741
BLAST score	566
E value	1.0e-58
Match length	105
% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -

	Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]
Seq. No.	137495
Seq. ID	LIB146-012-Q1-E1-G1
Method	BLASTN
NCBI GI	g2828278
BLAST score	170
E value	9.0e-91
Match length	327
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16 (ESSAII project)
Seq. No.	137496
Seq. ID	LIB146-012-Q1-E1-G11
Method	BLASTX
NCBI GI	g2642448
BLAST score	353
E value	1.0e-33
Match length	114
% identity	34
NCBI Description	(AC002391) hypothetical protein [Arabidopsis thaliana] >gi_3169187 (AC004401) hypothetical protein [Arabidopsis thaliana]
Seq. No.	137497
Seq. ID	LIB146-012-Q1-E1-G12
Method	BLASTN
NCBI GI	g4699904
BLAST score	25
E value	3.0e-04
Match length	412
% identity	79
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F1E22, complete sequence
Seq. No.	137498
Seq. ID	LIB146-012-Q1-E1-G4
Method	BLASTN
NCBI GI	g2058505
BLAST score	39
E value	1.0e-12
Match length	39
% identity	100
NCBI Description	Brassica rapa zinc-finger protein BcZFP1 (BcAFP1(3-2z)) gene, complete cds
Seq. No.	137499
Seq. ID	LIB146-012-Q1-E1-H8
Method	BLASTX
NCBI GI	g4467126
BLAST score	525
E value	8.0e-54

Match length	106
% identity	99
NCBI Description	(AL035538) guanine nucleotide-exchange protein-like [Arabidopsis thaliana]

Seq. No.	137500
Seq. ID	LIB146-012-Q1-E1-H9
Method	BLASTX
NCBI GI	g2274993
BLAST score	385
E value	2.0e-37
Match length	95
% identity	72
NCBI Description	(AJ000230) unnamed protein product [Hordeum vulgare]

Seq. No.	137501
Seq. ID	LIB146-013-Q1-E1-A12
Method	BLASTN
NCBI GI	g2104523
BLAST score	278
E value	1.0e-155
Match length	369
% identity	94
NCBI Description	Arabidopsis thaliana BAC T10M13 from chromosome IV, from 10.8 cM to 11.6 cM, complete sequence

Seq. No.	137502
Seq. ID	LIB146-013-Q1-E1-A5
Method	BLASTX
NCBI GI	g2529229
BLAST score	439
E value	1.0e-43
Match length	102
% identity	85
NCBI Description	(AB007907) 6-phosphogluconate dehydrogenase [Glycine max]

Seq. No.	137503
Seq. ID	LIB146-013-Q1-E1-B10
Method	BLASTN
NCBI GI	g3608126
BLAST score	200
E value	1.0e-108
Match length	305
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T32F12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137504
Seq. ID	LIB146-013-Q1-E1-C10
Method	BLASTX
NCBI GI	g729775
BLAST score	152
E value	6.0e-10
Match length	105
% identity	33
NCBI Description	HEAT SHOCK FACTOR PROTEIN HSF8 (HEAT SHOCK TRANSCRIPTION FACTOR 8) (HSTF 8) (HEAT STRESS TRANSCRIPTION FACTOR)

>gi_100264_pir__S25481 heat shock transcription factor 8 - Peruvian tomato >gi_19492_emb_CAA47869_ (X67600) heat shock transcription factor 8 [Lycopersicon peruvianum]

Seq. No.	137505
Seq. ID	LIB146-013-Q1-E1-C4
Method	BLASTN
NCBI GI	g4454022
BLAST score	187
E value	1.0e-101
Match length	361
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16 (ESSAII project)

Seq. No.	137506
Seq. ID	LIB146-013-Q1-E1-C7
Method	BLASTN
NCBI GI	g2358139
BLAST score	215
E value	1.0e-118
Match length	223
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 YAC yUP8H12 complete sequence [Arabidopsis thaliana]

Seq. No.	137507
Seq. ID	LIB146-013-Q1-E1-C8
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	137508
Seq. ID	LIB146-013-Q1-E1-D5
Method	BLASTX
NCBI GI	g131360
BLAST score	241
E value	2.0e-20
Match length	61
% identity	82
NCBI Description	PHOTOSYSTEM II 4 KD REACTION CENTRE PROTEIN PRECURSOR >gi_81727_pir__S02115 photosystem II protein psbK precursor - white mustard chloroplast >gi_12209_emb_CAA31909_ (X13558) K preprotein (AA -24 to 37) [Sinapis alba]

Seq. No.	137509
Seq. ID	LIB146-013-Q1-E1-D6
Method	BLASTX
NCBI GI	g4467126
BLAST score	690
E value	5.0e-73

Match length	136
% identity	99
NCBI Description	(AL035538) guanine nucleotide-exchange protein-like [Arabidopsis thaliana]

Seq. No.	137510
Seq. ID	LIB146-013-Q1-E1-D7
Method	BLASTX
NCBI GI	g112681
BLAST score	710
E value	2.0e-75
Match length	134
% identity	99
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	137511
Seq. ID	LIB146-013-Q1-E1-E1
Method	BLASTN
NCBI GI	g4757415
BLAST score	365
E value	0.0e+00
Match length	393
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN21, complete sequence

Seq. No.	137512
Seq. ID	LIB146-013-Q1-E1-E12
Method	BLASTX
NCBI GI	g2129738
BLAST score	643
E value	1.0e-67
Match length	124
% identity	100
NCBI Description	shaggy-like kinase dzeta - Arabidopsis thaliana >gi_1225913_emb_CAA64408_ (X94938) shaggy-like kinase dzeta [Arabidopsis thaliana] >gi_1669653_emb_CAA70483_ (Y09300) serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	137513
Seq. ID	LIB146-013-Q1-E1-F10
Method	BLASTX
NCBI GI	g4325282
BLAST score	306
E value	5.0e-28
Match length	59
% identity	93
NCBI Description	(AF123310) NAC domain protein NAM [Arabidopsis thaliana] >gi_4325286_gb_AAD17314_ (AF123311) NAC domain protein NAM [Arabidopsis thaliana]

Seq. No.	137514
Seq. ID	LIB146-013-Q1-E1-F9

Method	BLASTX
NCBI GI	g4512666
BLAST score	378
E value	2.0e-36
Match length	122
% identity	38
NCBI Description	(AC006931) putative mei2 protein [Arabidopsis thaliana]

Seq. No.	137515
Seq. ID	LIB146-013-Q1-E1-G5
Method	BLASTX
NCBI GI	g4406821
BLAST score	586
E value	8.0e-61
Match length	106
% identity	100
NCBI Description	(AC006201) hypothetical protein [Arabidopsis thaliana]

Seq. No.	137516
Seq. ID	LIB146-014-Q1-E1-B9
Method	BLASTX
NCBI GI	g3152576
BLAST score	189
E value	1.0e-14
Match length	64
% identity	59
NCBI Description	(AC002986) Similar to liver-specific transport protein gb_L27651 from Rattus norviegicus. [Arabidopsis thaliana]

Seq. No.	137517
Seq. ID	LIB146-014-Q1-E1-C1
Method	BLASTN
NCBI GI	g4539309
BLAST score	126
E value	1.0e-64
Match length	302
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F19H22 (ESSA project)

Seq. No.	137518
Seq. ID	LIB146-014-Q1-E1-C3
Method	BLASTN
NCBI GI	g2264309
BLAST score	183
E value	1.0e-98
Match length	217
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJJ3, complete sequence [Arabidopsis thaliana]

Seq. No.	137519
Seq. ID	LIB146-014-Q1-E1-C6
Method	BLASTX
NCBI GI	g4587526
BLAST score	267
E value	2.0e-23

Match length	112
% identity	48
NCBI Description	(AC007060) Strong similarity to F19I3.2 gi_3033375 putative berberine bridge enzyme from Arabidopsis thaliana BAC gb_AC004238. ESTs gb_F19886, gb_Z30784 and gb_Z30785 come from this gene

Seq. No.	137520
Seq. ID	LIB146-014-Q1-E1-D11
Method	BLASTN
NCBI GI	g4539290
BLAST score	349
E value	0.0e+00
Match length	373
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F14M19 (ESSA project)

Seq. No.	137521
Seq. ID	LIB146-014-Q1-E1-D12
Method	BLASTX
NCBI GI	g112681
BLAST score	564
E value	3.0e-58
Match length	132
% identity	83
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	137522
Seq. ID	LIB146-014-Q1-E1-E9
Method	BLASTX
NCBI GI	g112741
BLAST score	484
E value	4.0e-49
Match length	90
% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	137523
Seq. ID	LIB146-014-Q1-E1-F6
Method	BLASTX
NCBI GI	g4539452
BLAST score	372
E value	7.0e-36
Match length	100
% identity	70
NCBI Description	(AL049500) putative phosphoribosylanthranilate transferase

[Arabidopsis thaliana]

Seq. No.	137524
Seq. ID	LIB146-014-Q1-E1-H1
Method	BLASTN
NCBI GI	g2842474
BLAST score	228
E value	1.0e-125
Match length	260
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F2009 (ESSAII project)

Seq. No.	137525
Seq. ID	LIB146-014-Q1-E1-H12
Method	BLASTX
NCBI GI	g2829892
BLAST score	365
E value	6.0e-35
Match length	121
% identity	59
NCBI Description	(AC002311) putative pectinesterase [Arabidopsis thaliana]

Seq. No.	137526
Seq. ID	LIB146-014-Q1-E1-H3
Method	BLASTX
NCBI GI	g4510418
BLAST score	415
E value	4.0e-41
Match length	85
% identity	98
NCBI Description	(AC006929) hypothetical protein [Arabidopsis thaliana]

Seq. No.	137527
Seq. ID	LIB146-015-Q1-E1-A2
Method	BLASTX
NCBI GI	g1619602
BLAST score	313
E value	6.0e-29
Match length	73
% identity	82
NCBI Description	(Y08726) MtN3 [Medicago truncatula]

Seq. No.	137528
Seq. ID	LIB146-015-Q1-E1-B5
Method	BLASTX
NCBI GI	g112741
BLAST score	595
E value	6.0e-62
Match length	109
% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No.	137529
Seq. ID	LIB146-015-Q1-E1-C9
Method	BLASTX
NCBI GI	g2660672
BLAST score	534
E value	8.0e-55
Match length	115
% identity	41
NCBI Description	(AC002342) similar to pMS10 protein [Arabidopsis thaliana]

Seq. No.	137530
Seq. ID	LIB146-015-Q1-E1-E10
Method	BLASTX
NCBI GI	g4559380
BLAST score	648
E value	4.0e-68
Match length	123
% identity	100
NCBI Description	(AC006526) putative auxin-responsive GH3 protein [Arabidopsis thaliana]

Seq. No.	137531
Seq. ID	LIB146-015-Q1-E1-E11
Method	BLASTN
NCBI GI	g2760172
BLAST score	185
E value	1.0e-99
Match length	356
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUB3, complete sequence [Arabidopsis thaliana]

Seq. No.	137532
Seq. ID	LIB146-015-Q1-E1-F1
Method	BLASTN
NCBI GI	g3617740
BLAST score	87
E value	3.0e-41
Match length	99
% identity	97
NCBI Description	Arabidopsis thaliana BAC F1I21 from chromosome 1, near 59 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	137533
Seq. ID	LIB146-015-Q1-E1-G11
Method	BLASTX
NCBI GI	g2760830
BLAST score	607
E value	2.0e-63
Match length	117
% identity	100
NCBI Description	(AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No. 137534

Seq. ID	LIB146-015-Q1-E1-G4
Method	BLASTX
NCBI GI	g3341684
BLAST score	153
E value	4.0e-10
Match length	91
% identity	41
NCBI Description	(AC003672) hypothetical protein [Arabidopsis thaliana]

Seq. No.	137535
Seq. ID	LIB146-015-Q1-E1-H3
Method	BLASTN
NCBI GI	g2098816
BLAST score	333
E value	0.0e+00
Match length	337
% identity	100
NCBI Description	Arabidopsis thaliana BAC F19G10, complete sequence

Seq. No.	137536
Seq. ID	LIB146-015-Q1-E1-H6
Method	BLASTX
NCBI GI	g112741
BLAST score	618
E value	1.0e-64
Match length	114
% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	137537
Seq. ID	LIB146-016-Q1-E1-A6
Method	BLASTX
NCBI GI	g112737
BLAST score	464
E value	1.0e-46
Match length	116
% identity	78
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	137538
Seq. ID	LIB146-016-Q1-E1-B12
Method	BLASTX
NCBI GI	g3860272
BLAST score	209
E value	1.0e-16

Match length	41
% identity	100
NCBI Description	(AC005824) putative suppressor protein [Arabidopsis thaliana] >gi_4314399_gb_AAD15609_ (AC006232) putative skd1 protein [Arabidopsis thaliana]

Seq. No.	137539
Seq. ID	LIB146-016-Q1-E1-B9
Method	BLASTN
NCBI GI	g3510331
BLAST score	401
E value	0.0e+00
Match length	405
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K13P22, complete sequence [Arabidopsis thaliana]

Seq. No.	137540
Seq. ID	LIB146-016-Q1-E1-C10
Method	BLASTX
NCBI GI	g4689479
BLAST score	245
E value	8.0e-21
Match length	85
% identity	64
NCBI Description	(AC007213) hypothetical protein [Arabidopsis thaliana]

Seq. No.	137541
Seq. ID	LIB146-016-Q1-E1-D12
Method	BLASTX
NCBI GI	g1628583
BLAST score	663
E value	7.0e-70
Match length	127
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	137542
Seq. ID	LIB146-016-Q1-E1-F1
Method	BLASTX
NCBI GI	g3721856
BLAST score	318
E value	1.0e-29
Match length	89
% identity	62
NCBI Description	(AB014057) beta-Amyrin Synthase [Panax ginseng]

Seq. No.	137543
Seq. ID	LIB146-017-Q1-E1-A1
Method	BLASTN
NCBI GI	g4733984
BLAST score	340
E value	0.0e+00
Match length	356
% identity	49

NCBI Description	Arabidopsis thaliana chromosome II BAC F14O4 genomic sequence, complete sequence

Seq. No.	137544
Seq. ID	LIB146-017-Q1-E1-A11
Method	BLASTN
NCBI GI	g4732164
BLAST score	109
E value	2.0e-54
Match length	231
% identity	43
NCBI Description	Arabidopsis thaliana BAC F10A2

Seq. No.	137545
Seq. ID	LIB146-017-Q1-E1-B8
Method	BLASTN
NCBI GI	g3811319
BLAST score	134
E value	2.0e-69
Match length	212
% identity	98
NCBI Description	Arabidopsis thaliana ROOT HAIRLESS 1 (RHL1) gene, complete cds

Seq. No.	137546
Seq. ID	LIB146-017-Q1-E1-C2
Method	BLASTN
NCBI GI	g3763915
BLAST score	256
E value	1.0e-142
Match length	300
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F14B2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137547
Seq. ID	LIB146-017-Q1-E1-C3
Method	BLASTX
NCBI GI	g1628583
BLAST score	460
E value	2.0e-46
Match length	86
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	137548
Seq. ID	LIB146-017-Q1-E1-C7
Method	BLASTX
NCBI GI	g112741
BLAST score	691
E value	4.0e-73
Match length	128
% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -

	Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]
Seq. No.	137549
Seq. ID	LIB146-017-Q1-E1-D6
Method	BLASTX
NCBI GI	g3860250
BLAST score	268
E value	1.0e-23
Match length	103
% identity	61
NCBI Description	(AC005824) putative chloroplast prephenate dehydratase [Arabidopsis thaliana]
Seq. No.	137550
Seq. ID	LIB146-017-Q1-E1-E1
Method	BLASTX
NCBI GI	g2245048
BLAST score	446
E value	2.0e-44
Match length	124
% identity	74
NCBI Description	(Z97342) resistance gene homolog [Arabidopsis thaliana]
Seq. No.	137551
Seq. ID	LIB146-017-Q1-E1-E6
Method	BLASTN
NCBI GI	g3451055
BLAST score	271
E value	1.0e-151
Match length	371
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F16G20 (ESSAII project)
Seq. No.	137552
Seq. ID	LIB146-017-Q1-E1-E7
Method	BLASTX
NCBI GI	g112737
BLAST score	536
E value	6.0e-55
Match length	130
% identity	80
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]
Seq. No.	137553
Seq. ID	LIB146-017-Q1-E1-F1
Method	BLASTN

NCBI GI	g4725940
BLAST score	395
E value	0.0e+00
Match length	395
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T1P17 (ESSA project)

Seq. No.	137554
Seq. ID	LIB146-017-Q1-E1-G11
Method	BLASTX
NCBI GI	g1628583
BLAST score	480
E value	1.0e-48
Match length	95
% identity	96
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	137555
Seq. ID	LIB146-017-Q1-E1-G7
Method	BLASTN
NCBI GI	g2656026
BLAST score	207
E value	1.0e-113
Match length	379
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDF20

Seq. No.	137556
Seq. ID	LIB146-017-Q1-E1-H1
Method	BLASTN
NCBI GI	g3785992
BLAST score	291
E value	1.0e-163
Match length	345
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T6A23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137557
Seq. ID	LIB146-017-Q1-E1-H2
Method	BLASTN
NCBI GI	g3046852
BLAST score	351
E value	0.0e+00
Match length	351
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQJ16, complete sequence [Arabidopsis thaliana]

Seq. No.	137558
Seq. ID	LIB146-017-Q1-E1-H4
Method	BLASTX
NCBI GI	g3128192

BLAST score	271
E value	6.0e-24
Match length	87
% identity	63
NCBI Description	(AC004521) axi 1-like protein [Arabidopsis thaliana]

Seq. No.	137559
Seq. ID	LIB146-018-Q1-E1-A1
Method	BLASTN
NCBI GI	g4454587
BLAST score	336
E value	0.0e+00
Match length	336
% identity	100
NCBI Description	Arabidopsis thaliana BAC F21A20 from chromosome V near 61 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	137560
Seq. ID	LIB146-018-Q1-E1-A11
Method	BLASTN
NCBI GI	g4732168
BLAST score	25
E value	4.0e-04
Match length	355
% identity	45
NCBI Description	Arabidopsis thaliana BAC T1J24

Seq. No.	137561
Seq. ID	LIB146-018-Q1-E1-A5
Method	BLASTX
NCBI GI	g4033735
BLAST score	281
E value	1.0e-25
Match length	75
% identity	67
NCBI Description	(AF054284) spliceosomal protein SAP 155 [Homo sapiens]

Seq. No.	137562
Seq. ID	LIB146-018-Q1-E1-B10
Method	BLASTX
NCBI GI	g2160169
BLAST score	269
E value	1.0e-23
Match length	96
% identity	54
NCBI Description	(AC000132) No definition line found [Arabidopsis thaliana]

Seq. No.	137563
Seq. ID	LIB146-018-Q1-E1-B11
Method	BLASTN
NCBI GI	g4454447
BLAST score	207
E value	1.0e-113
Match length	328
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137564
Seq. ID	LIB146-018-Q1-E1-B2
Method	BLASTX
NCBI GI	g4558671
BLAST score	199
E value	2.0e-15
Match length	48
% identity	71
NCBI Description	(AC007063) hypothetical protein [Arabidopsis thaliana] >gi_4726111_gb_AAD28311.1_AC006436_2 (AC006436) hypothetical protein [Arabidopsis thaliana]

Seq. No.	137565
Seq. ID	LIB146-018-Q1-E1-B4
Method	BLASTX
NCBI GI	g3337361
BLAST score	443
E value	3.0e-44
Match length	96
% identity	79
NCBI Description	(AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	137566
Seq. ID	LIB146-018-Q1-E1-B6
Method	BLASTX
NCBI GI	g3819699
BLAST score	218
E value	1.0e-17
Match length	55
% identity	82
NCBI Description	(AJ009609) BnMAP4K alpha2 [Brassica napus]

Seq. No.	137567
Seq. ID	LIB146-018-Q1-E1-C1
Method	BLASTX
NCBI GI	g1628583
BLAST score	535
E value	6.0e-55
Match length	103
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	137568
Seq. ID	LIB146-018-Q1-E1-C11
Method	BLASTN
NCBI GI	g3080430
BLAST score	238
E value	1.0e-131
Match length	238
% identity	64
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T19P19 (ESSAII project)

Seq. No. 137569

Seq. ID	LIB146-018-Q1-E1-C9
Method	BLASTX
NCBI GI	g4726114
BLAST score	498
E value	2.0e-50
Match length	123
% identity	80
NCBI Description	(AC006436) putative retrotransposon Athila [Arabidopsis thaliana]

Seq. No.	137570
Seq. ID	LIB146-018-Q1-E1-D1
Method	BLASTX
NCBI GI	g4185738
BLAST score	366
E value	4.0e-35
Match length	116
% identity	59
NCBI Description	(AF079998) putative glutamate receptor [Arabidopsis thaliana]

Seq. No.	137571
Seq. ID	LIB146-018-Q1-E1-D12
Method	BLASTN
NCBI GI	g4512656
BLAST score	304
E value	1.0e-171
Match length	304
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	137572
Seq. ID	LIB146-018-Q1-E1-D2
Method	BLASTX
NCBI GI	g1628583
BLAST score	472
E value	2.0e-47
Match length	89
% identity	99
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	137573
Seq. ID	LIB146-018-Q1-E1-F6
Method	BLASTX
NCBI GI	g3687228
BLAST score	675
E value	3.0e-71
Match length	136
% identity	98
NCBI Description	(AC005169) putative malate dehydrogenase [Arabidopsis thaliana]

Seq. No.	137574
Seq. ID	LIB146-018-Q1-E1-G4

Method	BLASTX
NCBI GI	g1628583
BLAST score	663
E value	7.0e-70
Match length	127
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	137575
Seq. ID	LIB146-018-Q1-E1-H3
Method	BLASTX
NCBI GI	g112681
BLAST score	527
E value	6.0e-54
Match length	125
% identity	82
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	137576
Seq. ID	LIB146-019-Q1-E1-A10
Method	BLASTX
NCBI GI	g2832620
BLAST score	467
E value	6.0e-47
Match length	111
% identity	77
NCBI Description	(AL021711) hypothetical protein [Arabidopsis thaliana]

Seq. No.	137577
Seq. ID	LIB146-019-Q1-E1-A3
Method	BLASTN
NCBI GI	g4204173
BLAST score	346
E value	0.0e+00
Match length	358
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T2K10 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137578
Seq. ID	LIB146-019-Q1-E1-A9
Method	BLASTX
NCBI GI	g1628583
BLAST score	265
E value	2.0e-23
Match length	85
% identity	66
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	137579
Seq. ID	LIB146-019-Q1-E1-B5
Method	BLASTX
NCBI GI	g4773906
BLAST score	319
E value	2.0e-29
Match length	71
% identity	86
NCBI Description	(AF074021) putative symbiosis-related protein [Arabidopsis thaliana]

Seq. No.	137580
Seq. ID	LIB146-019-Q1-E1-C12
Method	BLASTX
NCBI GI	g1769568
BLAST score	213
E value	3.0e-17
Match length	64
% identity	73
NCBI Description	(U82202) fumarase; fumarate hydratase [Arabidopsis thaliana]

Seq. No.	137581
Seq. ID	LIB146-019-Q1-E1-C3
Method	BLASTX
NCBI GI	g112681
BLAST score	661
E value	1.0e-69
Match length	132
% identity	98
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	137582
Seq. ID	LIB146-019-Q1-E1-D3
Method	BLASTX
NCBI GI	g3184281
BLAST score	540
E value	2.0e-55
Match length	132
% identity	77
NCBI Description	(AC004136) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	137583
Seq. ID	LIB146-019-Q1-E1-D9
Method	BLASTN
NCBI GI	g4455321
BLAST score	242
E value	1.0e-134
Match length	310
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4I10 (ESSAII project)

Seq. No.	137584
Seq. ID	LIB146-019-Q1-E1-E12
Method	BLASTX
NCBI GI	g133320
BLAST score	304
E value	7.0e-28
Match length	101
% identity	57
NCBI Description	DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (A135) (RNA POLYMERASE I SUBUNIT 2) >gi_101446_pir__A39607 DNA-directed RNA polymerase (EC 2.7.7.6) I 135K chain - yeast (Saccharomyces cerevisiae) >gi_172464 (M62804) RNA polymerase I (second largest subunit) [Saccharomyces cerevisiae] >gi_887587_emb_CAA90154_ (Z49919) Rpa2p [Saccharomyces cerevisiae] >gi_939744 (U31900) Rpa135p [Saccharomyces cerevisiae] >gi_1314085_emb_CAA95050_ (Z71255) Rpa2p [Saccharomyces cerevisiae]

Seq. No.	137585
Seq. ID	LIB146-019-Q1-E1-E5
Method	BLASTX
NCBI GI	g1628583
BLAST score	663
E value	7.0e-70
Match length	127
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	137586
Seq. ID	LIB146-019-Q1-E1-F1
Method	BLASTN
NCBI GI	g2828187
BLAST score	34
E value	2.0e-09
Match length	50
% identity	44
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21C13, complete sequence [Arabidopsis thaliana]

Seq. No.	137587
Seq. ID	LIB146-019-Q1-E1-F3
Method	BLASTX
NCBI GI	g4544426
BLAST score	344
E value	2.0e-32
Match length	128
% identity	53
NCBI Description	(AC006955) putative transposase [Arabidopsis thaliana]

Seq. No.	137588
Seq. ID	LIB146-019-Q1-E1-G5
Method	BLASTX
NCBI GI	g112681
BLAST score	538
E value	3.0e-55

Match length	127
% identity	83
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	137589
Seq. ID	LIB146-019-Q1-E1-G9
Method	BLASTN
NCBI GI	g2656032
BLAST score	246
E value	1.0e-136
Match length	280
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZF18

Seq. No.	137590
Seq. ID	LIB146-019-Q1-E1-H2
Method	BLASTN
NCBI GI	g4587986
BLAST score	362
E value	0.0e+00
Match length	362
% identity	100
NCBI Description	Arabidopsis thaliana ABA-regulated gene cluster, complete sequence

Seq. No.	137591
Seq. ID	LIB146-020-Q1-E1-A7
Method	BLASTX
NCBI GI	g3169059
BLAST score	183
E value	1.0e-13
Match length	63
% identity	54
NCBI Description	(AL023704) weak similarity to B.subtilis spore outgrowth f actor B [Schizosaccharomyces pombe]

Seq. No.	137592
Seq. ID	LIB146-020-Q1-E1-B5
Method	BLASTN
NCBI GI	g2351061
BLAST score	344
E value	0.0e+00
Match length	344
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAF19, complete sequence [Arabidopsis thaliana]

Seq. No.	137593
Seq. ID	LIB146-020-Q1-E1-C4
Method	BLASTN
NCBI GI	g4581161
BLAST score	324

E value	0.0e+00
Match length	332
% identity	14
NCBI Description	Arabidopsis thaliana chromosome II BAC T20G20 genomic sequence, complete sequence

Seq. No.	137594
Seq. ID	LIB146-020-Q1-E1-E3
Method	BLASTN
NCBI GI	g3335356
BLAST score	298
E value	1.0e-167
Match length	336
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F16M14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137595
Seq. ID	LIB146-020-Q1-E1-G3
Method	BLASTX
NCBI GI	g112681
BLAST score	489
E value	2.0e-49
Match length	119
% identity	81
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	137596
Seq. ID	LIB146-020-Q1-E1-G4
Method	BLASTX
NCBI GI	g3152605
BLAST score	369
E value	2.0e-35
Match length	71
% identity	100
NCBI Description	(AC004482) hypothetical protein [Arabidopsis thaliana]

Seq. No.	137597
Seq. ID	LIB146-020-Q1-E1-H2
Method	BLASTX
NCBI GI	g112741
BLAST score	622
E value	4.0e-65
Match length	115
% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	137598
Seq. ID	LIB146-020-Q1-E1-H3
Method	BLASTX
NCBI GI	g2245017
BLAST score	491
E value	8.0e-50
Match length	114
% identity	90
NCBI Description	(Z97341) membrane protein homolog [Arabidopsis thaliana]

Seq. No.	137599
Seq. ID	LIB146-021-Q1-E1-A7
Method	BLASTN
NCBI GI	g4490717
BLAST score	400
E value	0.0e+00
Match length	400
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	137600
Seq. ID	LIB146-021-Q1-E1-B1
Method	BLASTN
NCBI GI	g4589415
BLAST score	23
E value	6.0e-03
Match length	365
% identity	55
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K14A3, complete sequence

Seq. No.	137601
Seq. ID	LIB146-021-Q1-E1-B10
Method	BLASTN
NCBI GI	g3831448
BLAST score	319
E value	1.0e-179
Match length	360
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T32F6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137602
Seq. ID	LIB146-021-Q1-E1-B6
Method	BLASTX
NCBI GI	g3184283
BLAST score	544
E value	6.0e-56
Match length	108
% identity	99
NCBI Description	(AC004136) putative TBP-binding protein [Arabidopsis thaliana]

Seq. No.	137603
Seq. ID	LIB146-021-Q1-E1-C11
Method	BLASTN

NCBI GI	g2182285
BLAST score	154
E value	3.0e-81
Match length	298
% identity	100
NCBI Description	Sequence of BAC F5I14 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	137604
Seq. ID	LIB146-021-Q1-E1-D12
Method	BLASTN
NCBI GI	g4027862
BLAST score	342
E value	0.0e+00
Match length	342
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T7A14 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137605
Seq. ID	LIB146-021-Q1-E1-E8
Method	BLASTX
NCBI GI	g112682
BLAST score	583
E value	2.0e-60
Match length	123
% identity	89
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	137606
Seq. ID	LIB146-021-Q1-E1-F3
Method	BLASTX
NCBI GI	g112682
BLAST score	550
E value	1.0e-56
Match length	117
% identity	88
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	137607
Seq. ID	LIB146-021-Q1-E1-F4
Method	BLASTX
NCBI GI	g112681
BLAST score	534
E value	9.0e-55
Match length	125
% identity	83
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana

	>gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]
Seq. No.	137608
Seq. ID	LIB146-021-Q1-E1-F6
Method	BLASTN
NCBI GI	g3738275
BLAST score	327
E value	0.0e+00
Match length	384
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F17A22 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	137609
Seq. ID	LIB146-021-Q1-E1-F8
Method	BLASTX
NCBI GI	g2335108
BLAST score	436
E value	9.0e-49
Match length	112
% identity	84
NCBI Description	(AC002339) putative isulinase [Arabidopsis thaliana]
Seq. No.	137610
Seq. ID	LIB146-021-Q1-E1-F9
Method	BLASTX
NCBI GI	g112741
BLAST score	575
E value	1.0e-59
Match length	106
% identity	100
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]
Seq. No.	137611
Seq. ID	LIB146-021-Q1-E1-G10
Method	BLASTN
NCBI GI	g3449334
BLAST score	41
E value	9.0e-14
Match length	53
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH9, complete sequence [Arabidopsis thaliana]
Seq. No.	137612
Seq. ID	LIB146-021-Q1-E1-G11
Method	BLASTN
NCBI GI	g2337888
BLAST score	227

E value	1.0e-124
Match length	361
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14J16, complete sequence [Arabidopsis thaliana]

Seq. No.	137613
Seq. ID	LIB146-021-Q1-E1-G12
Method	BLASTN
NCBI GI	g2264316
BLAST score	115
E value	6.0e-58
Match length	247
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRO11, complete sequence [Arabidopsis thaliana]

Seq. No.	137614
Seq. ID	LIB146-022-Q1-E1-A5
Method	BLASTN
NCBI GI	g2262097
BLAST score	348
E value	0.0e+00
Match length	373
% identity	98
NCBI Description	Arabidopsis thaliana chromosome IV BAC T19F6 genomic sequence, complete sequence

Seq. No.	137615
Seq. ID	LIB146-022-Q1-E1-B11
Method	BLASTN
NCBI GI	g3297806
BLAST score	313
E value	1.0e-176
Match length	342
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17I5 (ESSA project)

Seq. No.	137616
Seq. ID	LIB146-022-Q1-E1-C10
Method	BLASTN
NCBI GI	g16472
BLAST score	163
E value	2.0e-86
Match length	308
% identity	17
NCBI Description	A.thaliana rRNA repeat unit, most frequent IGR type

Seq. No.	137617
Seq. ID	LIB146-022-Q1-E1-C11
Method	BLASTX
NCBI GI	g112681
BLAST score	508
E value	1.0e-51
Match length	107
% identity	91

NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]
Seq. No.	137618
Seq. ID	LIB146-022-Q1-E1-C2
Method	BLASTN
NCBI GI	g2702261
BLAST score	181
E value	2.0e-97
Match length	230
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T21L14 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	137619
Seq. ID	LIB146-022-Q1-E1-C4
Method	BLASTN
NCBI GI	g3859610
BLAST score	126
E value	6.0e-65
Match length	138
% identity	49
NCBI Description	Arabidopsis thaliana BAC T9E19
Seq. No.	137620
Seq. ID	LIB146-022-Q1-E1-E12
Method	BLASTX
NCBI GI	g2275201
BLAST score	365
E value	6.0e-35
Match length	81
% identity	88
NCBI Description	(AC002337) unknown protein [Arabidopsis thaliana]
Seq. No.	137621
Seq. ID	LIB146-022-Q1-E1-E5
Method	BLASTX
NCBI GI	g3738297
BLAST score	176
E value	4.0e-13
Match length	41
% identity	16
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]
Seq. No.	137622
Seq. ID	LIB146-022-Q1-E1-F5
Method	BLASTX
NCBI GI	g2618701
BLAST score	182
E value	1.0e-13
Match length	61
% identity	59
NCBI Description	(AC002510) hypothetical protein [Arabidopsis thaliana]

Seq. No.	137623
Seq. ID	LIB146-022-Q1-E1-H4
Method	BLASTX
NCBI GI	g3695382
BLAST score	335
E value	2.0e-31
Match length	127
% identity	58
NCBI Description	(AF096370) contains similarity to Arabidopsis thaliana retrotransposon Ta11-1 (GB:L47193) [Arabidopsis thaliana]

Seq. No.	137624
Seq. ID	LIB146-023-Q1-E1-C1
Method	BLASTX
NCBI GI	g4102600
BLAST score	201
E value	5.0e-16
Match length	54
% identity	74
NCBI Description	(AF013467) ARF6 [Arabidopsis thaliana]

Seq. No.	137625
Seq. ID	LIB146-023-Q1-E1-D1
Method	BLASTX
NCBI GI	g3249105
BLAST score	161
E value	3.0e-11
Match length	51
% identity	59
NCBI Description	(AC003114) Contains similarity to protein phosphatase 2C (ABI1) gb_X78886 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	137626
Seq. ID	LIB146-023-Q1-E1-D7
Method	BLASTN
NCBI GI	g3128136
BLAST score	143
E value	8.0e-75
Match length	207
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1F13, complete sequence [Arabidopsis thaliana]

Seq. No.	137627
Seq. ID	LIB146-023-Q1-E1-H8
Method	BLASTN
NCBI GI	g4220645
BLAST score	114
E value	9.0e-58
Match length	145
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYA6, complete sequence [Arabidopsis thaliana]

Seq. No.	137628
Seq. ID	LIB146-024-Q1-E1-A3
Method	BLASTX

NCBI GI	g112739
BLAST score	232
E value	7.0e-20
Match length	55
% identity	78
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	137629
Seq. ID	LIB146-024-Q1-E1-A7
Method	BLASTN
NCBI GI	g12212
BLAST score	116
E value	9.0e-59
Match length	164
% identity	93
NCBI Description	S.alba chloroplast rp123 and rp12 genes for ribosomal proteins L23 and L2

Seq. No.	137630
Seq. ID	LIB146-024-Q1-E1-A8
Method	BLASTN
NCBI GI	g4220643
BLAST score	123
E value	5.0e-63
Match length	191
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD22, complete sequence [Arabidopsis thaliana]

Seq. No.	137631
Seq. ID	LIB146-024-Q1-E1-C7
Method	BLASTN
NCBI GI	g2264305
BLAST score	96
E value	6.0e-47
Match length	180
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK23, complete sequence [Arabidopsis thaliana]

Seq. No.	137632
Seq. ID	LIB146-024-Q1-E1-G7
Method	BLASTN
NCBI GI	g4388816
BLAST score	43
E value	4.0e-15
Match length	149
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC F9B22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137633
Seq. ID	LIB146-024-Q1-E1-H10
Method	BLASTN
NCBI GI	g3420042
BLAST score	258
E value	1.0e-143
Match length	310
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T13E15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137634
Seq. ID	LIB146-025-Q1-E1-B5
Method	BLASTN
NCBI GI	g2351073
BLAST score	368
E value	0.0e+00
Match length	376
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	137635
Seq. ID	LIB146-025-Q1-E1-C1
Method	BLASTN
NCBI GI	g4589434
BLAST score	273
E value	1.0e-152
Match length	293
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNJ7, complete sequence

Seq. No.	137636
Seq. ID	LIB146-025-Q1-E1-C12
Method	BLASTX
NCBI GI	g3335216
BLAST score	256
E value	4.0e-22
Match length	62
% identity	82
NCBI Description	(AF074928) 1-aminocyclopropane-1-carboxylate synthase 2 [Sinapis arvensis]

Seq. No.	137637
Seq. ID	LIB146-025-Q1-E1-C3
Method	BLASTX
NCBI GI	g2642450
BLAST score	355
E value	8.0e-34
Match length	106
% identity	68
NCBI Description	(AC002391) putative metal ion transporter (Nramp) [Arabidopsis thaliana] >gi_3169188 (AC004401) putative metal ion transporter (Nramp) [Arabidopsis thaliana]

Seq. No.	137638

Seq. ID LIB146-025-Q1-E1-D4
Method BLASTN
NCBI GI g2760170
BLAST score 336
E value 0.0e+00
Match length 356
% identity 99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIO24, complete sequence [Arabidopsis thaliana]

Seq. No. 137639
Seq. ID LIB146-025-Q1-E1-E11
Method BLASTX
NCBI GI g3128169
BLAST score 83
E value 1.0e-09
Match length 82
% identity 50
NCBI Description (AC004521) hypothetical protein [Arabidopsis thaliana]

Seq. No. 137640
Seq. ID LIB146-025-Q1-E1-E12
Method BLASTN
NCBI GI g4558590
BLAST score 408
E value 0.0e+00
Match length 412
% identity 100
NCBI Description Arabidopsis thaliana chromosome II BAC T17C22 genomic sequence, complete sequence

Seq. No. 137641
Seq. ID LIB146-025-Q1-E1-H10
Method BLASTX
NCBI GI g112681
BLAST score 578
E value 8.0e-60
Match length 139
% identity 81
NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No. 137642
Seq. ID LIB146-025-Q1-E1-H11
Method BLASTX
NCBI GI g4377180
BLAST score 276
E value 8.0e-25
Match length 84
% identity 61
NCBI Description (AE001667) Phosphoglycerate Mutase [Chlamydia pneumoniae]

Seq. No. 137643
Seq. ID LIB146-025-Q1-E1-H12

Method	BLASTX
NCBI GI	g2924784
BLAST score	645
E value	1.0e-67
Match length	123
% identity	100
NCBI Description	(AC002334) similar to jasmonate inducible protein [Arabidopsis thaliana]

Seq. No.	137644
Seq. ID	LIB146-025-Q1-E1-H2
Method	BLASTN
NCBI GI	g4757662
BLAST score	356
E value	0.0e+00
Match length	360
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome I, complete sequence

Seq. No.	137645
Seq. ID	LIB146-025-Q1-E1-H7
Method	BLASTX
NCBI GI	g2244868
BLAST score	93
E value	1.0e-13
Match length	104
% identity	43
NCBI Description	(Z97337) cytochrome P450 [Arabidopsis thaliana]

Seq. No.	137646
Seq. ID	LIB146-026-Q1-K1-A10
Method	BLASTN
NCBI GI	g3805839
BLAST score	80
E value	5.0e-37
Match length	374
% identity	43
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4B14 (ESSAII project)

Seq. No.	137647
Seq. ID	LIB146-026-Q1-K1-A11
Method	BLASTN
NCBI GI	g3176693
BLAST score	142
E value	4.0e-74
Match length	333
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC T27I1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137648
Seq. ID	LIB146-026-Q1-K1-A12
Method	BLASTN
NCBI GI	g3643588
BLAST score	361

E value	0.0e+00
Match length	373
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F17H15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137649
Seq. ID	LIB146-026-Q1-K1-A2
Method	BLASTX
NCBI GI	g1076529
BLAST score	382
E value	7.0e-37
Match length	77
% identity	95
NCBI Description	heat shock protein HSP71.2 - garden pea >gi_562006 (U08848) PsHSP71.2 [Pisum sativum] >gi_1771479_emb_CAA67867_ (X99515) heat shock protein hsp70 [Pisum sativum]

Seq. No.	137650
Seq. ID	LIB146-026-Q1-K1-A4
Method	BLASTN
NCBI GI	g3659491
BLAST score	370
E value	0.0e+00
Match length	434
% identity	100
NCBI Description	Sequence of BAC T22H22 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	137651
Seq. ID	LIB146-026-Q1-K1-B11
Method	BLASTX
NCBI GI	g2642158
BLAST score	125
E value	1.0e-09
Match length	68
% identity	50
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	137652
Seq. ID	LIB146-026-Q1-K1-B3
Method	BLASTN
NCBI GI	g4757417
BLAST score	209
E value	1.0e-114
Match length	420
% identity	57
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: T30G6, complete sequence

Seq. No.	137653
Seq. ID	LIB146-026-Q1-K1-B5
Method	BLASTN
NCBI GI	g4589950
BLAST score	230
E value	1.0e-126
Match length	418

% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T28P16 genomic sequence, complete sequence

Seq. No.	137654
Seq. ID	LIB146-026-Q1-K1-B7
Method	BLASTN
NCBI GI	g11571
BLAST score	116
E value	7.0e-59
Match length	168
% identity	92
NCBI Description	Soybean chloroplast rps12 and rps7 genes

Seq. No.	137655
Seq. ID	LIB146-026-Q1-K1-B8
Method	BLASTX
NCBI GI	g4206210
BLAST score	714
E value	9.0e-76
Match length	142
% identity	63
NCBI Description	(AF071527) putative calcium channel [Arabidopsis thaliana] >gi_4263043_gb_AAD15312_ (AC005142) putative calcium channel [Arabidopsis thaliana]

Seq. No.	137656
Seq. ID	LIB146-026-Q1-K1-C12
Method	BLASTN
NCBI GI	g4581161
BLAST score	123
E value	1.0e-62
Match length	209
% identity	87
NCBI Description	Arabidopsis thaliana chromosome II BAC T20G20 genomic sequence, complete sequence

Seq. No.	137657
Seq. ID	LIB146-026-Q1-K1-C2
Method	BLASTX
NCBI GI	g3056598
BLAST score	293
E value	2.0e-26
Match length	60
% identity	93
NCBI Description	(AC004255) T1F9.19 [Arabidopsis thaliana]

Seq. No.	137658
Seq. ID	LIB146-026-Q1-K1-C9
Method	BLASTN
NCBI GI	g3985949
BLAST score	210
E value	1.0e-114
Match length	358
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOB24, complete sequence [Arabidopsis thaliana]

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Seq. No.	137659
Seq. ID	LIB146-026-Q1-K1-D1
Method	BLASTN
NCBI GI	g2760172
BLAST score	388
E value	0.0e+00
Match length	400
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUB3, complete sequence [Arabidopsis thaliana]

Seq. No.	137660
Seq. ID	LIB146-026-Q1-K1-E1
Method	BLASTX
NCBI GI	g3860247
BLAST score	720
E value	2.0e-76
Match length	140
% identity	96
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]

Seq. No.	137661
Seq. ID	LIB146-026-Q1-K1-E5
Method	BLASTX
NCBI GI	g3328240
BLAST score	307
E value	4.0e-28
Match length	106
% identity	51
NCBI Description	(AF064775) early nodule-specific protein [Medicago truncatula]

Seq. No.	137662
Seq. ID	LIB146-026-Q1-K1-E6
Method	BLASTX
NCBI GI	g2529229
BLAST score	549
E value	2.0e-56
Match length	117
% identity	90
NCBI Description	(AB007907) 6-phosphogluconate dehydrogenase [Glycine max]

Seq. No.	137663
Seq. ID	LIB146-026-Q1-K1-E7
Method	BLASTX
NCBI GI	g2980771
BLAST score	486
E value	4.0e-49
Match length	111
% identity	87
NCBI Description	(AL022198) chloroplast omega-6 fatty acid desaturase (fad6) [Arabidopsis thaliana]

Seq. No.	137664
Seq. ID	LIB146-026-Q1-K1-E9
Method	BLASTN

NCBI GI	g2570223
BLAST score	75
E value	1.0e-34
Match length	120
% identity	89
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F20D22 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137665
Seq. ID	LIB146-026-Q1-K1-F12
Method	BLASTN
NCBI GI	g2832639
BLAST score	56
E value	8.0e-23
Match length	128
% identity	86
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28J12 (ESSAII project)

Seq. No.	137666
Seq. ID	LIB146-026-Q1-K1-F7
Method	BLASTX
NCBI GI	g2062169
BLAST score	106
E value	1.0e-15
Match length	72
% identity	57
NCBI Description	(AC001645) ABC transporter (PDR5-like) isolog [Arabidopsis thaliana]

Seq. No.	137667
Seq. ID	LIB146-026-Q1-K1-G7
Method	BLASTX
NCBI GI	g4529972
BLAST score	581
E value	3.0e-60
Match length	140
% identity	86
NCBI Description	(AC002330) putative chloroplast outer envelope 86-like protein [Arabidopsis thaliana]

Seq. No.	137668
Seq. ID	LIB146-026-Q1-K1-H1
Method	BLASTX
NCBI GI	g1628583
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	137669
Seq. ID	LIB146-026-Q1-K1-H2
Method	BLASTX
NCBI GI	g4262216

BLAST score	658
E value	3.0e-69
Match length	128
% identity	98
NCBI Description	(AC006161) putative DNA binding protein [Arabidopsis thaliana]

Seq. No.	137670
Seq. ID	LIB146-026-Q1-K1-H6
Method	BLASTN
NCBI GI	g3243214
BLAST score	319
E value	1.0e-179
Match length	327
% identity	99
NCBI Description	Arabidopsis thaliana BAC T19B17 from chromsome IV, near 19.3 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	137671
Seq. ID	LIB146-027-Q1-K1-A2
Method	BLASTN
NCBI GI	g3928074
BLAST score	184
E value	5.0e-99
Match length	406
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T7F6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137672
Seq. ID	LIB146-027-Q1-K1-B5
Method	BLASTX
NCBI GI	g267055
BLAST score	387
E value	5.0e-38
Match length	75
% identity	99
NCBI Description	SUCROSE SYNTHASE (SUCROSE-UDP GLUCOSYLTRANSFERASE) >gi_66572_pir__YUMU sucrose synthase (EC 2.4.1.13) - Arabidopsis thaliana >gi_16526_emb_CAA43303_ (X60987) sucrose synthase [Arabidopsis thaliana]

Seq. No.	137673
Seq. ID	LIB146-027-Q1-K1-D2
Method	BLASTX
NCBI GI	g4115379
BLAST score	141
E value	8.0e-09
Match length	42
% identity	69
NCBI Description	(AC005967) putative carbonyl reductase [Arabidopsis thaliana]

Seq. No.	137674
Seq. ID	LIB146-027-Q1-K1-D8
Method	BLASTX
NCBI GI	g1173151

BLAST score	300
E value	9.0e-28
Match length	65
% identity	89
NCBI Description	DNA-DIRECTED RNA POLYMERASE BETA CHAIN >gi_629607_pir__S48842 DNA-directed RNA polymerase (EC 2.7.7.6) beta chain - white mustard chloroplast >gi_563343_emb_CAA57814_ (X82417) RNA polymerase subunit beta [Sinapis alba]

Seq. No.	137675
Seq. ID	LIB146-027-Q1-K1-G3
Method	BLASTX
NCBI GI	g3080389
BLAST score	234
E value	2.0e-19
Match length	116
% identity	47
NCBI Description	(AL022603) putative membrane associated protein [Arabidopsis thaliana]

Seq. No.	137676
Seq. ID	LIB146-027-Q1-K1-G4
Method	BLASTX
NCBI GI	g4678299
BLAST score	560
E value	6.0e-58
Match length	110
% identity	96
NCBI Description	(AL049655) cysteine proteinase precursor-like protein [Arabidopsis thaliana]

Seq. No.	137677
Seq. ID	LIB146-027-Q1-K1-H3
Method	BLASTN
NCBI GI	g4455262
BLAST score	190
E value	1.0e-102
Match length	356
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22 (ESSAII project)

Seq. No.	137678
Seq. ID	LIB146-027-Q1-K1-H5
Method	BLASTN
NCBI GI	g3299824
BLAST score	324
E value	0.0e+00
Match length	352
% identity	97
NCBI Description	Arabidopsis thaliana BAC F4C21 from chromosome IV, top arm, near 17 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	137679
Seq. ID	LIB146-029-Q1-K1-A3
Method	BLASTX

NCBI GI	g4559342
BLAST score	181
E value	2.0e-13
Match length	37
% identity	92
NCBI Description	(AC007087) putative copper methylamine oxidase [Arabidopsis thaliana]

Seq. No.	137680
Seq. ID	LIB146-029-Q1-K1-A8
Method	BLASTN
NCBI GI	g4432793
BLAST score	314
E value	1.0e-176
Match length	370
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC T19K21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137681
Seq. ID	LIB146-029-Q1-K1-B2
Method	BLASTN
NCBI GI	g3135250
BLAST score	121
E value	5.0e-62
Match length	121
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F27F23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137682
Seq. ID	LIB146-029-Q1-K1-D11
Method	BLASTN
NCBI GI	g4539331
BLAST score	157
E value	5.0e-83
Match length	306
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22I13 (ESSA project)

Seq. No.	137683
Seq. ID	LIB146-029-Q1-K1-D7
Method	BLASTN
NCBI GI	g4432793
BLAST score	165
E value	7.0e-88
Match length	277
% identity	75
NCBI Description	Arabidopsis thaliana chromosome II BAC T19K21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137684
Seq. ID	LIB146-029-Q1-K1-E1
Method	BLASTX
NCBI GI	g4580462
BLAST score	237

E value	5.0e-20
Match length	109
% identity	55
NCBI Description	(AC006081) hypothetical protein [Arabidopsis thaliana]

Seq. No.	137685
Seq. ID	LIB146-029-Q1-K1-E10
Method	BLASTN
NCBI GI	g4678291
BLAST score	272
E value	1.0e-151
Match length	299
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F28P10 (ESSA project)

Seq. No.	137686
Seq. ID	LIB146-029-Q1-K1-E3
Method	BLASTN
NCBI GI	g2815519
BLAST score	157
E value	3.0e-83
Match length	178
% identity	77
NCBI Description	Arabidopsis thaliana BAC T5J8 from chromosome IV, top arm, complete sequence [Arabidopsis thaliana]

Seq. No.	137687
Seq. ID	LIB146-029-Q1-K1-E6
Method	BLASTX
NCBI GI	g1170247
BLAST score	199
E value	2.0e-15
Match length	43
% identity	91
NCBI Description	HEVEIN-LIKE PROTEIN PRECURSOR >gi_407248 (U01880) pre-hevein-like protein [Arabidopsis thaliana]

Seq. No.	137688
Seq. ID	LIB146-029-Q1-K1-E7
Method	BLASTN
NCBI GI	g4512656
BLAST score	204
E value	1.0e-111
Match length	204
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	137689
Seq. ID	LIB146-029-Q1-K1-F11
Method	BLASTX
NCBI GI	g3548806
BLAST score	150
E value	3.0e-10
Match length	63
% identity	52

NCBI Description	(AC005313) unknown protein [Arabidopsis thaliana]

Seq. No.	137690
Seq. ID	LIB146-029-Q1-K1-F4
Method	BLASTX
NCBI GI	g1723643
BLAST score	155
E value	4.0e-17
Match length	109
% identity	43
NCBI Description	HYPOTHETICAL 44.9 KD PROTEIN IN SEC9-MSB2 INTERGENIC REGION >gi_2132582_pir__S64299 probable membrane protein YGR010w - yeast (Saccharomyces cerevisiae) >gi_1322971_emb_CAA96993_ (Z72795) ORF YGR010w [Saccharomyces cerevisiae]

Seq. No.	137691
Seq. ID	LIB146-029-Q1-K1-G1
Method	BLASTN
NCBI GI	g3869072
BLAST score	256
E value	1.0e-142
Match length	346
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJB24, complete sequence [Arabidopsis thaliana]

Seq. No.	137692
Seq. ID	LIB146-029-Q1-K1-G12
Method	BLASTN
NCBI GI	g3193305
BLAST score	126
E value	6.0e-65
Match length	134
% identity	99
NCBI Description	Arabidopsis thaliana BAC F3D13

Seq. No.	137693
Seq. ID	LIB146-029-Q1-K1-H5
Method	BLASTX
NCBI GI	g3033400
BLAST score	430
E value	1.0e-42
Match length	118
% identity	71
NCBI Description	(AC004238) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No.	137694
Seq. ID	LIB146-029-Q1-K1-H7
Method	BLASTN
NCBI GI	g4699904
BLAST score	131
E value	1.0e-67
Match length	261
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F1E22, complete sequence

Seq. No.	137695
Seq. ID	LIB146-030-Q1-K1-A5
Method	BLASTN
NCBI GI	g4335744
BLAST score	353
E value	0.0e+00
Match length	426
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T4M8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137696
Seq. ID	LIB146-030-Q1-K1-A8
Method	BLASTX
NCBI GI	g3172044
BLAST score	241
E value	6.0e-21
Match length	54
% identity	91
NCBI Description	(AB010080) aldehyde oxidase [Arabidopsis thaliana]

Seq. No.	137697
Seq. ID	LIB146-030-Q1-K1-B4
Method	BLASTN
NCBI GI	g432445
BLAST score	346
E value	0.0e+00
Match length	374
% identity	98
NCBI Description	Arabidopsis thaliana (FUS6) gene, complete cds

Seq. No.	137698
Seq. ID	LIB146-030-Q1-K1-B6
Method	BLASTX
NCBI GI	g3335378
BLAST score	277
E value	1.0e-24
Match length	109
% identity	51
NCBI Description	(AC003028) Myb-related transcription activator [Arabidopsis thaliana]

Seq. No.	137699
Seq. ID	LIB146-030-Q1-K1-C5
Method	BLASTN
NCBI GI	g4388714
BLAST score	292
E value	1.0e-163
Match length	392
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F5K7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137700
Seq. ID	LIB146-030-Q1-K1-C7
Method	BLASTX

NCBI GI	g3695399
BLAST score	486
E value	4.0e-49
Match length	96
% identity	94
NCBI Description	(AF096372) contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801) [Arabidopsis thaliana]

Seq. No.	137701
Seq. ID	LIB146-030-Q1-K1-D10
Method	BLASTN
NCBI GI	g4063735
BLAST score	84
E value	1.0e-39
Match length	159
% identity	93
NCBI Description	Arabidopsis thaliana BAC F18G18 from chromosome V near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	137702
Seq. ID	LIB146-030-Q1-K1-D11
Method	BLASTX
NCBI GI	g4309698
BLAST score	474
E value	9.0e-48
Match length	118
% identity	81
NCBI Description	(AC006266) putative glucosyltransferase [Arabidopsis thaliana]

Seq. No.	137703
Seq. ID	LIB146-030-Q1-K1-E1
Method	BLASTX
NCBI GI	g3184275
BLAST score	222
E value	1.0e-18
Match length	42
% identity	98
NCBI Description	(AC004136) hypothetical protein [Arabidopsis thaliana]

Seq. No.	137704
Seq. ID	LIB146-030-Q1-K1-E8
Method	BLASTN
NCBI GI	g4191771
BLAST score	404
E value	0.0e+00
Match length	412
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F3P11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137705
Seq. ID	LIB146-030-Q1-K1-F1
Method	BLASTN
NCBI GI	g2760172
BLAST score	328
E value	0.0e+00

Match length	336
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUB3, complete sequence [Arabidopsis thaliana]

Seq. No.	137706
Seq. ID	LIB146-030-Q1-K1-G10
Method	BLASTN
NCBI GI	g3004543
BLAST score	168
E value	2.0e-89
Match length	415
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F19F24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137707
Seq. ID	LIB146-030-Q1-K1-G3
Method	BLASTN
NCBI GI	g3831437
BLAST score	337
E value	0.0e+00
Match length	365
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T3A4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137708
Seq. ID	LIB146-030-Q1-K1-G8
Method	BLASTN
NCBI GI	g4755185
BLAST score	206
E value	1.0e-112
Match length	234
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F5G3 genomic sequence, complete sequence

Seq. No.	137709
Seq. ID	LIB146-030-Q1-K1-H11
Method	BLASTN
NCBI GI	g3241916
BLAST score	305
E value	1.0e-171
Match length	402
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15N18, complete sequence [Arabidopsis thaliana]

Seq. No.	137710
Seq. ID	LIB146-030-Q1-K1-H7
Method	BLASTX
NCBI GI	g3738316
BLAST score	368
E value	3.0e-35
Match length	102
% identity	69

NCBI Description	(AC005170) unknown protein [Arabidopsis thaliana]
Seq. No.	137711
Seq. ID	LIB22-001-Q1-E1-C5
Method	BLASTX
NCBI GI	g2047324
BLAST score	485
E value	4.0e-49
Match length	92
% identity	100
NCBI Description	(U80192) HAL3 homolog [Arabidopsis thaliana]
Seq. No.	137712
Seq. ID	LIB22-001-Q1-E1-C6
Method	BLASTN
NCBI GI	g3985955
BLAST score	347
E value	0.0e+00
Match length	384
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTH16, complete sequence [Arabidopsis thaliana]
Seq. No.	137713
Seq. ID	LIB22-001-Q1-E1-C8
Method	BLASTN
NCBI GI	g2827140
BLAST score	170
E value	1.0e-90
Match length	170
% identity	100
NCBI Description	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds
Seq. No.	137714
Seq. ID	LIB22-001-Q1-E1-D7
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1
Seq. No.	137715
Seq. ID	LIB22-001-Q1-E1-E6
Method	BLASTN
NCBI GI	g2160155
BLAST score	397
E value	0.0e+00
Match length	397
% identity	100
NCBI Description	Sequence of BAC F21M12 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]
Seq. No.	137716
Seq. ID	LIB22-001-Q1-E1-F2

Method	BLASTX
NCBI GI	g1491615
BLAST score	459
E value	5.0e-46
Match length	121
% identity	69
NCBI Description	(X99923) male sterility 2-like protein [Arabidopsis thaliana]

Seq. No.	137717
Seq. ID	LIB22-001-Q1-E1-G1
Method	BLASTX
NCBI GI	g4033469
BLAST score	170
E value	3.0e-12
Match length	36
% identity	86
NCBI Description	ARGININE/SERINE-RICH SPLICING FACTOR RSP41 >gi_1707370_emb_CAA67799_ (X99436) splicing factor [Arabidopsis thaliana]

Seq. No.	137718
Seq. ID	LIB22-001-Q1-E1-G3
Method	BLASTN
NCBI GI	g2760168
BLAST score	350
E value	0.0e+00
Match length	350
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MEE6, complete sequence [Arabidopsis thaliana]

Seq. No.	137719
Seq. ID	LIB22-001-Q1-E1-G6
Method	BLASTN
NCBI GI	g4587582
BLAST score	431
E value	0.0e+00
Match length	431
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T16B14 genomic sequence, complete sequence

Seq. No.	137720
Seq. ID	LIB22-001-Q1-E1-G7
Method	BLASTX
NCBI GI	g4757762
BLAST score	184
E value	1.0e-13
Match length	126
% identity	29
NCBI Description	androgen receptor associated protein 54 >gi_4530066_gb_AAD21842.1_ (AF060544) androgen receptor associated protein 54 [Homo sapiens]

Seq. No.	137721
Seq. ID	LIB22-002-Q1-E1-A10

Method	BLASTX
NCBI GI	g4210330
BLAST score	595
E value	7.0e-62
Match length	126
% identity	87
NCBI Description	(AJ223802) 2-oxoglutarate dehydrogenase, E1 subunit [Arabidopsis thaliana]

Seq. No.	137722
Seq. ID	LIB22-002-Q1-E1-B2
Method	BLASTN
NCBI GI	g4589433
BLAST score	379
E value	0.0e+00
Match length	379
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNI5, complete sequence

Seq. No.	137723
Seq. ID	LIB22-002-Q1-E1-B9
Method	BLASTX
NCBI GI	g2245060
BLAST score	368
E value	2.0e-35
Match length	76
% identity	99
NCBI Description	(Z97342) allergen homolog [Arabidopsis thaliana]

Seq. No.	137724
Seq. ID	LIB22-002-Q1-E1-C5
Method	BLASTN
NCBI GI	g3702731
BLAST score	34
E value	7.0e-10
Match length	170
% identity	80
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFC19, complete sequence [Arabidopsis thaliana]

Seq. No.	137725
Seq. ID	LIB22-002-Q1-E1-D1
Method	BLASTN
NCBI GI	g4732164
BLAST score	82
E value	3.0e-38
Match length	175
% identity	91
NCBI Description	Arabidopsis thaliana BAC F10A2

Seq. No.	137726
Seq. ID	LIB22-002-Q1-E1-D3
Method	BLASTX
NCBI GI	g401213
BLAST score	585
E value	8.0e-61

Match length	116
% identity	100
NCBI Description	ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE PRECURSOR >gi_166792 (M96073) phosphoribosylanthranilate transferase [Arabidopsis thaliana] >gi_445600_prf__1909347A phosphoribosylanthranilate transferase [Arabidopsis thaliana]

Seq. No.	137727
Seq. ID	LIB22-002-Q1-E1-D4
Method	BLASTX
NCBI GI	g4371296
BLAST score	460
E value	3.0e-46
Match length	90
% identity	99
NCBI Description	(AC006260) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	137728
Seq. ID	LIB22-002-Q1-E1-D6
Method	BLASTX
NCBI GI	g1279640
BLAST score	338
E value	1.0e-31
Match length	88
% identity	73
NCBI Description	(X92204) NAM [Petunia x hybrida]

Seq. No.	137729
Seq. ID	LIB22-002-Q1-E1-E10
Method	BLASTX
NCBI GI	g2244910
BLAST score	159
E value	7.0e-11
Match length	108
% identity	35
NCBI Description	(Z97339) unnamed protein product [Arabidopsis thaliana]

Seq. No.	137730
Seq. ID	LIB22-002-Q1-E1-E12
Method	BLASTN
NCBI GI	g2832639
BLAST score	303
E value	1.0e-170
Match length	401
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28J12 (ESSAII project)

Seq. No.	137731
Seq. ID	LIB22-002-Q1-E1-E2
Method	BLASTN
NCBI GI	g3869071
BLAST score	134
E value	1.0e-69
Match length	190

% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MIL23, complete sequence [Arabidopsis thaliana]

Seq. No.	137732
Seq. ID	LIB22-002-Q1-E1-E5
Method	BLASTX
NCBI GI	g603074
BLAST score	360
E value	2.0e-34
Match length	110
% identity	60
NCBI Description	(U18197) ATP:citrate lyase [Homo sapiens]

Seq. No.	137733
Seq. ID	LIB22-002-Q1-E1-E9
Method	BLASTX
NCBI GI	g3258573
BLAST score	245
E value	7.0e-21
Match length	92
% identity	53
NCBI Description	(U89959) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	137734
Seq. ID	LIB22-002-Q1-E1-F12
Method	BLASTN
NCBI GI	g3869066
BLAST score	79
E value	1.0e-36
Match length	246
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBM17, complete sequence [Arabidopsis thaliana]

Seq. No.	137735
Seq. ID	LIB22-002-Q1-E1-F5
Method	BLASTN
NCBI GI	g4314374
BLAST score	398
E value	0.0e+00
Match length	398
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137736
Seq. ID	LIB22-002-Q1-E1-F6
Method	BLASTX
NCBI GI	g1684913
BLAST score	344
E value	1.0e-32
Match length	107
% identity	62
NCBI Description	(U77888) receptor-like protein kinase [Ipomoea nil]

Seq. No. 137737

Seq. ID	LIB22-002-Q1-E1-G12
Method	BLASTX
NCBI GI	g681904
BLAST score	455
E value	2.0e-45
Match length	106
% identity	86
NCBI Description	(D31711) cp29 [Arabidopsis thaliana]

Seq. No.	137738
Seq. ID	LIB22-002-Q1-E1-G8
Method	BLASTN
NCBI GI	g2264311
BLAST score	189
E value	1.0e-102
Match length	322
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLN1, complete sequence [Arabidopsis thaliana]

Seq. No.	137739
Seq. ID	LIB22-002-Q1-E1-H2
Method	BLASTX
NCBI GI	g2832641
BLAST score	501
E value	5.0e-51
Match length	100
% identity	99
NCBI Description	(AL021710) glycolate oxidase - like protein [Arabidopsis thaliana]

Seq. No.	137740
Seq. ID	LIB22-002-Q1-E1-H6
Method	BLASTN
NCBI GI	g4589438
BLAST score	387
E value	0.0e+00
Match length	391
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQJ2, complete sequence

Seq. No.	137741
Seq. ID	LIB22-002-Q1-E1-H7
Method	BLASTX
NCBI GI	g4138282
BLAST score	307
E value	5.0e-28
Match length	118
% identity	56
NCBI Description	(AJ011576) RNA-directed RNA polymerase [Nicotiana tabacum]

Seq. No.	137742
Seq. ID	LIB22-003-Q1-E1-B11
Method	BLASTX
NCBI GI	g4006865
BLAST score	297

E value 2.0e-27
Match length 67
% identity 85
NCBI Description (Z99707) putative protein [Arabidopsis thaliana]

Seq. No. 137743
Seq. ID LIB22-003-Q1-E1-B12
Method BLASTN
NCBI GI g2252823
BLAST score 127
E value 3.0e-65
Match length 230
% identity 99
NCBI Description Arabidopsis thaliana BAC IG005I10

Seq. No. 137744
Seq. ID LIB22-003-Q1-E1-B5
Method BLASTX
NCBI GI g2244863
BLAST score 209
E value 1.0e-16
Match length 47
% identity 81
NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No. I37745
Seq. ID LIB22-003-Q1-E1-C3
Method BLASTX
NCBI GI g3540207
BLAST score 512
E value 3.0e-52
Match length 126
% identity 87
NCBI Description (AC004260) Putative protein kinase [Arabidopsis thaliana]

Seq. No. 137746
Seq. ID LIB22-003-Q1-E1-C4
Method BLASTN
NCBI GI g2182287
BLAST score 200
E value 1.0e-109
Match length 227
% identity 97
NCBI Description Genomic sequence for Arabidopsis thaliana BAC T7N9, complete sequence [Arabidopsis thaliana]

Seq. No. 137747
Seq. ID LIB22-003-Q1-E1-D11
Method BLASTX
NCBI GI g2738248
BLAST score 158
E value 1.0e-10
Match length 101
% identity 75
NCBI Description (U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No.	137748
Seq. ID	LIB22-003-Q1-E1-F11
Method	BLASTX
NCBI GI	g2191131
BLAST score	445
E value	1.0e-44
Match length	93
% identity	86
NCBI Description	(AF007269) A_IG002N01.8 gene product [Arabidopsis thaliana]

Seq. No.	137749
Seq. ID	LIB22-003-Q1-E1-F12
Method	BLASTN
NCBI GI	g4490291
BLAST score	270
E value	1.0e-150
Match length	273
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17M5 (ESSA project)

Seq. No.	137750
Seq. ID	LIB22-003-Q1-E1-G7
Method	BLASTX
NCBI GI	g1169128
BLAST score	412
E value	1.0e-40
Match length	90
% identity	90
NCBI Description	SERINE/THREONINE-PROTEIN KINASE CTR1 >gi_166680 (L08789) protein kinase [Arabidopsis thaliana] >gi_166682 (L08790) protein kinase [Arabidopsis thaliana]

Seq. No.	137751
Seq. ID	LIB22-003-Q1-E1-G8
Method	BLASTN
NCBI GI	g4263694
BLAST score	241
E value	1.0e-133
Match length	241
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F22D22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137752
Seq. ID	LIB22-003-Q1-E1-H3
Method	BLASTN
NCBI GI	g3241917
BLAST score	172
E value	4.0e-92
Match length	224
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19B1, complete sequence [Arabidopsis thaliana]

Seq. No.	137753
Seq. ID	LIB22-003-Q1-E1-H7

Method	BLASTX
NCBI GI	g4630748
BLAST score	388
E value	5.0e-38
Match length	81
% identity	93
NCBI Description	(AC007236) putative anion exchange protein 3 [Arabidopsis thaliana]

Seq. No.	137754
Seq. ID	LIB22-004-Q1-E1-A10
Method	BLASTX
NCBI GI	g3184258
BLAST score	183
E value	1.0e-13
Match length	80
% identity	41
NCBI Description	(U82130) tumor susceptibility protein [Homo sapiens]

Seq. No.	137755
Seq. ID	LIB22-004-Q1-E1-B7
Method	BLASTN
NCBI GI	g3299824
BLAST score	251
E value	1.0e-139
Match length	338
% identity	100
NCBI Description	Arabidopsis thaliana BAC F4C21 from chromosome IV, top arm, near 17 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	137756
Seq. ID	LIB22-004-Q1-E1-B8
Method	BLASTX
NCBI GI	g2702281
BLAST score	469
E value	3.0e-47
Match length	104
% identity	86
NCBI Description	(AC003033) putative protein disulfide isomerase precursor [Arabidopsis thaliana]

Seq. No.	137757
Seq. ID	LIB22-004-Q1-E1-B9
Method	BLASTX
NCBI GI	g3776005
BLAST score	614
E value	4.0e-64
Match length	135
% identity	90
NCBI Description	(AJ010466) RNA helicase [Arabidopsis thaliana]

Seq. No.	137758
Seq. ID	LIB22-004-Q1-E1-C11
Method	BLASTN
NCBI GI	g4589950
BLAST score	331
E value	0.0e+00

Match length	408
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T28P16 genomic sequence, complete sequence

Seq. No.	137759
Seq. ID	LIB22-004-Q1-E1-C2
Method	BLASTX
NCBI GI	g3193284
BLAST score	213
E value	5.0e-17
Match length	90
% identity	46
NCBI Description	(AF069298) No definition line found [Arabidopsis thaliana]

Seq. No.	137760
Seq. ID	LIB22-004-Q1-E1-C3
Method	BLASTX
NCBI GI	g4406780
BLAST score	407
E value	7.0e-40
Match length	116
% identity	69
NCBI Description	(AC006532) putative multispanning membrane protein [Arabidopsis thaliana]

Seq. No.	137761
Seq. ID	LIB22-004-Q1-E1-C5
Method	BLASTX
NCBI GI	g2961356
BLAST score	530
E value	3.0e-54
Match length	122
% identity	78
NCBI Description	(AL022140) alcohol dehydrogenase like protein [Arabidopsis thaliana]

Seq. No.	137762
Seq. ID	LIB22-004-Q1-E1-C7
Method	BLASTX
NCBI GI	g3056594
BLAST score	693
E value	2.0e-73
Match length	124
% identity	100
NCBI Description	(AC004255) T1F9.15 [Arabidopsis thaliana]

Seq. No.	137763
Seq. ID	LIB22-004-Q1-E1-D10
Method	BLASTX
NCBI GI	g4580469
BLAST score	438
E value	2.0e-43
Match length	102
% identity	82
NCBI Description	(AC006081) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	137764
Seq. ID	LIB22-004-Q1-E1-D12
Method	BLASTN
NCBI GI	g2281632
BLAST score	46
E value	1.0e-16
Match length	46
% identity	100
NCBI Description	Arabidopsis thaliana AP2 domain containing protein RAP2.4 mRNA, partial cds

Seq. No.	137765
Seq. ID	LIB22-004-Q1-E1-E10
Method	BLASTX
NCBI GI	g1546698
BLAST score	697
E value	8.0e-74
Match length	136
% identity	100
NCBI Description	(X98808) peroxidase ATP3a [Arabidopsis thaliana]

Seq. No.	137766
Seq. ID	LIB22-004-Q1-E1-F2
Method	BLASTN
NCBI GI	g2182287
BLAST score	407
E value	0.0e+00
Match length	407
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T7N9, complete sequence [Arabidopsis thaliana]

Seq. No.	137767
Seq. ID	LIB22-004-Q1-E1-F5
Method	BLASTX
NCBI GI	g2688828
BLAST score	123
E value	7.0e-26
Match length	132
% identity	47
NCBI Description	(U97530) ethylene-forming-enzyme-like dioxygenase [Prunus armeniaca]

Seq. No.	137768
Seq. ID	LIB22-004-Q1-E1-G12
Method	BLASTN
NCBI GI	g3434972
BLAST score	159
E value	2.0e-84
Match length	197
% identity	100
NCBI Description	Arabidopsis thaliana AtERF-4 mRNA for ethylene responsive element binding factor 4, complete cds

Seq. No.	137769
Seq. ID	LIB22-005-Q1-E1-A7

Method	BLASTX
NCBI GI	g1490554
BLAST score	636
E value	1.0e-66
Match length	141
% identity	91
NCBI Description	(U63633) S-adenosylmethionine decarboxylase [Arabidopsis thaliana]

Seq. No.	137770
Seq. ID	LIB22-005-Q1-E1-B11
Method	BLASTN
NCBI GI	g4454022
BLAST score	65
E value	1.0e-28
Match length	97
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16 (ESSAII project)

Seq. No.	137771
Seq. ID	LIB22-005-Q1-E1-B3
Method	BLASTX
NCBI GI	g4680659
BLAST score	222
E value	4.0e-18
Match length	104
% identity	41
NCBI Description	(AF132944) CGI-10 protein [Homo sapiens]

Seq. No.	137772
Seq. ID	LIB22-005-Q1-E1-C10
Method	BLASTX
NCBI GI	g3600030
BLAST score	330
E value	9.0e-31
Match length	104
% identity	62
NCBI Description	(AF080119) contains similarity to ankyrin repeats (Pfam: ank.hmm, score: 13.93, 14.93 and 27.78) [Arabidopsis thaliana]

Seq. No.	137773
Seq. ID	LIB22-005-Q1-E1-C8
Method	BLASTX
NCBI GI	g4432830
BLAST score	239
E value	1.0e-20
Match length	59
% identity	85
NCBI Description	(AC006283) similar to pheromone receptor deficient mutant [Arabidopsis thaliana]

Seq. No.	137774
Seq. ID	LIB22-005-Q1-E1-C9
Method	BLASTN
NCBI GI	g2924729

BLAST score	358
E value	0.0e+00
Match length	358
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNA5, complete sequence [Arabidopsis thaliana]

Seq. No.	137775
Seq. ID	LIB22-005-Q1-E1-D2
Method	BLASTN
NCBI GI	g2979540
BLAST score	148
E value	1.0e-77
Match length	357
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F17K2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137776
Seq. ID	LIB22-005-Q1-E1-D8
Method	BLASTN
NCBI GI	g4757678
BLAST score	85
E value	3.0e-40
Match length	216
% identity	92
NCBI Description	Arabidopsis thaliana chromosome I BAC F9H16 genomic sequence, complete sequence

Seq. No.	137777
Seq. ID	LIB22-005-Q1-E1-F4
Method	BLASTN
NCBI GI	g4096078
BLAST score	245
E value	1.0e-135
Match length	378
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC T5A14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137778
Seq. ID	LIB22-005-Q1-E1-G1
Method	BLASTX
NCBI GI	g231586
BLAST score	210
E value	6.0e-17
Match length	101
% identity	54
NCBI Description	ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR >gi_82027_pir__S20504 H+-transporting ATP synthase (EC 3.6.1.34) beta chain, mitochondrial - Para rubber tree >gi_18831_emb_CAA41401_ (X58498) mitochondrial ATP synthase beta-subunit [Hevea brasiliensis]

Seq. No.	137779
Seq. ID	LIB22-005-Q1-E1-G12
Method	BLASTX

NCBI GI	g4539452
BLAST score	364
E value	8.0e-35
Match length	125
% identity	54
NCBI Description	(AL049500) putative phosphoribosylanthranilate transferase [Arabidopsis thaliana]

Seq. No.	137780
Seq. ID	LIB22-005-Q1-E1-G3
Method	BLASTN
NCBI GI	g4586098
BLAST score	283
E value	1.0e-158
Match length	304
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F16J13 (ESSA project)

Seq. No.	137781
Seq. ID	LIB22-005-Q1-E1-G4
Method	BLASTX
NCBI GI	g2244946
BLAST score	505
E value	1.0e-51
Match length	99
% identity	100
NCBI Description	(Z97339) unnamed protein product [Arabidopsis thaliana] >gi_2326344_emb_CAA72072_ (Y11187) G14587-6 [Arabidopsis thaliana]

Seq. No.	137782
Seq. ID	LIB22-005-Q1-E1-H6
Method	BLASTN
NCBI GI	g2749918
BLAST score	268
E value	1.0e-149
Match length	343
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC F3I6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137783
Seq. ID	LIB22-006-Q1-E1-A1
Method	BLASTX
NCBI GI	g3337361
BLAST score	166
E value	7.0e-12
Match length	59
% identity	49
NCBI Description	(AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	137784
Seq. ID	LIB22-006-Q1-E1-A7
Method	BLASTN
NCBI GI	g3766106
BLAST score	59

E value	1.0e-24
Match length	226
% identity	94
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F9K20 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137785
Seq. ID	LIB22-006-Q1-E1-B8
Method	BLASTN
NCBI GI	g3399678
BLAST score	137
E value	2.0e-71
Match length	189
% identity	94
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F13M7 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137786
Seq. ID	LIB22-006-Q1-E1-C4
Method	BLASTN
NCBI GI	g2245126
BLAST score	300
E value	1.0e-168
Match length	338
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	137787
Seq. ID	LIB22-006-Q1-E1-C8
Method	BLASTX
NCBI GI	g4454043
BLAST score	171
E value	3.0e-12
Match length	70
% identity	44
NCBI Description	(AL035394) putative receptor kinase [Arabidopsis thaliana]

Seq. No.	137788
Seq. ID	LIB22-006-Q1-E1-D10
Method	BLASTX
NCBI GI	g3334441
BLAST score	343
E value	2.0e-32
Match length	116
% identity	34
NCBI Description	HYPOTHETICAL 47.9 KD PROTEIN T5I7.9 IN CHROMOSOME II >gi_2642161 (AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	137789
Seq. ID	LIB22-006-Q1-E1-D2
Method	BLASTX
NCBI GI	g3377813
BLAST score	254
E value	6.0e-22
Match length	56

% identity	71
NCBI Description	(AF076275) No definition line found [Arabidopsis thaliana]

Seq. No.	137790
Seq. ID	LIB22-006-Q1-E1-E12
Method	BLASTN
NCBI GI	g2618683
BLAST score	281
E value	1.0e-157
Match length	410
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T32G6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137791
Seq. ID	LIB22-006-Q1-E1-F12
Method	BLASTN
NCBI GI	g487790
BLAST score	138
E value	1.0e-71
Match length	178
% identity	94
NCBI Description	Arabidopsis thaliana GF14omega isoform (GRF2) gene, complete cds

Seq. No.	137792
Seq. ID	LIB22-006-Q1-E1-G10
Method	BLASTX
NCBI GI	g2811066
BLAST score	255
E value	3.0e-22
Match length	95
% identity	47
NCBI Description	PUTATIVE PROTEIN-TYROSINE PHOSPHATASE PTEN (MUTATED IN MULTIPLE ADVANCED CANCERS 1) >gi_1916330 (U92437) MMAC1 [Mus musculus]

Seq. No.	137793
Seq. ID	LIB22-006-Q1-E1-G11
Method	BLASTX
NCBI GI	g2980773
BLAST score	623
E value	3.0e-65
Match length	129
% identity	73
NCBI Description	(AL022198) putative protein [Arabidopsis thaliana]

Seq. No.	137794
Seq. ID	LIB22-006-Q1-E1-H4
Method	BLASTX
NCBI GI	g4581132
BLAST score	258
E value	2.0e-22
Match length	86
% identity	64
NCBI Description	(AC005825) hypothetical protein [Arabidopsis thaliana]

Seq. No.	137795
Seq. ID	LIB22-007-Q1-E1-A12
Method	BLASTX
NCBI GI	g2911082
BLAST score	428
E value	2.0e-42
Match length	100
% identity	56
NCBI Description	(AL021960) hypothetical protein [Arabidopsis thaliana]

Seq. No.	137796
Seq. ID	LIB22-007-Q1-E1-A6
Method	BLASTX
NCBI GI	g4455750
BLAST score	175
E value	1.0e-12
Match length	111
% identity	36
NCBI Description	(AL035478) putative dehydrogenase [Streptomyces coelicolor]

Seq. No.	137797
Seq. ID	LIB22-007-Q1-E1-B2
Method	BLASTX
NCBI GI	g1335862
BLAST score	186
E value	2.0e-14
Match length	42
% identity	83
NCBI Description	(U42608) clathrin heavy chain [Glycine max]

Seq. No.	137798
Seq. ID	LIB22-007-Q1-E1-C12
Method	BLASTN
NCBI GI	g4586241
BLAST score	80
E value	3.0e-37
Match length	236
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T20K18 (ESSA project)

Seq. No.	137799
Seq. ID	LIB22-007-Q1-E1-C3
Method	BLASTX
NCBI GI	g2062169
BLAST score	85
E value	4.4e-02
Match length	88
% identity	37
NCBI Description	(AC001645) ABC transporter (PDR5-like) isolog [Arabidopsis thaliana]

Seq. No.	137800
Seq. ID	LIB22-007-Q1-E1-C9
Method	BLASTX
NCBI GI	g2244750
BLAST score	581

09604746 "09604746"

E value	3.0e-60
Match length	124
% identity	89
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	137801
Seq. ID	LIB22-007-Q1-E1-E10
Method	BLASTX
NCBI GI	g2498731
BLAST score	448
E value	1.0e-44
Match length	126
% identity	67
NCBI Description	PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1 >gi_1362013_pir__S57611 zeta-crystallin homolog - Arabidopsis thaliana >gi_886428_emb_CAA89838_ (Z49768) zeta-crystallin homologue [Arabidopsis thaliana]

Seq. No.	137802
Seq. ID	LIB22-007-Q1-E1-F10
Method	BLASTN
NCBI GI	g4263586
BLAST score	342
E value	0.0e+00
Match length	342
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F28K20 sequence, complete sequence

Seq. No.	137803
Seq. ID	LIB22-007-Q1-E1-G12
Method	BLASTN
NCBI GI	g4539378
BLAST score	145
E value	4.0e-76
Match length	189
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28A21 (ESSA project)

Seq. No.	137804
Seq. ID	LIB22-007-Q1-E1-G7
Method	BLASTX
NCBI GI	g3377517
BLAST score	235
E value	1.0e-19
Match length	116
% identity	39
NCBI Description	(AF073361) nitrate transporter NTL1 [Arabidopsis thaliana]

Seq. No.	137805
Seq. ID	LIB22-008-Q1-E1-B2
Method	BLASTX
NCBI GI	g4586021
BLAST score	102

E value	3.0e-55
Match length	113
% identity	98
NCBI Description	(AC007170) putative cytoplasmic aconitate hydratase [Arabidopsis thaliana]

Seq. No.	137806
Seq. ID	LIB22-008-Q1-E1-C1
Method	BLASTN
NCBI GI	g2098816
BLAST score	38
E value	5.0e-12
Match length	94
% identity	85
NCBI Description	Arabidopsis thaliana BAC F19G10, complete sequence

Seq. No.	137807
Seq. ID	LIB22-008-Q1-E1-C10
Method	BLASTX
NCBI GI	g1563719
BLAST score	303
E value	1.0e-27
Match length	88
% identity	68
NCBI Description	(Y08320) cyclophylin [Digitalis lanata]

Seq. No.	137808
Seq. ID	LIB22-008-Q1-E1-C11
Method	BLASTN
NCBI GI	g4589950
BLAST score	230
E value	1.0e-127
Match length	230
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T28P16 genomic sequence, complete sequence

Seq. No.	137809
Seq. ID	LIB22-008-Q1-E1-C5
Method	BLASTX
NCBI GI	g2760844
BLAST score	363
E value	4.0e-35
Match length	76
% identity	100
NCBI Description	(AC003105) hypothetical protein [Arabidopsis thaliana]

Seq. No.	137810
Seq. ID	LIB22-008-Q1-E1-D10
Method	BLASTX
NCBI GI	g3915085
BLAST score	541
E value	1.0e-55
Match length	113
% identity	93
NCBI Description	TRANS-CINNAMATE 4-MONOOXYGENASE (CINNAMIC ACID 4-HYDROXYLASE) (CA4H) (P450C4H) (CYTOCHROME P450 73)

>gi_1773289 (U71081) cinnamate-4-hydroxylase [Arabidopsis thaliana] >gi_1946370 (U93215) cinnamate-4-hydroxylase [Arabidopsis thaliana]

Seq. No.	137811
Seq. ID	LIB22-008-Q1-E1-E12
Method	BLASTN
NCBI GI	g2583106
BLAST score	189
E value	1.0e-102
Match length	333
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC F4L23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137812
Seq. ID	LIB22-008-Q1-E1-F11
Method	BLASTX
NCBI GI	g2827143
BLAST score	200
E value	2.0e-15
Match length	139
% identity	77
NCBI Description	(AF027174) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	137813
Seq. ID	LIB22-008-Q1-E1-F5
Method	BLASTN
NCBI GI	g2832667
BLAST score	93
E value	7.0e-45
Match length	234
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T10I14 (ESSAII project)

Seq. No.	137814
Seq. ID	LIB22-008-Q1-E1-G3
Method	BLASTX
NCBI GI	g3980378
BLAST score	656
E value	5.0e-69
Match length	119
% identity	97
NCBI Description	(AC004561) putative RNA binding protein [Arabidopsis thaliana]

Seq. No.	137815
Seq. ID	LIB22-009-Q1-E1-A7
Method	BLASTX
NCBI GI	g4191779
BLAST score	499
E value	1.0e-50
Match length	100
% identity	100
NCBI Description	(AC005917) putative recA protein [Arabidopsis thaliana]

Seq. No.	137816
Seq. ID	LIB22-009-Q1-E1-B6
Method	BLASTX
NCBI GI	g1402912
BLAST score	147
E value	6.0e-10
Match length	28
% identity	100
NCBI Description	(X98317) peroxidase [Arabidopsis thaliana]

Seq. No.	137817
Seq. ID	LIB22-009-Q1-E1-D10
Method	BLASTX
NCBI GI	g2245378
BLAST score	459
E value	4.0e-46
Match length	104
% identity	85
NCBI Description	(U83245) auxin response factor 1 [Arabidopsis thaliana]

Seq. No.	137818
Seq. ID	LIB22-009-Q1-E1-D6
Method	BLASTX
NCBI GI	g2190558
BLAST score	559
E value	1.0e-57
Match length	122
% identity	85
NCBI Description	(AC001229) F5I14.14 [Arabidopsis thaliana]

Seq. No.	137819
Seq. ID	LIB22-009-Q1-E1-D7
Method	BLASTX
NCBI GI	g4220462
BLAST score	461
E value	2.0e-46
Match length	91
% identity	100
NCBI Description	(AC006216) Strong similarity to gb_Z50851 HD-zip (athb-8) gene from Arabidopsis thaliana containing Homeobox PF_00046 and bZIP PF_00170 domains. [Arabidopsis thaliana]

Seq. No.	137820
Seq. ID	LIB22-009-Q1-E1-E9
Method	BLASTX
NCBI GI	g1361982
BLAST score	330
E value	3.0e-31
Match length	75
% identity	85
NCBI Description	4-coumarate--CoA ligase (EC 6.2.1.12) - Arabidopsis thaliana >gi_609340 (U18675) 4-coumarate--coenzyme A ligase [Arabidopsis thaliana]

Seq. No.	137821
Seq. ID	LIB22-009-Q1-E1-F12

Method	BLASTN
NCBI GI	g4519192
BLAST score	304
E value	1.0e-171
Match length	311
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MBK21, complete sequence

Seq. No.	137822
Seq. ID	LIB22-009-Q1-E1-G6
Method	BLASTX
NCBI GI	g3582329
BLAST score	673
E value	5.0e-71
Match length	125
% identity	99
NCBI Description	(AC005496) unknown protein [Arabidopsis thaliana]

Seq. No.	137823
Seq. ID	LIB22-009-Q1-E1-H8
Method	BLASTN
NCBI GI	g4519182
BLAST score	83
E value	3.0e-39
Match length	144
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K13H13, complete sequence

Seq. No.	137824
Seq. ID	LIB22-010-Q1-E1-B5
Method	BLASTN
NCBI GI	g1742964
BLAST score	424
E value	0.0e+00
Match length	436
% identity	99
NCBI Description	A.thaliana mRNA for HAPp48,5 protein

Seq. No.	137825
Seq. ID	LIB22-010-Q1-E1-B6
Method	BLASTX
NCBI GI	g3492806
BLAST score	264
E value	5.0e-23
Match length	101
% identity	51
NCBI Description	(AJ225045) adventitious rooting related oxygenase [Malus domestica]

Seq. No.	137826
Seq. ID	LIB22-010-Q1-E1-C2
Method	BLASTX
NCBI GI	g4056467
BLAST score	549
E value	2.0e-56

Match length	104
% identity	100
NCBI Description	(AC005990) Strong similarity to gb_AB006693 spermidine synthase from Arabidopsis thaliana. ESTs gb_AA389822, gb_T41794, gb_N38455, gb_AI100106, gb_F14442 and gb_F14256 come from this gene. [Arabidopsis thaliana]

Seq. No.	137827
Seq. ID	LIB22-010-Q1-E1-C6
Method	BLASTX
NCBI GI	g2335096
BLAST score	337
E value	1.0e-31
Match length	147
% identity	47
NCBI Description	(AC002339) hypothetical protein [Arabidopsis thaliana]

Seq. No.	137828
Seq. ID	LIB22-010-Q1-E1-C9
Method	BLASTN
NCBI GI	g4586098
BLAST score	156
E value	2.0e-82
Match length	314
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F16J13 (ESSA project)

Seq. No.	137829
Seq. ID	LIB22-010-Q1-E1-D1
Method	BLASTN
NCBI GI	g4519195
BLAST score	298
E value	1.0e-167
Match length	308
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MQC12, complete sequence

Seq. No.	137830
Seq. ID	LIB22-010-Q1-E1-E1
Method	BLASTN
NCBI GI	g4056476
BLAST score	169
E value	3.0e-90
Match length	190
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F3G5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137831
Seq. ID	LIB22-010-Q1-E1-E4
Method	BLASTN
NCBI GI	g2833627
BLAST score	339
E value	0.0e+00
Match length	339

% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F17O7 complete sequence [Arabidopsis thaliana]

Seq. No.	137832
Seq. ID	LIB22-010-Q1-E1-E5
Method	BLASTN
NCBI GI	g2244870
BLAST score	191
E value	1.0e-103
Match length	337
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	137833
Seq. ID	LIB22-010-Q1-E1-E8
Method	BLASTN
NCBI GI	g3522932
BLAST score	218
E value	1.0e-119
Match length	234
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137834
Seq. ID	LIB22-010-Q1-E1-F1
Method	BLASTN
NCBI GI	g2980787
BLAST score	299
E value	1.0e-168
Match length	299
% identity	50
NCBI Description	Arabidopsis thaliana DNA chromosome 4, P1 clone M7J2 (ESSAII project)

Seq. No.	137835
Seq. ID	LIB22-010-Q1-E1-G10
Method	BLASTX
NCBI GI	g4455184
BLAST score	569
E value	5.0e-59
Match length	106
% identity	100
NCBI Description	(AL035521) extra-large G-protein-like [Arabidopsis thaliana]

Seq. No.	137836
Seq. ID	LIB22-010-Q1-E1-G11
Method	BLASTX
NCBI GI	g4115377
BLAST score	405
E value	7.0e-40
Match length	95
% identity	81
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	137837
Seq. ID	LIB22-010-Q1-E1-G4
Method	BLASTX
NCBI GI	g3426038
BLAST score	466
E value	8.0e-47
Match length	114
% identity	52
NCBI Description	(AC005168) unknown protein [Arabidopsis thaliana]

Seq. No.	137838
Seq. ID	LIB22-010-Q1-E1-H2
Method	BLASTX
NCBI GI	g3608155
BLAST score	461
E value	6.0e-49
Match length	130
% identity	81
NCBI Description	(AC005314) putative RNA helicase [Arabidopsis thaliana]

Seq. No.	137839
Seq. ID	LIB22-010-Q1-E1-H8
Method	BLASTN
NCBI GI	g2244788
BLAST score	263
E value	1.0e-146
Match length	368
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	137840
Seq. ID	LIB22-011-Q1-E1-C11
Method	BLASTX
NCBI GI	g3250696
BLAST score	314
E value	3.0e-29
Match length	89
% identity	39
NCBI Description	(AL024486) putative protein [Arabidopsis thaliana]

Seq. No.	137841
Seq. ID	LIB22-011-Q1-E1-C5
Method	BLASTN
NCBI GI	g2618683
BLAST score	279
E value	1.0e-156
Match length	307
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T32G6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137842
Seq. ID	LIB22-011-Q1-E1-E6
Method	BLASTN
NCBI GI	g2262155

BLAST score	167
E value	3.0e-89
Match length	211
% identity	95
NCBI Description	DNA sequence of Arabidopsis thaliana BAC F5J6 from chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No.	137843
Seq. ID	LIB22-011-Q1-E1-F7
Method	BLASTX
NCBI GI	g2854117
BLAST score	67
E value	6.4e+00
Match length	130
% identity	45
NCBI Description	(AF045453) protein kinase YakA [Dictyostelium discoideum]

Seq. No.	137844
Seq. ID	LIB22-011-Q1-E1-G12
Method	BLASTX
NCBI GI	g4572674
BLAST score	352
E value	2.0e-33
Match length	85
% identity	82
NCBI Description	(AC006954) unknown protein [Arabidopsis thaliana]

Seq. No.	137845
Seq. ID	LIB22-011-Q1-E1-H11
Method	BLASTX
NCBI GI	g3869280
BLAST score	249
E value	1.0e-21
Match length	76
% identity	64
NCBI Description	(AF064786) beta-galactosidase precursor [Carica papaya]

Seq. No.	137846
Seq. ID	LIB22-011-Q1-K1-A12
Method	BLASTN
NCBI GI	g4206762
BLAST score	225
E value	1.0e-123
Match length	335
% identity	96
NCBI Description	Arabidopsis thaliana cell wall-plasma membrane linker protein homolog (CWLP) mRNA, complete cds

Seq. No.	137847
Seq. ID	LIB22-011-Q1-K1-A6
Method	BLASTX
NCBI GI	g3046696
BLAST score	180
E value	4.0e-13
Match length	116
% identity	39
NCBI Description	(AL022224) CTP synthase like protein [Arabidopsis thaliana]

Seq. No.	137848
Seq. ID	LIB22-011-Q1-K1-D10
Method	BLASTX
NCBI GI	g1684855
BLAST score	285
E value	1.0e-25
Match length	58
% identity	22
NCBI Description	(U77939) ubiquitin-like protein [Phaseolus vulgaris]

Seq. No.	137849
Seq. ID	LIB22-011-Q1-K1-E9
Method	BLASTN
NCBI GI	g3132469
BLAST score	239
E value	1.0e-131
Match length	542
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T29F13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137850
Seq. ID	LIB22-011-Q1-K1-F12
Method	BLASTN
NCBI GI	g3831437
BLAST score	544
E value	0.0e+00
Match length	552
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T3A4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137851
Seq. ID	LIB22-011-Q1-K1-G8
Method	BLASTX
NCBI GI	g3668097
BLAST score	210
E value	1.0e-16
Match length	118
% identity	44
NCBI Description	(AC004667) putative glycine cleavage system protein H precursor [Arabidopsis thaliana]

Seq. No.	137852
Seq. ID	LIB22-012-Q1-E1-A11
Method	BLASTN
NCBI GI	g3449312
BLAST score	179
E value	4.0e-96
Match length	332
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K16L22, complete sequence [Arabidopsis thaliana]

Seq. No.	137853
Seq. ID	LIB22-012-Q1-E1-A6

Method	BLASTX
NCBI GI	g4512697
BLAST score	258
E value	3.0e-22
Match length	98
% identity	57
NCBI Description	(AC006569) unknown protein [Arabidopsis thaliana]

Seq. No.	137854
Seq. ID	LIB22-012-Q1-E1-B5
Method	BLASTN
NCBI GI	g4220641
BLAST score	41
E value	7.0e-14
Match length	268
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUL3, complete sequence [Arabidopsis thaliana]

Seq. No.	137855
Seq. ID	LIB22-012-Q1-E1-D1
Method	BLASTX
NCBI GI	g4587602
BLAST score	393
E value	2.0e-38
Match length	90
% identity	86
NCBI Description	(AC006951) putative retrotransposon hopscotch polyprotein [Arabidopsis thaliana]

Seq. No.	137856
Seq. ID	LIB22-012-Q1-E1-D11
Method	BLASTX
NCBI GI	g3688173
BLAST score	556
E value	2.0e-57
Match length	123
% identity	82
NCBI Description	(AL031804) putative protein [Arabidopsis thaliana]

Seq. No.	137857
Seq. ID	LIB22-012-Q1-E1-E9
Method	BLASTN
NCBI GI	g4159708
BLAST score	286
E value	1.0e-160
Match length	321
% identity	64
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MKP6, complete sequence

Seq. No.	137858
Seq. ID	LIB22-012-Q1-E1-F11
Method	BLASTN
NCBI GI	g3702735
BLAST score	156
E value	2.0e-82

09604750.1600

Match length	277
% identity	42
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQL5, complete sequence [Arabidopsis thaliana]

Seq. No.	137859
Seq. ID	LIB22-012-Q1-E1-F4
Method	BLASTN
NCBI GI	g2828185
BLAST score	151
E value	9.0e-80
Match length	155
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUD21, complete sequence [Arabidopsis thaliana]

Seq. No.	137860
Seq. ID	LIB22-012-Q1-E1-H4
Method	BLASTN
NCBI GI	g4056476
BLAST score	209
E value	1.0e-114
Match length	213
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F3G5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137861
Seq. ID	LIB22-012-Q1-E1-H5
Method	BLASTN
NCBI GI	g469113
BLAST score	108
E value	3.0e-54
Match length	108
% identity	100
NCBI Description	A.thaliana (Columbia) Dr4 mRNA

Seq. No.	137862
Seq. ID	LIB22-013-Q1-E1-B2
Method	BLASTN
NCBI GI	g4337186
BLAST score	145
E value	7.0e-76
Match length	310
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T28I24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137863
Seq. ID	LIB22-013-Q1-E1-B5
Method	BLASTX
NCBI GI	g1531758
BLAST score	509
E value	5.0e-52
Match length	97
% identity	95
NCBI Description	(X98772) AUX1 [Arabidopsis thaliana] >gi_3335360 (AC003028)

unknown protein [Arabidopsis thaliana]

Seq. No.	137864
Seq. ID	LIB22-013-Q1-E1-C8
Method	BLASTN
NCBI GI	g2494106
BLAST score	345
E value	0.0e+00
Match length	357
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137865
Seq. ID	LIB22-013-Q1-E1-D12
Method	BLASTN
NCBI GI	g4567300
BLAST score	293
E value	1.0e-164
Match length	329
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II P1 MHK10 genomic sequence, complete sequence

Seq. No.	137866
Seq. ID	LIB22-013-Q1-E1-D2
Method	BLASTN
NCBI GI	g2853071
BLAST score	89
E value	2.0e-42
Match length	263
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F24J7 (ESSA project)

Seq. No.	137867
Seq. ID	LIB22-013-Q1-E1-D6
Method	BLASTX
NCBI GI	g4454452
BLAST score	423
E value	7.0e-42
Match length	81
% identity	66
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	137868
Seq. ID	LIB22-013-Q1-E1-D8
Method	BLASTN
NCBI GI	g3386593
BLAST score	341
E value	0.0e+00
Match length	341
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F4I18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 137869

Seq. ID	LIB22-013-Q1-E1-D9
Method	BLASTX
NCBI GI	g120675
BLAST score	526
E value	9.0e-54
Match length	121
% identity	84
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66011_pir__DEIS3C glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - white mustard >gi_21143_emb_CAA27844_ (X04301) GAPDH (aa 1-338) [Sinapis alba]

Seq. No.	137870
Seq. ID	LIB22-013-Q1-E1-E2
Method	BLASTX
NCBI GI	g549060
BLAST score	367
E value	3.0e-35
Match length	96
% identity	75
NCBI Description	T-COMPLEX PROTEIN 1, ETA SUBUNIT (TCP-1-ETA) (CCT-ETA) >gi_631656_pir__S43058 CCTeta protein eta chain - mouse >gi_468504_emb_CAA83274_ (Z31399) CCTeta, eta subunit of the chaperonin containing TCP-1 (CCT) [Mus musculus]

Seq. No.	137871
Seq. ID	LIB22-013-Q1-E1-E6
Method	BLASTN
NCBI GI	g2924652
BLAST score	191
E value	1.0e-103
Match length	350
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9L2, complete sequence [Arabidopsis thaliana]

Seq. No.	137872
Seq. ID	LIB22-013-Q1-E1-G3
Method	BLASTN
NCBI GI	g4733984
BLAST score	187
E value	1.0e-101
Match length	357
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F14O4 genomic sequence, complete sequence

Seq. No.	137873
Seq. ID	LIB22-013-Q1-E1-G4
Method	BLASTN
NCBI GI	g4586024
BLAST score	331
E value	0.0e+00
Match length	335
% identity	53
NCBI Description	Arabidopsis thaliana chromosome II BAC T13C7 genomic

sequence, complete sequence

Seq. No.	137874
Seq. ID	LIB22-013-Q1-E1-G9
Method	BLASTN
NCBI GI	g4757403
BLAST score	140
E value	9.0e-73
Match length	432
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJL12, complete sequence

Seq. No.	137875
Seq. ID	LIB22-013-Q1-E1-H6
Method	BLASTX
NCBI GI	g3450842
BLAST score	257
E value	8.0e-23
Match length	68
% identity	71
NCBI Description	(AF080436) mitogen activated protein kinase kinase [Oryza sativa]

Seq. No.	137876
Seq. ID	LIB22-014-Q1-E1-A1
Method	BLASTX
NCBI GI	g3377820
BLAST score	473
E value	1.0e-47
Match length	96
% identity	100
NCBI Description	(AF076275) contains similarity to coatomer zeta chains [Arabidopsis thaliana]

Seq. No.	137877
Seq. ID	LIB22-014-Q1-E1-B12
Method	BLASTX
NCBI GI	g4263784
BLAST score	294
E value	1.0e-26
Match length	127
% identity	57
NCBI Description	(AC006068) putative glycogenin-2 protein [Arabidopsis thaliana]

Seq. No.	137878
Seq. ID	LIB22-014-Q1-E1-B9
Method	BLASTX
NCBI GI	g2117612
BLAST score	449
E value	7.0e-45
Match length	90
% identity	97
NCBI Description	catalase (EC 1.11.1.6) 3 - Arabidopsis thaliana

Seq. No. 137879

Seq. ID	LIB22-014-Q1-E1-D5
Method	BLASTN
NCBI GI	g4699904
BLAST score	244
E value	1.0e-135
Match length	274
% identity	96
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F1E22, complete sequence

Seq. No.	137880
Seq. ID	LIB22-014-Q1-E1-D8
Method	BLASTX
NCBI GI	g1586551
BLAST score	284
E value	2.0e-25
Match length	104
% identity	69
NCBI Description	CCAAT-binding factor:SUBUNIT=B [Brassica napus]

Seq. No.	137881
Seq. ID	LIB22-014-Q1-E1-E6
Method	BLASTN
NCBI GI	g2335089
BLAST score	130
E value	6.0e-67
Match length	308
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T11A7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137882
Seq. ID	LIB22-014-Q1-E1-F12
Method	BLASTX
NCBI GI	g4558592
BLAST score	615
E value	3.0e-64
Match length	127
% identity	100
NCBI Description	(AC006555) hypothetical protein [Arabidopsis thaliana]

Seq. No.	137883
Seq. ID	LIB22-014-Q1-E1-H10
Method	BLASTX
NCBI GI	g2191159
BLAST score	325
E value	2.0e-30
Match length	91
% identity	79
NCBI Description	(AF007270) Similar to serine hydroxymethyltransferase; coded for by A. thaliana cDNA T42313; coded for by A. thaliana cDNA W43384 [Arabidopsis thaliana]

Seq. No.	137884
Seq. ID	LIB22-014-Q1-E1-H7
Method	BLASTN
NCBI GI	g4589430

BLAST score	244
E value	1.0e-135
Match length	410
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLD14, complete sequence

Seq. No.	137885
Seq. ID	LIB22-015-Q1-E1-F12
Method	BLASTN
NCBI GI	g4519193
BLAST score	169
E value	4.0e-90
Match length	328
% identity	63
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC11, complete sequence

Seq. No.	137886
Seq. ID	LIB22-016-Q1-E1-A12
Method	BLASTN
NCBI GI	g2245031
BLAST score	197
E value	1.0e-107
Match length	269
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	137887
Seq. ID	LIB22-016-Q1-E1-B4
Method	BLASTN
NCBI GI	g3451055
BLAST score	311
E value	1.0e-175
Match length	360
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F16G20 (ESSAII project)

Seq. No.	137888
Seq. ID	LIB22-016-Q1-E1-F1
Method	BLASTX
NCBI GI	g417073
BLAST score	183
E value	4.0e-14
Match length	62
% identity	60
NCBI Description	GLUTAMATE SYNTHASE (NADH) PRECURSOR (NADH-GOGAT) >gi_484529_pir__JQ1977 glutamate synthase (NADH) (EC 1.4.1.14) - alfalfa >gi_166412 (L01660) NADH-glutamate synthase [Medicago sativa]

Seq. No.	137889
Seq. ID	LIB22-016-Q1-E1-G1
Method	BLASTX
NCBI GI	g4263711

BLAST score	385
E value	1.0e-37
Match length	85
% identity	88
NCBI Description	(AC006223) putative CCR4-associated transcription factor [Arabidopsis thaliana]

Seq. No.	137890
Seq. ID	LIB22-016-Q1-E1-G10
Method	BLASTN
NCBI GI	g4572664
BLAST score	415
E value	0.0e+00
Match length	415
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F25P17 genomic sequence, complete sequence

Seq. No.	137891
Seq. ID	LIB22-016-Q1-E1-H3
Method	BLASTX
NCBI GI	g4337188
BLAST score	161
E value	2.0e-11
Match length	40
% identity	82
NCBI Description	(AC006403) hypothetical protein [Arabidopsis thaliana]

Seq. No.	137892
Seq. ID	LIB22-016-Q1-E1-H7
Method	BLASTN
NCBI GI	g4263753
BLAST score	260
E value	1.0e-144
Match length	409
% identity	100
NCBI Description	Arabidopsis thaliana chromosome V map near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	137893
Seq. ID	LIB22-017-Q1-E1-A2
Method	BLASTX
NCBI GI	g4581150
BLAST score	171
E value	2.0e-12
Match length	41
% identity	83
NCBI Description	(AC006919) hypothetical protein [Arabidopsis thaliana]

Seq. No.	137894
Seq. ID	LIB22-017-Q1-E1-A4
Method	BLASTN
NCBI GI	g4558586
BLAST score	218
E value	1.0e-119
Match length	303
% identity	100

NCBI Description	Arabidopsis thaliana chromosome 1 BAC T5I8 sequence, complete sequence

Seq. No.	137895
Seq. ID	LIB22-017-Q1-E1-A5
Method	BLASTX
NCBI GI	g4585991
BLAST score	285
E value	1.0e-25
Match length	91
% identity	54
NCBI Description	(AC005287) very similar to mouse Dhm1 and Dhm2 [Arabidopsis thaliana]

Seq. No.	137896
Seq. ID	LIB22-017-Q1-E1-B8
Method	BLASTX
NCBI GI	g2781394
BLAST score	418
E value	3.0e-41
Match length	87
% identity	100
NCBI Description	(U70424) O-methyltransferase 1 [Arabidopsis thaliana]

Seq. No.	137897
Seq. ID	LIB22-017-Q1-E1-C11
Method	BLASTX
NCBI GI	g4581146
BLAST score	421
E value	1.0e-41
Match length	91
% identity	93
NCBI Description	(AC006919) putative fructose-bisphosphate aldolase, cytoplasmic [Arabidopsis thaliana]

Seq. No.	137898
Seq. ID	LIB22-017-Q1-E1-C8
Method	BLASTX
NCBI GI	g4115377
BLAST score	141
E value	3.0e-09
Match length	44
% identity	55
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	137899
Seq. ID	LIB22-017-Q1-E1-D3
Method	BLASTX
NCBI GI	g2911057
BLAST score	431
E value	9.0e-43
Match length	83
% identity	100
NCBI Description	(AL021961) caffeoyl-CoA O-methyltransferase - like protein [Arabidopsis thaliana]

Seq. No.	137900

Seq. ID	LIB22-017-Q1-E1-E3
Method	BLASTN
NCBI GI	g2244950
BLAST score	88
E value	2.0e-42
Match length	88
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	137901
Seq. ID	LIB22-017-Q1-E1-E5
Method	BLASTX
NCBI GI	g3335375
BLAST score	284
E value	5.0e-26
Match length	69
% identity	80
NCBI Description	(AC003028) putative amidase [Arabidopsis thaliana]

Seq. No.	137902
Seq. ID	LIB22-017-Q1-E1-E7
Method	BLASTN
NCBI GI	g3763915
BLAST score	207
E value	1.0e-113
Match length	366
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F14B2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137903
Seq. ID	LIB22-017-Q1-E1-F1
Method	BLASTN
NCBI GI	g2828182
BLAST score	211
E value	1.0e-115
Match length	246
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOJ9, complete sequence [Arabidopsis thaliana]

Seq. No.	137904
Seq. ID	LIB22-017-Q1-E1-F11
Method	BLASTX
NCBI GI	g1402904
BLAST score	473
E value	8.0e-48
Match length	90
% identity	100
NCBI Description	(X98313) peroxidase [Arabidopsis thaliana]

Seq. No.	137905
Seq. ID	LIB22-017-Q1-E1-F12
Method	BLASTN
NCBI GI	g3241924
BLAST score	383

E value	0.0e+00
Match length	387
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNC6, complete sequence [Arabidopsis thaliana]

Seq. No.	137906
Seq. ID	LIB22-017-Q1-E1-F7
Method	BLASTX
NCBI GI	g2129759
BLAST score	334
E value	3.0e-31
Match length	68
% identity	99
NCBI Description	UDPglucose 4-epimerase (EC 5.1.3.2) - Arabidopsis thaliana >gi_1143392_emb_CAA90941_ (Z54214) uridine diphosphate glucose epimerase [Arabidopsis thaliana]

Seq. No.	137907
Seq. ID	LIB22-017-Q1-E1-G1
Method	BLASTX
NCBI GI	g4572681
BLAST score	635
E value	1.0e-66
Match length	127
% identity	98
NCBI Description	(AC006954) putative ubiquitin carboxyl terminal hydrolase [Arabidopsis thaliana]

Seq. No.	137908
Seq. ID	LIB22-017-Q1-E1-G11
Method	BLASTX
NCBI GI	g2894574
BLAST score	427
E value	2.0e-42
Match length	81
% identity	100
NCBI Description	(AL021890) peroxidase prxr1 [Arabidopsis thaliana] >gi_2961341_emb_CAA18099.1_ (AL022140) peroxidase prxr1 [Arabidopsis thaliana]

Seq. No.	137909
Seq. ID	LIB22-018-Q1-E1-A2
Method	BLASTX
NCBI GI	g2104949
BLAST score	380
E value	5.0e-37
Match length	84
% identity	83
NCBI Description	(U96716) MAP kinase-like protein [Selaginella lepidophylla]

Seq. No.	137910
Seq. ID	LIB22-018-Q1-E1-A5
Method	BLASTN
NCBI GI	g4006885
BLAST score	146
E value	1.0e-76

Match length	182
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	137911
Seq. ID	LIB22-018-Q1-E1-E11
Method	BLASTN
NCBI GI	g3702734
BLAST score	327
E value	0.0e+00
Match length	327
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNB8, complete sequence [Arabidopsis thaliana]

Seq. No.	137912
Seq. ID	LIB22-018-Q1-E1-F3
Method	BLASTN
NCBI GI	g4581084
BLAST score	207
E value	1.0e-113
Match length	304
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC T30F21 genomic sequence, complete sequence

Seq. No.	137913
Seq. ID	LIB22-018-Q1-E1-G12
Method	BLASTN
NCBI GI	g2760169
BLAST score	223
E value	1.0e-122
Match length	283
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFB13, complete sequence [Arabidopsis thaliana]

Seq. No.	137914
Seq. ID	LIB22-018-Q1-E1-H12
Method	BLASTX
NCBI GI	g4567235
BLAST score	353
E value	9.0e-34
Match length	92
% identity	70
NCBI Description	(AC007119) putative phosphatidylinositol/phophatidylcholine transfer protein [Arabidopsis thaliana]

Seq. No.	137915
Seq. ID	LIB22-019-Q1-E1-A4
Method	BLASTN
NCBI GI	g3869070
BLAST score	46
E value	5.0e-17
Match length	195
% identity	72

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MGO3, complete sequence [Arabidopsis thaliana]
Seq. No.	137916
Seq. ID	LIB22-019-Q1-E1-E10
Method	BLASTX
NCBI GI	g4835226
BLAST score	262
E value	1.0e-22
Match length	85
% identity	58
NCBI Description	(AL049862) putative protein [Arabidopsis thaliana]
Seq. No.	137917
Seq. ID	LIB22-019-Q1-E1-F2
Method	BLASTX
NCBI GI	g3582329
BLAST score	241
E value	2.0e-20
Match length	103
% identity	47
NCBI Description	(AC005496) unknown protein [Arabidopsis thaliana]
Seq. No.	137918
Seq. ID	LIB22-020-Q1-E1-A10
Method	BLASTX
NCBI GI	g3319344
BLAST score	576
E value	1.0e-59
Match length	130
% identity	87
NCBI Description	(AF077407) contains similarity to UDP-glucoronosyl and UDP-glucosyl transferases (Pfam: UDPGT.hmm, score: 85.94) [Arabidopsis thaliana]
Seq. No.	137919
Seq. ID	LIB22-020-Q1-E1-B12
Method	BLASTN
NCBI GI	g4539290
BLAST score	110
E value	4.0e-55
Match length	194
% identity	90
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F14M19 (ESSA project)
Seq. No.	137920
Seq. ID	LIB22-020-Q1-E1-B5
Method	BLASTX
NCBI GI	g4263777
BLAST score	207
E value	2.0e-16
Match length	58
% identity	62
NCBI Description	(AC006068) putative serine carboxypeptidase II [Arabidopsis thaliana] >gi_4510391_gb_AAD21479.1_ (AC007017) putative serine carboxypeptidase II [Arabidopsis thaliana]

Seq. No.	137921
Seq. ID	LIB22-020-Q1-E1-D9
Method	BLASTX
NCBI GI	g4768986
BLAST score	148
E value	1.0e-09
Match length	99
% identity	34
NCBI Description	(AF140493) hypothetical protein [Oryza sativa]

Seq. No.	137922
Seq. ID	LIB22-020-Q1-E1-E4
Method	BLASTN
NCBI GI	g4454022
BLAST score	47
E value	1.0e-17
Match length	132
% identity	74
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16 (ESSAII project)

Seq. No.	137923
Seq. ID	LIB22-020-Q1-E1-G7
Method	BLASTN
NCBI GI	g2924768
BLAST score	62
E value	9.0e-27
Match length	126
% identity	87
NCBI Description	Arabidopsis thaliana chromosome II BAC F25I18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137924
Seq. ID	LIB22-021-Q1-E1-B12
Method	BLASTX
NCBI GI	g3152589
BLAST score	587
E value	5.0e-61
Match length	125
% identity	81
NCBI Description	(AC002986) Strong similarity to lupeol synthase gb_U49919 from A. thaliana (second gene in a series of three with similar homologies). [Arabidopsis thaliana]

Seq. No.	137925
Seq. ID	LIB22-021-Q1-E1-B2
Method	BLASTN
NCBI GI	g3449317
BLAST score	124
E value	9.0e-64
Match length	124
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKM21, complete sequence [Arabidopsis thaliana]

Seq. No.	137926

Seq. ID	LIB22-021-Q1-E1-B9
Method	BLASTN
NCBI GI	g4586349
BLAST score	65
E value	5.0e-28
Match length	89
% identity	93
NCBI Description	Arabidopsis thaliana DNA for glucose-1-phosphate adenylyltransferase, complete cds

Seq. No.	137927
Seq. ID	LIB22-021-Q1-E1-C10
Method	BLASTN
NCBI GI	g3046848
BLAST score	115
E value	6.0e-58
Match length	353
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18C1, complete sequence [Arabidopsis thaliana]

Seq. No.	137928
Seq. ID	LIB22-021-Q1-E1-F6
Method	BLASTX
NCBI GI	g4587541
BLAST score	611
E value	9.0e-64
Match length	118
% identity	100
NCBI Description	(AC006577) Belongs to the PF_00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb_T44453, gb_T04815, gb_T45993, gb_R30138, gb_AI099570 and gb_T22281 come from this gene. [Arabidopsis thaliana]

Seq. No.	137929
Seq. ID	LIB22-021-Q1-E1-G10
Method	BLASTX
NCBI GI	g4388828
BLAST score	169
E value	2.0e-12
Match length	56
% identity	70
NCBI Description	(AC006528) putative zinc-finger protein [Arabidopsis thaliana]

Seq. No.	137930
Seq. ID	LIB22-021-Q1-E1-H10
Method	BLASTX
NCBI GI	g4335737
BLAST score	172
E value	3.0e-12
Match length	79
% identity	46
NCBI Description	(AC006248) putative serine/threonine kinase [Arabidopsis thaliana]

Seq. No. 137931

Seq. ID	LIB22-022-Q1-E1-A12
Method	BLASTN
NCBI GI	g3080430
BLAST score	82
E value	1.0e-38
Match length	122
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T19P19 (ESSAII project)

Seq. No.	137932
Seq. ID	LIB22-022-Q1-E1-E9
Method	BLASTX
NCBI GI	g3757529
BLAST score	366
E value	3.0e-35
Match length	73
% identity	100
NCBI Description	(AC005167) tetracycline transporter-like protein [Arabidopsis thaliana]

Seq. No.	137933
Seq. ID	LIB22-022-Q1-E1-G1
Method	BLASTN
NCBI GI	g3132469
BLAST score	178
E value	1.0e-95
Match length	320
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T29F13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137934
Seq. ID	LIB22-022-Q1-E1-G2
Method	BLASTX
NCBI GI	g4758356
BLAST score	375
E value	4.0e-36
Match length	115
% identity	66
NCBI Description	flap structure-specific endonuclease 1; MATURATION FACTOR 1 (MF1); DNase IV; RAD2_HUMAN >gi_729475_sp_P39748_FEN1_HUMAN FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) >gi_1362788_pir__A56531 DNA structure-specific endonuclease FEN1 - human >gi_704377_bbs_157592 DNase IV=nuclear 42 kda 5' -> 3' exonuclease [human, HeLa cells, Peptide, 380 aa] >gi_642090 (L37374) endonuclease [Homo sapiens] >gi_3169155 (AC004770) FEN1_HUMAN; MATURATION FACTOR 1 (MF1); DNase IV; RAD2_HUMAN [Homo sapiens] >gi_3980293_emb_CAA54166_ (X76771) flap endonuclease-1 [Homo sapiens]

Seq. No.	137935
Seq. ID	LIB22-022-Q1-E1-G8
Method	BLASTN
NCBI GI	g3548797
BLAST score	40
E value	3.0e-13

Match length	84
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC T18E12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137936
Seq. ID	LIB22-023-Q1-E1-A11
Method	BLASTX
NCBI GI	g2213597
BLAST score	431
E value	1.0e-42
Match length	88
% identity	98
NCBI Description	(AC000348) T7N9.17 [Arabidopsis thaliana]

Seq. No.	137937
Seq. ID	LIB22-023-Q1-E1-D11
Method	BLASTX
NCBI GI	g1170711
BLAST score	326
E value	3.0e-30
Match length	88
% identity	75
NCBI Description	SHAGGY RELATED PROTEIN KINASE ASK-ALPHA >gi_541901_pir__S41596 protein kinase ASK-alpha (EC 2.7.1.-) - Arabidopsis thaliana >gi_460832_emb_CAA53181_ (X75432) shaggy related kinase [Arabidopsis thaliana] >gi_1769889_emb_CAA48538_ (X68525) serine /threonine protein kinase [Arabidopsis thaliana]

Seq. No.	137938
Seq. ID	LIB22-023-Q1-E1-E11
Method	BLASTX
NCBI GI	g3510250
BLAST score	590
E value	3.0e-61
Match length	114
% identity	100
NCBI Description	(AC005310) unknown protein [Arabidopsis thaliana]

Seq. No.	137939
Seq. ID	LIB22-023-Q1-E1-E9
Method	BLASTX
NCBI GI	g1495269
BLAST score	465
E value	1.0e-46
Match length	126
% identity	74
NCBI Description	(X97829) product similar to ccr protein, Citrus paradisi; PIR: S52663 [Arabidopsis thaliana] >gi_1550735_emb_CAA66824_ (X98130) unknown [Arabidopsis thaliana]

Seq. No.	137940
Seq. ID	LIB22-023-Q1-E1-F11
Method	BLASTX
NCBI GI	g1495804

BLAST score	159
E value	1.0e-10
Match length	118
% identity	40
NCBI Description	(X96406) 13-lipoxygenase [Solanum tuberosum]

Seq. No.	137941
Seq. ID	LIB22-023-Q1-E1-F9
Method	BLASTN
NCBI GI	g2264321
BLAST score	252
E value	1.0e-139
Match length	443
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXM12, complete sequence [Arabidopsis thaliana]

Seq. No.	137942
Seq. ID	LIB22-023-Q1-E1-G2
Method	BLASTX
NCBI GI	g3142290
BLAST score	567
E value	1.0e-58
Match length	122
% identity	99
NCBI Description	(AC002411) Contains similarity to gb_Z69902 from C. elegans. [Arabidopsis thaliana]

Seq. No.	137943
Seq. ID	LIB22-023-Q1-E1-G9
Method	BLASTX
NCBI GI	g1652892
BLAST score	280
E value	7.0e-25
Match length	142
% identity	26
NCBI Description	(D90909) ABC transporter [Synechocystis sp.]

Seq. No.	137944
Seq. ID	LIB22-023-Q1-E1-H10
Method	BLASTN
NCBI GI	g3386593
BLAST score	327
E value	0.0e+00
Match length	384
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F4I18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137945
Seq. ID	LIB22-024-Q1-E1-A1
Method	BLASTX
NCBI GI	g4633131
BLAST score	703
E value	1.0e-74
Match length	133
% identity	99

NCBI Description	(AF110407) ATP sulfurylase precursor [Arabidopsis thaliana] >gi_4803653_emb_CAB42640.1_ (AJ012586) sulfate adenylyltransferase [Arabidopsis thaliana]
Seq. No.	137946
Seq. ID	LIB22-024-Q1-E1-A2
Method	BLASTN
NCBI GI	g2477521
BLAST score	28
E value	5.0e-06
Match length	348
% identity	16
NCBI Description	Arabidopsis thaliana chromosome I BAC F22K20 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	137947
Seq. ID	LIB22-024-Q1-E1-A3
Method	BLASTX
NCBI GI	g2129559
BLAST score	371
E value	1.0e-35
Match length	128
% identity	64
NCBI Description	cellulase homolog OR16pep - Arabidopsis thaliana >gi_1022807 (U37702) cellulase [Arabidopsis thaliana] >gi_3493633 (AF074092) cellulase [Arabidopsis thaliana] >gi_3598956 (AF074375) cellulase [Arabidopsis thaliana] >gi_3978258 (AF073875) endo-1,4-beta-D-glucanase KORRIGAN [Arabidopsis thaliana]
Seq. No.	137948
Seq. ID	LIB22-024-Q1-E1-A4
Method	BLASTX
NCBI GI	g4567286
BLAST score	101
E value	4.0e-04
Match length	78
% identity	7
NCBI Description	(AC006841) putative coatomer alpha subunit [Arabidopsis thaliana]
Seq. No.	137949
Seq. ID	LIB22-024-Q1-E1-C3
Method	BLASTX
NCBI GI	g4572671
BLAST score	357
E value	4.0e-34
Match length	116
% identity	54
NCBI Description	(AC006954) putative cyclic nucleotide regulated ion channel [Arabidopsis thaliana]
Seq. No.	137950
Seq. ID	LIB22-024-Q1-E1-C8
Method	BLASTX
NCBI GI	g4539438
BLAST score	256

E value	3.0e-22
Match length	101
% identity	58
NCBI Description	(AL049523) hypothetical protein [Arabidopsis thaliana]

Seq. No.	137951
Seq. ID	LIB22-024-Q1-E1-D3
Method	BLASTN
NCBI GI	g4335744
BLAST score	301
E value	1.0e-169
Match length	301
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC T4M8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137952
Seq. ID	LIB22-024-Q1-E1-E10
Method	BLASTX
NCBI GI	g2062169
BLAST score	441
E value	6.0e-44
Match length	113
% identity	71
NCBI Description	(AC001645) ABC transporter (PDR5-like) isolog [Arabidopsis thaliana]

Seq. No.	137953
Seq. ID	LIB22-024-Q1-E1-E6
Method	BLASTN
NCBI GI	g17681
BLAST score	226
E value	1.0e-124
Match length	226
% identity	100
NCBI Description	A.thaliana mRNA for Wilm's tumor suppressor homologue

Seq. No.	137954
Seq. ID	LIB22-024-Q1-E1-F1
Method	BLASTN
NCBI GI	g2462930
BLAST score	137
E value	2.0e-71
Match length	141
% identity	99
NCBI Description	dArabidopsis thaliana mRNA for UDP-glucose:sterol glucosyltransferase

Seq. No.	137955
Seq. ID	LIB22-024-Q1-E1-H10
Method	BLASTX
NCBI GI	g728905
BLAST score	207
E value	6.0e-17
Match length	64
% identity	66
NCBI Description	PROBABLE CALCIUM-TRANSPORTING ATPASE 3 (ENDOPLASMIC

D0074960.960

RETICULUM CA2+-ATPASE) >gi_1078206_pir__S51995 probable ATPase (EC 3.6.1.-) DRS2 - yeast (Saccharomyces cerevisiae) >gi_171114 (L01795) ATPase [Saccharomyces cerevisiae] >gi_595560 (U12980) Drs2p: Membrane spanning Ca-ATPase(P-type), member of the cation transport(E1-E2) ATPase [Saccharomyces cerevisiae]

Seq. No.	137956
Seq. ID	LIB22-025-Q1-E1-A1
Method	BLASTN
NCBI GI	g4006885
BLAST score	231
E value	1.0e-127
Match length	235
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	137957
Seq. ID	LIB22-025-Q1-E1-A10
Method	BLASTX
NCBI GI	g2134982
BLAST score	280
E value	5.0e-25
Match length	102
% identity	55
NCBI Description	de-ubiquitinase - human >gi_1122278_emb_CAA62690_ (X91349) de-ubiquitinase [Homo sapiens]

Seq. No.	137958
Seq. ID	LIB22-025-Q1-E1-A6
Method	BLASTX
NCBI GI	g2281113
BLAST score	587
E value	6.0e-61
Match length	123
% identity	88
NCBI Description	(AC002333) endochitinase isolog [Arabidopsis thaliana] >gi_2288989 (AC002335) endochitinase isolog [Arabidopsis thaliana]

Seq. No.	137959
Seq. ID	LIB22-025-Q1-E1-B1
Method	BLASTN
NCBI GI	g4587641
BLAST score	142
E value	3.0e-74
Match length	176
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No.	137960
Seq. ID	LIB22-025-Q1-E1-B6
Method	BLASTX
NCBI GI	g3894168
BLAST score	245

E value	7.0e-21
Match length	105
% identity	43
NCBI Description	(AC005312) similar to phloem-specific lectin [Arabidopsis thaliana]

Seq. No.	137961
Seq. ID	LIB22-025-Q1-E1-B8
Method	BLASTX
NCBI GI	g135497
BLAST score	639
E value	5.0e-67
Match length	121
% identity	96
NCBI Description	TUBULIN BETA CHAIN (BETA-1 AND BETA-2) >gi_84375_pir__S00683 tubulin beta-1 chain - Stylonychia lemnae (SGC5) >gi_10159_emb_CAA29853_ (X06653) beta-1 tubulin (AA 1 - 442) [Stylonychia lemnae] >gi_578493_emb_CAA29995_ (X06874) beta-2 tubulin (AA 1 - 442) [Stylonychia lemnae]

Seq. No.	137962
Seq. ID	LIB22-025-Q1-E1-B9
Method	BLASTN
NCBI GI	g3241925
BLAST score	276
E value	1.0e-154
Match length	318
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK9, complete sequence [Arabidopsis thaliana]

Seq. No.	137963
Seq. ID	LIB22-025-Q1-E1-D9
Method	BLASTX
NCBI GI	g4588001
BLAST score	295
E value	9.0e-27
Match length	119
% identity	61
NCBI Description	(AF085279) hypothetical Ser-Thr protein kinase [Arabidopsis thaliana]

Seq. No.	137964
Seq. ID	LIB22-025-Q1-E1-E1
Method	BLASTX
NCBI GI	g4585978
BLAST score	306
E value	9.0e-64
Match length	120
% identity	98
NCBI Description	(AC005287) NADP specific isocitrate dehydrogenase [Arabidopsis thaliana]

Seq. No.	137965
Seq. ID	LIB22-025-Q1-E1-E4
Method	BLASTN

NCBI GI	g3873174
BLAST score	319
E value	1.0e-179
Match length	323
% identity	61
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14N23, complete sequence [Arabidopsis thaliana]

Seq. No.	137966
Seq. ID	LIB22-025-Q1-E1-F5
Method	BLASTN
NCBI GI	g2494106
BLAST score	126
E value	2.0e-64
Match length	416
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137967
Seq. ID	LIB22-025-Q1-E1-H3
Method	BLASTX
NCBI GI	g2827143
BLAST score	225
E value	3.0e-33
Match length	81
% identity	88
NCBI Description	(AF027174) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	137968
Seq. ID	LIB22-026-Q1-E1-A6
Method	BLASTX
NCBI GI	g2558657
BLAST score	495
E value	2.0e-50
Match length	93
% identity	98
NCBI Description	(AC002354) No definition line found [Arabidopsis thaliana]

Seq. No.	137969
Seq. ID	LIB22-026-Q1-E1-A7
Method	BLASTN
NCBI GI	g3894179
BLAST score	42
E value	2.0e-14
Match length	62
% identity	92
NCBI Description	Arabidopsis thaliana chromosome II BAC F13H10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	137970
Seq. ID	LIB22-026-Q1-E1-B10
Method	BLASTX
NCBI GI	g450880
BLAST score	636
E value	1.0e-66

Match length	124
% identity	99
NCBI Description	(X77199) heat shock cognate 70-1 [Arabidopsis thaliana]

Seq. No.	137971
Seq. ID	LIB22-026-Q1-E1-B6
Method	BLASTX
NCBI GI	g3738340
BLAST score	412
E value	2.0e-40
Match length	111
% identity	68
NCBI Description	(AC005170) GMP synthase-like protein [Arabidopsis thaliana]

Seq. No.	137972
Seq. ID	LIB22-026-Q1-E1-B9
Method	BLASTX
NCBI GI	g4567273
BLAST score	702
E value	2.0e-74
Match length	132
% identity	100
NCBI Description	(AC006841) putative vacuolar proton ATPase subunit [Arabidopsis thaliana]

Seq. No.	137973
Seq. ID	LIB22-026-Q1-E1-C5
Method	BLASTX
NCBI GI	g3289002
BLAST score	118
E value	6.0e-06
Match length	139
% identity	3
NCBI Description	(AF073522) CRP1 [Zea mays]

Seq. No.	137974
Seq. ID	LIB22-026-Q1-E1-D4
Method	BLASTX
NCBI GI	g458969
BLAST score	229
E value	5.0e-19
Match length	99
% identity	46
NCBI Description	(U00033) similar to ACV synthetase and other enzymes which act via an atp-dependent covalent binding of AMP to their substrate [Caenorhabditis elegans]

Seq. No.	137975
Seq. ID	LIB22-026-Q1-E1-E10
Method	BLASTX
NCBI GI	g3757524
BLAST score	287
E value	9.0e-26
Match length	58
% identity	100
NCBI Description	(AC005167) tetracycline transporter-like protein [Arabidopsis thaliana]

Seq. No.	137976
Seq. ID	LIB22-026-Q1-E1-E6
Method	BLASTN
NCBI GI	g3449321
BLAST score	63
E value	4.0e-27
Match length	176
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTG10, complete sequence [Arabidopsis thaliana]

Seq. No.	137977
Seq. ID	LIB22-026-Q1-E1-F8
Method	BLASTX
NCBI GI	g4371286
BLAST score	102
E value	6.0e-21
Match length	54
% identity	96
NCBI Description	(AC006260) putative C-terminal RING-finger protein [Arabidopsis thaliana]

Seq. No.	137978
Seq. ID	LIB22-027-Q1-E1-A8
Method	BLASTN
NCBI GI	g2262135
BLAST score	196
E value	1.0e-106
Match length	401
% identity	99
NCBI Description	Arabidopsis thaliana BAC T10P11 from chromosome IV, near 15 cM, complete sequence

Seq. No.	137979
Seq. ID	LIB22-027-Q1-E1-C12
Method	BLASTX
NCBI GI	g1169228
BLAST score	215
E value	3.0e-17
Match length	73
% identity	56
NCBI Description	RNA HELICASE-LIKE PROTEIN DB10 >gi_1084413_pir__S42639 helicase-like protein - Wood tobacco >gi_563986_dbj_BAA03763_ (D16247) RNA helicase like protein DB10 [Nicotiana sylvestris]

Seq. No.	137980
Seq. ID	LIB22-027-Q1-E1-C4
Method	BLASTX
NCBI GI	g3176687
BLAST score	666
E value	3.0e-70
Match length	123
% identity	99
NCBI Description	(AC003671) Strong similarity to trehalose-6-phosphate synthase homolog from A. thaliana chromosome 4 contig

gb_Z97344. ESTs gb_H37594, gb_R65023, gb_H37578 and gb_R64855 come from this gene. [Arabidopsis thaliana]

Seq. No.	137981
Seq. ID	LIB22-027-Q1-E1-C7
Method	BLASTN
NCBI GI	g3868722
BLAST score	47
E value	2.0e-17
Match length	83
% identity	89
NCBI Description	Arabidopsis thaliana BAC T19G15, from chromosome V near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	137982
Seq. ID	LIB22-027-Q1-E1-E1
Method	BLASTX
NCBI GI	g2618687
BLAST score	260
E value	9.0e-23
Match length	102
% identity	54
NCBI Description	(AC002510) hypothetical protein [Arabidopsis thaliana]

Seq. No.	137983
Seq. ID	LIB22-027-Q1-E1-F12
Method	BLASTN
NCBI GI	g1699056
BLAST score	365
E value	0.0e+00
Match length	369
% identity	100
NCBI Description	Arabidopsis thaliana 27 kDa unknown protein mRNA, complete cds

Seq. No.	137984
Seq. ID	LIB22-027-Q1-E1-G2
Method	BLASTN
NCBI GI	g2244870
BLAST score	347
E value	0.0e+00
Match length	375
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	137985
Seq. ID	LIB22-028-Q1-E1-A3
Method	BLASTX
NCBI GI	g2809246
BLAST score	178
E value	4.0e-13
Match length	66
% identity	48
NCBI Description	(AC002560) F24O1.15 [Arabidopsis thaliana]

Seq. No. 137986

09604960 - 970204

Seq. ID	LIB22-028-Q1-E1-B11
Method	BLASTN
NCBI GI	g3449330
BLAST score	381
E value	0.0e+00
Match length	400
% identity	62
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDJ14, complete sequence [Arabidopsis thaliana]

Seq. No.	137987
Seq. ID	LIB22-028-Q1-E1-B6
Method	BLASTN
NCBI GI	g285954
BLAST score	41
E value	9.0e-14
Match length	173
% identity	92
NCBI Description	Human mRNA for KIAA0021 gene, complete cds

Seq. No.	137988
Seq. ID	LIB22-028-Q1-E1-B9
Method	BLASTX
NCBI GI	g2244762
BLAST score	304
E value	9.0e-28
Match length	66
% identity	79
NCBI Description	(Z97335) major latex protein [Arabidopsis thaliana]

Seq. No.	137989
Seq. ID	LIB22-028-Q1-E1-C2
Method	BLASTX
NCBI GI	g452470
BLAST score	490
E value	1.0e-49
Match length	99
% identity	99
NCBI Description	(U05218) ATP sulfurylase [Arabidopsis thaliana]

Seq. No.	137990
Seq. ID	LIB22-028-Q1-E1-D4
Method	BLASTX
NCBI GI	g2459445
BLAST score	228
E value	7.0e-19
Match length	103
% identity	24
NCBI Description	(AC002332) putative ribonucleoprotein [Arabidopsis thaliana]

Seq. No.	137991
Seq. ID	LIB22-028-Q1-E1-D7
Method	BLASTN
NCBI GI	g4235150
BLAST score	86
E value	3.0e-41

Match length	90
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC T25B24 genomic sequence, complete sequence

Seq. No.	137992
Seq. ID	LIB22-028-Q1-E1-F11
Method	BLASTX
NCBI GI	g1076334
BLAST score	557
E value	2.0e-57
Match length	108
% identity	100
NCBI Description	hypothetical protein HYP1 - Arabidopsis thaliana >gi_499168_emb_CAA56145_ (X79707) HYP1 [Arabidopsis thaliana]

Seq. No.	137993
Seq. ID	LIB22-028-Q1-E1-F5
Method	BLASTX
NCBI GI	g1399277
BLAST score	339
E value	5.0e-32
Match length	62
% identity	100
NCBI Description	(U31836) calmodulin-domain protein kinase CDPK isoform 7 [Arabidopsis thaliana]

Seq. No.	137994
Seq. ID	LIB22-028-Q1-E1-F8
Method	BLASTX
NCBI GI	g4490750
BLAST score	163
E value	2.0e-11
Match length	33
% identity	97
NCBI Description	(AL035708) GTP-binding protein GB3 [Arabidopsis thaliana]

Seq. No.	137995
Seq. ID	LIB22-028-Q1-E1-G11
Method	BLASTX
NCBI GI	g4587550
BLAST score	187
E value	4.0e-14
Match length	75
% identity	52
NCBI Description	(AC006577) EST gb_R64848 comes from this gene. [Arabidopsis thaliana]

Seq. No.	137996
Seq. ID	LIB22-028-Q1-E1-G8
Method	BLASTX
NCBI GI	g4581146
BLAST score	426
E value	4.0e-42
Match length	93
% identity	92

NCBI Description	(AC006919) putative fructose-bisphosphate aldolase, cytoplasmic [Arabidopsis thaliana]

Seq. No.	137997
Seq. ID	LIB22-028-Q1-E1-H12
Method	BLASTX
NCBI GI	g4220514
BLAST score	423
E value	1.0e-41
Match length	102
% identity	77
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	137998
Seq. ID	LIB22-028-Q1-E1-H7
Method	BLASTX
NCBI GI	g4165154
BLAST score	509
E value	7.0e-52
Match length	119
% identity	81
NCBI Description	(AF115482) topoisomerase I [Nicotiana tabacum]

Seq. No.	137999
Seq. ID	LIB22-028-Q1-E1-H8
Method	BLASTN
NCBI GI	g4646215
BLAST score	276
E value	1.0e-154
Match length	296
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T22O13 genomic sequence, complete sequence

Seq. No.	138000
Seq. ID	LIB22-028-Q1-E1-H9
Method	BLASTN
NCBI GI	g3702724
BLAST score	312
E value	1.0e-175
Match length	384
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K17N15, complete sequence [Arabidopsis thaliana]

Seq. No.	138001
Seq. ID	LIB22-029-Q1-E1-D6
Method	BLASTN
NCBI GI	g4581138
BLAST score	76
E value	6.0e-35
Match length	189
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC F1O11 genomic sequence, complete sequence

Seq. No.	138002

Seq. ID	LIB22-029-Q1-E1-E12
Method	BLASTN
NCBI GI	g3241922
BLAST score	143
E value	6.0e-75
Match length	167
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLM24, complete sequence [Arabidopsis thaliana]

Seq. No.	138003
Seq. ID	LIB22-029-Q1-E1-F2
Method	BLASTX
NCBI GI	g4588002
BLAST score	471
E value	1.0e-47
Match length	92
% identity	100
NCBI Description	(AF085279) hypothetical ankyrin-like protein [Arabidopsis thaliana]

Seq. No.	138004
Seq. ID	LIB22-029-Q1-E1-F4
Method	BLASTN
NCBI GI	g4415905
BLAST score	261
E value	1.0e-145
Match length	261
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F13K3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138005
Seq. ID	LIB22-029-Q1-E1-G12
Method	BLASTX
NCBI GI	g3859595
BLAST score	361
E value	2.0e-34
Match length	79
% identity	94
NCBI Description	(AF104919) No definition line found [Arabidopsis thaliana]

Seq. No.	138006
Seq. ID	LIB22-029-Q1-E1-G4
Method	BLASTX
NCBI GI	g1514643
BLAST score	428
E value	2.0e-42
Match length	102
% identity	42
NCBI Description	(Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]

Seq. No.	138007
Seq. ID	LIB22-029-Q1-E1-G5
Method	BLASTX
NCBI GI	g1363489
BLAST score	496

E value	2.0e-50
Match length	91
% identity	99
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	138008
Seq. ID	LIB22-029-Q1-E1-G9
Method	BLASTX
NCBI GI	g4510401
BLAST score	525
E value	7.0e-54
Match length	104
% identity	98
NCBI Description	(AC006587) putative general negative regulator of transcription [Arabidopsis thaliana]

Seq. No.	138009
Seq. ID	LIB22-029-Q1-E1-H9
Method	BLASTX
NCBI GI	g4508069
BLAST score	309
E value	6.0e-29
Match length	62
% identity	97
NCBI Description	(AC005882) 12246 [Arabidopsis thaliana]

Seq. No.	138010
Seq. ID	LIB22-030-Q1-E1-B5
Method	BLASTX
NCBI GI	g2894306
BLAST score	396
E value	1.0e-38
Match length	106
% identity	79
NCBI Description	(AJ223329) ubiquitin extension protein [Nicotiana tabacum]

Seq. No.	138011
Seq. ID	LIB22-030-Q1-E1-B9
Method	BLASTX
NCBI GI	g3912953
BLAST score	163
E value	2.0e-11
Match length	58
% identity	57
NCBI Description	PUTATIVE 1-AMINOCYCLOPROPANE-1-CARBOXYLATE DEAMINASE (ACC DEAMINASE) >gi_3256439_dbj_BAA29122.1_ (AP000001) 328aa long hypothetical 1-aminocyclopropane-1-carboxylate deaminase [Pyrococcus horikoshii]

Seq. No.	138012
Seq. ID	LIB22-030-Q1-E1-C8
Method	BLASTN
NCBI GI	g2564051
BLAST score	318
E value	1.0e-179

Match length	318
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD9, complete sequence [Arabidopsis thaliana]

Seq. No.	138013
Seq. ID	LIB22-030-Q1-E1-D2
Method	BLASTX
NCBI GI	g2388580
BLAST score	321
E value	8.0e-30
Match length	82
% identity	67
NCBI Description	(AC000098) Similar to Sequence 10 from patent 5477002 (gb_1253956). [Arabidopsis thaliana]

Seq. No.	138014
Seq. ID	LIB22-030-Q1-E1-D3
Method	BLASTN
NCBI GI	g2618602
BLAST score	116
E value	9.0e-59
Match length	220
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	138015
Seq. ID	LIB22-030-Q1-E1-E1
Method	BLASTX
NCBI GI	g2702281
BLAST score	502
E value	4.0e-51
Match length	112
% identity	50
NCBI Description	(AC003033) putative protein disulfide isomerase precursor [Arabidopsis thaliana]

Seq. No.	138016
Seq. ID	LIB22-030-Q1-E1-F1
Method	BLASTX
NCBI GI	g3522939
BLAST score	674
E value	4.0e-71
Match length	127
% identity	99
NCBI Description	(AC004411) putative squamosa-promoter binding protein [Arabidopsis thaliana]

Seq. No.	138017
Seq. ID	LIB22-030-Q1-E1-F2
Method	BLASTN
NCBI GI	g4587641
BLAST score	287
E value	1.0e-160
Match length	287
% identity	100

NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence
Seq. No.	138018
Seq. ID	LIB22-030-Q1-E1-F4
Method	BLASTX
NCBI GI	g3482977
BLAST score	603
E value	6.0e-63
Match length	116
% identity	99
NCBI Description	(AL031369) putative protein [Arabidopsis thaliana]
Seq. No.	138019
Seq. ID	LIB22-030-Q1-E1-G1
Method	BLASTX
NCBI GI	g3080433
BLAST score	324
E value	4.0e-30
Match length	112
% identity	52
NCBI Description	(AL022605) putative gamma-glutamyltransferase [Arabidopsis thaliana]
Seq. No.	138020
Seq. ID	LIB22-031-Q1-E1-A2
Method	BLASTN
NCBI GI	g3688169
BLAST score	178
E value	1.0e-95
Match length	253
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F26P21 (ESSAII project)
Seq. No.	138021
Seq. ID	LIB22-031-Q1-E1-B12
Method	BLASTX
NCBI GI	g3913379
BLAST score	414
E value	1.0e-40
Match length	77
% identity	100
NCBI Description	CRYPTOCHROME 2 APOPROTEIN (BLUE LIGHT PHOTORECEPTOR) >gi_1857038 (U43397) cryptochrome 2 apoprotein [Arabidopsis thaliana]
Seq. No.	138022
Seq. ID	LIB22-031-Q1-E1-C8
Method	BLASTN
NCBI GI	g3132469
BLAST score	195
E value	1.0e-105
Match length	381
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T29F13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138023
Seq. ID	LIB22-031-Q1-E1-D5
Method	BLASTX
NCBI GI	g4008006
BLAST score	223
E value	3.0e-18
Match length	76
% identity	57
NCBI Description	(AF084034) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	138024
Seq. ID	LIB22-031-Q1-E1-E3
Method	BLASTN
NCBI GI	g2914688
BLAST score	84
E value	1.0e-39
Match length	241
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F24L7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138025
Seq. ID	LIB22-031-Q1-E1-F11
Method	BLASTX
NCBI GI	g3924613
BLAST score	484
E value	7.0e-49
Match length	92
% identity	100
NCBI Description	(AF069442) hypothetical protein [Arabidopsis thaliana] >gi_4263512_gb_AAD15338_ (AC004044) hypothetical protein [Arabidopsis thaliana]

Seq. No.	138026
Seq. ID	LIB22-031-Q1-E1-F5
Method	BLASTN
NCBI GI	g4757401
BLAST score	214
E value	1.0e-117
Match length	287
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGH6, complete sequence

Seq. No.	138027
Seq. ID	LIB22-031-Q1-E1-F8
Method	BLASTN
NCBI GI	g3985957
BLAST score	345
E value	0.0e+00
Match length	373
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN8, complete sequence [Arabidopsis thaliana]

Seq. No.	138028
Seq. ID	LIB22-031-Q1-E1-G3
Method	BLASTN
NCBI GI	g3859658
BLAST score	130
E value	6.0e-67
Match length	311
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1 (ESSAII project)

Seq. No.	138029
Seq. ID	LIB22-031-Q1-E1-H9
Method	BLASTX
NCBI GI	g2827139
BLAST score	274
E value	8.0e-25
Match length	55
% identity	87
NCBI Description	(AF027172) cellulose synthase catalytic subunit [Arabidopsis thaliana] >gi_4049343_emb_CAA22568_ (AL034567) cellulose synthase catalytic subunit (RSW1) [Arabidopsis thaliana]

Seq. No.	138030
Seq. ID	LIB22-032-Q1-E1-C10
Method	BLASTX
NCBI GI	g3249084
BLAST score	429
E value	1.0e-42
Match length	83
% identity	35
NCBI Description	(AC004473) Similar to red-1 (related to thioredoxin) gene gb_X92750 from Mus musculus. ESTs gb_AA712687 and gb_Z37223 come from this gene [Arabidopsis thaliana]

Seq. No.	138031
Seq. ID	LIB22-032-Q1-E1-C12
Method	BLASTX
NCBI GI	g2829921
BLAST score	384
E value	2.0e-37
Match length	102
% identity	81
NCBI Description	(AC002291) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	138032
Seq. ID	LIB22-032-Q1-E1-C2
Method	BLASTX
NCBI GI	g4160532
BLAST score	297
E value	5.0e-27
Match length	108
% identity	53
NCBI Description	(AJ011304) sphingosine-1-phosphate lyase [Homo sapiens]

Seq. No.	138033

Seq. ID	LIB22-032-Q1-E1-D6
Method	BLASTN
NCBI GI	g3510336
BLAST score	47
E value	2.0e-17
Match length	59
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18J17, complete sequence [Arabidopsis thaliana]

Seq. No.	138034
Seq. ID	LIB22-032-Q1-E1-F10
Method	BLASTX
NCBI GI	g4455787
BLAST score	206
E value	2.0e-16
Match length	73
% identity	47
NCBI Description	(AL035536) putative DNA polymerase accessory protein [Schizosaccharomyces pombe]

Seq. No.	138035
Seq. ID	LIB22-032-Q1-E1-G9
Method	BLASTX
NCBI GI	g1161926
BLAST score	84
E value	3.0e-11
Match length	53
% identity	72
NCBI Description	(U34392) alpha-carboxyltransferase aCT-1 precursor [Glycine max]

Seq. No.	138036
Seq. ID	LIB22-032-Q1-E1-H11
Method	BLASTN
NCBI GI	g4262221
BLAST score	143
E value	1.0e-74
Match length	297
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138037
Seq. ID	LIB22-033-Q1-E1-C4
Method	BLASTN
NCBI GI	g4544405
BLAST score	363
E value	0.0e+00
Match length	363
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F28I8 genomic sequence, complete sequence

Seq. No.	138038
Seq. ID	LIB22-033-Q1-E2-A9
Method	BLASTN

NCBI GI	g2979540
BLAST score	320
E value	1.0e-180
Match length	320
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F17K2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138039
Seq. ID	LIB22-033-Q1-E2-B12
Method	BLASTN
NCBI GI	g3702731
BLAST score	233
E value	1.0e-128
Match length	377
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFC19, complete sequence [Arabidopsis thaliana]

Seq. No.	138040
Seq. ID	LIB22-033-Q1-E2-C12
Method	BLASTX
NCBI GI	g3142302
BLAST score	486
E value	3.0e-49
Match length	101
% identity	66
NCBI Description	(AC002411) Strong similarity to myosin heavy chain gb_Z34293 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	138041
Seq. ID	LIB22-033-Q1-E2-F11
Method	BLASTX
NCBI GI	g2262167
BLAST score	546
E value	3.0e-56
Match length	104
% identity	100
NCBI Description	(AC002329) cytosolic ribosomal protein S4 [Arabidopsis thaliana]

Seq. No.	138042
Seq. ID	LIB22-033-Q1-E2-G9
Method	BLASTN
NCBI GI	g3789706
BLAST score	263
E value	1.0e-146
Match length	360
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F15K9 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138043
Seq. ID	LIB22-034-Q1-E2-A1
Method	BLASTX
NCBI GI	g3880145
BLAST score	207

E value	1.0e-16
Match length	85
% identity	46
NCBI Description	(Z68319) similar to tyrosine specific protein phosphatase; cDNA EST yk460c9.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	138044
Seq. ID	LIB22-034-Q1-E2-B7
Method	BLASTX
NCBI GI	g4558665
BLAST score	203
E value	4.0e-16
Match length	98
% identity	48
NCBI Description	(AC007063) putative white protein [Arabidopsis thaliana]

Seq. No.	138045
Seq. ID	LIB22-034-Q1-E2-B8
Method	BLASTN
NCBI GI	g4455321
BLAST score	49
E value	6.0e-19
Match length	145
% identity	84
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4I10 (ESSAII project)

Seq. No.	138046
Seq. ID	LIB22-034-Q1-E2-D6
Method	BLASTN
NCBI GI	g3201608
BLAST score	45
E value	1.0e-16
Match length	109
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC F7F1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138047
Seq. ID	LIB22-034-Q1-E2-E12
Method	BLASTN
NCBI GI	g4469002
BLAST score	256
E value	1.0e-142
Match length	256
% identity	48
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15 (ESSA project)

Seq. No.	138048
Seq. ID	LIB22-034-Q1-E2-E7
Method	BLASTN
NCBI GI	g4586098
BLAST score	191
E value	1.0e-103
Match length	251

% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F16J13 (ESSA project)

Seq. No.	138049
Seq. ID	LIB22-034-Q1-E2-E8
Method	BLASTN
NCBI GI	g4589445
BLAST score	214
E value	1.0e-117
Match length	334
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWL2, complete sequence

Seq. No.	138050
Seq. ID	LIB22-034-Q1-E2-F10
Method	BLASTN
NCBI GI	g4049332
BLAST score	144
E value	2.0e-75
Match length	230
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F8B4 (ESSAII project)

Seq. No.	138051
Seq. ID	LIB22-034-Q1-E2-F11
Method	BLASTN
NCBI GI	g2244829
BLAST score	319
E value	1.0e-179
Match length	343
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	138052
Seq. ID	LIB22-034-Q1-E2-G12
Method	BLASTN
NCBI GI	g3413696
BLAST score	227
E value	1.0e-124
Match length	413
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T19L18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138053
Seq. ID	LIB22-034-Q1-E2-H1
Method	BLASTN
NCBI GI	g4092471
BLAST score	194
E value	1.0e-105
Match length	363
% identity	100
NCBI Description	Arabidopsis thaliana BAC F9M13 from chromosome IV near 21.5

cM, complete sequence

Seq. No.	138054
Seq. ID	LIB22-034-Q1-E2-H8
Method	BLASTX
NCBI GI	g2244884
BLAST score	131
E value	9.0e-29
Match length	79
% identity	91
NCBI Description	(Z97338) glucosyltransferase [Arabidopsis thaliana]

Seq. No.	138055
Seq. ID	LIB22-035-Q1-E1-B11
Method	BLASTX
NCBI GI	g3046694
BLAST score	191
E value	7.0e-15
Match length	54
% identity	74
NCBI Description	(AL022224) vacuolar sorting receptor-like protein [Arabidopsis thaliana]

Seq. No.	138056
Seq. ID	LIB22-035-Q1-E1-B9
Method	BLASTX
NCBI GI	g3292829
BLAST score	180
E value	3.0e-13
Match length	82
% identity	50
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	138057
Seq. ID	LIB22-035-Q1-E1-C12
Method	BLASTX
NCBI GI	g1402916
BLAST score	470
E value	3.0e-47
Match length	90
% identity	100
NCBI Description	(X98319) peroxidase [Arabidopsis thaliana] >gi_1429217_emb_CAA67311_ (X98775) peroxidase ATP12a [Arabidopsis thaliana]

Seq. No.	138058
Seq. ID	LIB22-035-Q1-E1-C3
Method	BLASTN
NCBI GI	g4432847
BLAST score	130
E value	7.0e-67
Match length	359
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F13B15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 138059

Seq. ID	LIB22-035-Q1-E1-E1
Method	BLASTX
NCBI GI	g2997755
BLAST score	211
E value	6.0e-17
Match length	118
% identity	39
NCBI Description	(AF054823) TFIIH transcription/DNA repair factor p52 subunit [Mus musculus]

Seq. No.	138060
Seq. ID	LIB22-035-Q1-E1-F9
Method	BLASTX
NCBI GI	g4580531
BLAST score	550
E value	1.0e-56
Match length	125
% identity	86
NCBI Description	(AF036309) scarecrow-like 14 [Arabidopsis thaliana]

Seq. No.	138061
Seq. ID	LIB22-035-Q1-E1-H10
Method	BLASTX
NCBI GI	g3559805
BLAST score	213
E value	1.0e-45
Match length	105
% identity	88
NCBI Description	(AJ006787) putative phytochelatin synthetase [Arabidopsis thaliana]

Seq. No.	138062
Seq. ID	LIB22-035-Q1-E1-H12
Method	BLASTX
NCBI GI	g4753653
BLAST score	320
E value	1.0e-29
Match length	118
% identity	86
NCBI Description	(AL049751) putative protein [Arabidopsis thaliana]

Seq. No.	138063
Seq. ID	LIB22-035-Q1-E1-H7
Method	BLASTX
NCBI GI	g2245110
BLAST score	262
E value	6.0e-23
Match length	49
% identity	98
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	138064
Seq. ID	LIB22-036-Q1-E1-A11
Method	BLASTN
NCBI GI	g3241926
BLAST score	200
E value	1.0e-108

Match length	204
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSG15, complete sequence [Arabidopsis thaliana]

Seq. No.	138065
Seq. ID	LIB22-036-Q1-E1-C12
Method	BLASTN
NCBI GI	g4589415
BLAST score	70
E value	3.0e-31
Match length	175
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K14A3, complete sequence

Seq. No.	138066
Seq. ID	LIB22-036-Q1-E1-G1
Method	BLASTX
NCBI GI	g4583544
BLAST score	203
E value	6.0e-16
Match length	46
% identity	85
NCBI Description	(Z95637) acyl-CoA:1-acylglycerol-3-phosphate acyltransferase [Brassica napus]

Seq. No.	138067
Seq. ID	LIB22-036-Q1-E1-G11
Method	BLASTN
NCBI GI	g4732167
BLAST score	89
E value	1.0e-42
Match length	212
% identity	100
NCBI Description	Arabidopsis thaliana BAC F28D6

Seq. No.	138068
Seq. ID	LIB22-037-Q1-E1-B8
Method	BLASTX
NCBI GI	g1791309
BLAST score	178
E value	1.0e-13
Match length	37
% identity	95
NCBI Description	(U83500) cystathionine gamma-synthase [Arabidopsis thaliana] >gi_2852454_dbj_BAA24699_ (AB010888) cystathionine gamma-synthase [Arabidopsis thaliana]

Seq. No.	138069
Seq. ID	LIB22-037-Q1-E1-C8
Method	BLASTX
NCBI GI	g1168470
BLAST score	410
E value	4.0e-40
Match length	82
% identity	100

NCBI Description	PROTEIN KINASE APK1A >gi_282877_pir__S28615 protein kinase, tyrosine/serine/threonine-specific (EC 2.7.1.-) - Arabidopsis thaliana >gi_217829_dbj_BAA02092_ (D12522) protein tyrosine-serine-threonine kinase [Arabidopsis thaliana]
Seq. No.	138070
Seq. ID	LIB22-037-Q1-E1-D2
Method	BLASTX
NCBI GI	g4468807
BLAST score	437
E value	3.0e-43
Match length	131
% identity	68
NCBI Description	(AL035601) cytochrome P450 monooxygenase-like protein [Arabidopsis thaliana]
Seq. No.	138071
Seq. ID	LIB22-037-Q1-E1-F4
Method	BLASTX
NCBI GI	g2632103
BLAST score	449
E value	4.0e-45
Match length	86
% identity	99
NCBI Description	(Z98759) arginyl-tRNA synthetase [Arabidopsis thaliana]
Seq. No.	138072
Seq. ID	LIB22-037-Q1-E1-H8
Method	BLASTX
NCBI GI	g1906000
BLAST score	530
E value	3.0e-54
Match length	112
% identity	88
NCBI Description	(U90428) blue copper-binding protein II [Arabidopsis thaliana]
Seq. No.	138073
Seq. ID	LIB22-038-Q1-E1-B6
Method	BLASTN
NCBI GI	g4519193
BLAST score	127
E value	5.0e-65
Match length	422
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC11, complete sequence
Seq. No.	138074
Seq. ID	LIB22-038-Q1-E1-D8
Method	BLASTN
NCBI GI	g3859658
BLAST score	155
E value	5.0e-82
Match length	199
% identity	94

NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1 (ESSAII project)
Seq. No.	138075
Seq. ID	LIB22-038-Q1-E1-F4
Method	BLASTN
NCBI GI	g4757407
BLAST score	32
E value	1.0e-08
Match length	75
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQD19, complete sequence
Seq. No.	138076
Seq. ID	LIB22-038-Q1-E1-G10
Method	BLASTN
NCBI GI	g4757388
BLAST score	36
E value	1.0e-10
Match length	161
% identity	80
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F15L12, complete sequence
Seq. No.	138077
Seq. ID	LIB22-038-Q1-E1-G12
Method	BLASTX
NCBI GI	g4415908
BLAST score	278
E value	9.0e-25
Match length	95
% identity	54
NCBI Description	(AC006282) unknown protein [Arabidopsis thaliana]
Seq. No.	138078
Seq. ID	LIB22-038-Q1-E1-G7
Method	BLASTX
NCBI GI	g1702987
BLAST score	553
E value	6.0e-57
Match length	122
% identity	93
NCBI Description	14-3-3-LIKE PROTEIN GF14 PHI >gi_1493805 (L09111) GF14 protein phi chain [Arabidopsis thaliana] >gi_2232146 (AF001414) 14-3-3-like protein GF14 phi [Arabidopsis thaliana]
Seq. No.	138079
Seq. ID	LIB22-038-Q1-E1-H11
Method	BLASTN
NCBI GI	g2506048
BLAST score	391
E value	0.0e+00
Match length	391
% identity	100
NCBI Description	Arabidopsis thaliana DNA for alternative oxidase (AOX1c

gene), complete cds

Seq. No.	138080
Seq. ID	LIB22-039-Q1-E1-A11
Method	BLASTX
NCBI GI	g2088654
BLAST score	216
E value	2.0e-17
Match length	64
% identity	72
NCBI Description	(AF002109) 60S acidic ribosomal protein P0 isolog [Arabidopsis thaliana]

Seq. No.	138081
Seq. ID	LIB22-039-Q1-E1-B2
Method	BLASTN
NCBI GI	g4185128
BLAST score	146
E value	9.0e-77
Match length	170
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II P1 MSF3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138082
Seq. ID	LIB22-039-Q1-E1-C5
Method	BLASTX
NCBI GI	g1518540
BLAST score	353
E value	2.0e-33
Match length	71
% identity	87
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	138083
Seq. ID	LIB22-039-Q1-E1-C7
Method	BLASTN
NCBI GI	g3402745
BLAST score	295
E value	1.0e-165
Match length	315
% identity	85
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F18E5 (ESSAII project)

Seq. No.	138084
Seq. ID	LIB22-039-Q1-E1-E7
Method	BLASTN
NCBI GI	g2618602
BLAST score	246
E value	1.0e-136
Match length	369
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No. 138085

Seq. ID	LIB22-039-Q1-E1-E9
Method	BLASTN
NCBI GI	g4519187
BLAST score	198
E value	1.0e-107
Match length	389
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K1G2, complete sequence

Seq. No.	138086
Seq. ID	LIB22-039-Q1-E1-F1
Method	BLASTX
NCBI GI	g730526
BLAST score	205
E value	1.0e-16
Match length	35
% identity	100
NCBI Description	60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG) >gi_480787_pir__S37271 ribosomal protein L13 - Arabidopsis thaliana >gi_404166_emb_CAA53005_ (X75162) BBC1 protein [Arabidopsis thaliana]

Seq. No.	138087
Seq. ID	LIB22-039-Q1-E1-F11
Method	BLASTN
NCBI GI	g4558521
BLAST score	63
E value	2.0e-27
Match length	101
% identity	93
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T10O24, complete sequence

Seq. No.	138088
Seq. ID	LIB22-039-Q1-E1-F7
Method	BLASTN
NCBI GI	g2351062
BLAST score	295
E value	1.0e-165
Match length	328
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAH20, complete sequence [Arabidopsis thaliana]

Seq. No.	138089
Seq. ID	LIB22-039-Q1-E1-F9
Method	BLASTN
NCBI GI	g2642152
BLAST score	157
E value	4.0e-83
Match length	235
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T5I7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138090

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Seq. ID	LIB22-039-Q1-E1-G12
Method	BLASTN
NCBI GI	g4006885
BLAST score	137
E value	5.0e-71
Match length	386
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	138091
Seq. ID	LIB22-039-Q1-E1-H1
Method	BLASTX
NCBI GI	g2895510
BLAST score	395
E value	1.0e-38
Match length	73
% identity	100
NCBI Description	(AF033204) putative pectin methylesterase [Arabidopsis thaliana]

Seq. No.	138092
Seq. ID	LIB22-039-Q1-E1-H4
Method	BLASTX
NCBI GI	g4049399
BLAST score	516
E value	1.0e-52
Match length	96
% identity	100
NCBI Description	(Y09581) FRO2 [Arabidopsis thaliana]

Seq. No.	138093
Seq. ID	LIB22-039-Q1-E1-H6
Method	BLASTX
NCBI GI	g2384673
BLAST score	426
E value	5.0e-42
Match length	81
% identity	100
NCBI Description	(AF012658) putative potassium transporter AtKT3p [Arabidopsis thaliana]

Seq. No.	138094
Seq. ID	LIB22-040-Q1-E1-A5
Method	BLASTX
NCBI GI	g2897946
BLAST score	150
E value	1.0e-09
Match length	115
% identity	37
NCBI Description	(AF007544) prostate-specific membrane antigen [Homo sapiens]

Seq. No.	138095
Seq. ID	LIB22-040-Q1-E1-B6
Method	BLASTX
NCBI GI	g2642448

BLAST score	250
E value	5.0e-22
Match length	57
% identity	40
NCBI Description	(AC002391) hypothetical protein [Arabidopsis thaliana] >gi_3169187 (AC004401) hypothetical protein [Arabidopsis thaliana]

Seq. No.	138096
Seq. ID	LIB22-040-Q1-E1-C7
Method	BLASTN
NCBI GI	g4559375
BLAST score	261
E value	1.0e-145
Match length	321
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F11C10 genomic sequence, complete sequence

Seq. No.	138097
Seq. ID	LIB22-040-Q1-E1-E11
Method	BLASTN
NCBI GI	g3212846
BLAST score	243
E value	1.0e-134
Match length	418
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138098
Seq. ID	LIB22-040-Q1-E1-E12
Method	BLASTN
NCBI GI	g1402907
BLAST score	160
E value	7.0e-85
Match length	160
% identity	100
NCBI Description	A.thaliana mRNA for peroxidase, prxr3

Seq. No.	138099
Seq. ID	LIB22-040-Q1-E1-G1
Method	BLASTN
NCBI GI	g4519193
BLAST score	201
E value	1.0e-109
Match length	245
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC11, complete sequence

Seq. No.	138100
Seq. ID	LIB22-040-Q1-E1-G8
Method	BLASTN
NCBI GI	g3193282
BLAST score	44
E value	1.0e-15

Match length	128
% identity	84
NCBI Description	Arabidopsis thaliana BAC T14P8

Seq. No.	138101
Seq. ID	LIB22-041-Q1-E1-A12
Method	BLASTX
NCBI GI	g3063472
BLAST score	623
E value	4.0e-65
Match length	116
% identity	99
NCBI Description	(AC003981) F22O13.34 [Arabidopsis thaliana]

Seq. No.	138102
Seq. ID	LIB22-041-Q1-E1-A9
Method	BLASTN
NCBI GI	g4757417
BLAST score	130
E value	3.0e-67
Match length	166
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: T30G6, complete sequence

Seq. No.	138103
Seq. ID	LIB22-041-Q1-E1-B5
Method	BLASTX
NCBI GI	g2499608
BLAST score	475
E value	9.0e-48
Match length	118
% identity	81
NCBI Description	MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 4 (MAP KINASE 4) (ATMPK4) >gi_2129645_pir__S40470 mitogen-activated protein kinase 4 (EC 2.7.1.-) - Arabidopsis thaliana >gi_457400_dbj_BAA04867_ (D21840) MAP kinase [Arabidopsis thaliana]

Seq. No.	138104
Seq. ID	LIB22-041-Q1-E1-B6
Method	BLASTX
NCBI GI	g3193309
BLAST score	148
E value	4.0e-24
Match length	83
% identity	77
NCBI Description	(AF069300) No definition line found [Arabidopsis thaliana]

Seq. No.	138105
Seq. ID	LIB22-041-Q1-E1-B9
Method	BLASTX
NCBI GI	g4469023
BLAST score	528
E value	5.0e-54
Match length	118
% identity	85

NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	138106
Seq. ID	LIB22-041-Q1-E1-C4
Method	BLASTN
NCBI GI	g4519190
BLAST score	186
E value	1.0e-100
Match length	395
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K6A12, complete sequence

Seq. No.	138107
Seq. ID	LIB22-041-Q1-E1-C9
Method	BLASTN
NCBI GI	g2980787
BLAST score	203
E value	1.0e-110
Match length	327
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, P1 clone M7J2 (ESSAII project)

Seq. No.	138108
Seq. ID	LIB22-041-Q1-E1-D11
Method	BLASTX
NCBI GI	g3063691
BLAST score	222
E value	1.0e-18
Match length	45
% identity	84
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]

Seq. No.	138109
Seq. ID	LIB22-041-Q1-E1-G2
Method	BLASTN
NCBI GI	g4567237
BLAST score	258
E value	1.0e-143
Match length	309
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T22F11 genomic sequence, complete sequence

Seq. No.	138110
Seq. ID	LIB22-042-Q1-E1-B1
Method	BLASTX
NCBI GI	g134976
BLAST score	42
E value	6.0e-43
Match length	90
% identity	100
NCBI Description	GLUCOSE TRANSPORTER (SUGAR CARRIER) >gi_81619_pir__S12042 glucose transport protein STP1 - Arabidopsis thaliana >gi_16520_emb_CAA39037_ (X55350) glucose transporter [Arabidopsis thaliana]

Seq. No.	138111
Seq. ID	LIB22-042-Q1-E1-C5
Method	BLASTN
NCBI GI	g633027
BLAST score	244
E value	1.0e-135
Match length	244
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for protein phosphatase 2C

Seq. No.	138112
Seq. ID	LIB22-042-Q1-E1-F3
Method	BLASTX
NCBI GI	g2576361
BLAST score	600
E value	2.0e-62
Match length	112
% identity	100
NCBI Description	(U39782) lysine and histidine specific transporter [Arabidopsis thaliana]

Seq. No.	138113
Seq. ID	LIB22-042-Q1-E1-H11
Method	BLASTX
NCBI GI	g99697
BLAST score	713
E value	1.0e-75
Match length	135
% identity	99
NCBI Description	glutamate--ammonia ligase (EC 6.3.1.2), cytosolic (clone lambdaAtgsr2) - Arabidopsis thaliana

Seq. No.	138114
Seq. ID	LIB22-043-Q1-E1-B5
Method	BLASTX
NCBI GI	g4454049
BLAST score	225
E value	1.0e-18
Match length	60
% identity	80
NCBI Description	(AL035394) 98b like protein [Arabidopsis thaliana]

Seq. No.	138115
Seq. ID	LIB22-043-Q1-E1-B6
Method	BLASTX
NCBI GI	g2144191
BLAST score	151
E value	8.0e-10
Match length	82
% identity	46
NCBI Description	glucan 1,4-beta-glucosidase (EC 3.2.1.74) - Microbispora bispora >gi_149826 (L06134) glucan-glucohydrolase [Microbispora bispora]

Seq. No.	138116
Seq. ID	LIB22-043-Q1-E1-C1

Method	BLASTX
NCBI GI	g128405
BLAST score	284
E value	1.0e-25
Match length	75
% identity	71
NCBI Description	NODULIN 21 (N-21) >gi_99942_pir__S08632 nodulin-21 - soybean >gi_18694_emb_CAA34506_ (X16488) nodulin-21 (AA 1-201) [Glycine max]

Seq. No.	138117
Seq. ID	LIB22-043-Q1-E1-C10
Method	BLASTN
NCBI GI	g4469002
BLAST score	91
E value	5.0e-44
Match length	134
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15 (ESSA project)

Seq. No.	138118
Seq. ID	LIB22-043-Q1-E1-C12
Method	BLASTX
NCBI GI	g1170373
BLAST score	686
E value	1.0e-72
Match length	133
% identity	100
NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_1072473_pir__S46302 heat shock cognate protein 70-1 - Arabidopsis thaliana >gi_397482_emb_CAA52684_ (X74604) heat shock protein 70 cognate [Arabidopsis thaliana]

Seq. No.	138119
Seq. ID	LIB22-043-Q1-E1-C5
Method	BLASTN
NCBI GI	g2760168
BLAST score	259
E value	1.0e-144
Match length	384
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MEE6, complete sequence [Arabidopsis thaliana]

Seq. No.	138120
Seq. ID	LIB22-043-Q1-E1-C9
Method	BLASTX
NCBI GI	g4522003
BLAST score	466
E value	9.0e-47
Match length	90
% identity	100
NCBI Description	(AC007069) putative protein kinase [Arabidopsis thaliana]

Seq. No.	138121
Seq. ID	LIB22-043-Q1-E1-D11

Method	BLASTX
NCBI GI	g1490554
BLAST score	401
E value	4.0e-39
Match length	81
% identity	100
NCBI Description	(U63633) S-adenosylmethionine decarboxylase [Arabidopsis thaliana]

Seq. No.	138122
Seq. ID	LIB22-043-Q1-E1-E10
Method	BLASTX
NCBI GI	g1063415
BLAST score	624
E value	3.0e-65
Match length	118
% identity	100
NCBI Description	(L40948) K+ channel protein [Arabidopsis thaliana]

Seq. No.	138123
Seq. ID	LIB22-043-Q1-E1-E6
Method	BLASTX
NCBI GI	g1708461
BLAST score	474
E value	1.0e-47
Match length	113
% identity	85
NCBI Description	IAA-AMINO ACID HYDROLASE HOMOLOG 1 PRECURSOR >gi_902789 (U23795) ILL1 [Arabidopsis thaliana] >gi_2921829_gb_AAC04865.1_ (AF047031) IAA-amino acid hydrolase [Arabidopsis thaliana]

Seq. No.	138124
Seq. ID	LIB22-043-Q1-E1-F12
Method	BLASTN
NCBI GI	g4678219
BLAST score	193
E value	1.0e-104
Match length	323
% identity	82
NCBI Description	Arabidopsis thaliana chromosome II BAC F9C22 genomic sequence, complete sequence

Seq. No.	138125
Seq. ID	LIB22-043-Q1-E1-H11
Method	BLASTX
NCBI GI	g99741
BLAST score	328
E value	1.0e-30
Match length	130
% identity	25
NCBI Description	P-glycoprotein pgp1 - Arabidopsis thaliana

Seq. No.	138126
Seq. ID	LIB22-044-Q1-E1-F12
Method	BLASTN
NCBI GI	g2244829

BLAST score	401
E value	0.0e+00
Match length	401
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	138127
Seq. ID	LIB22-044-Q1-E1-G8
Method	BLASTX
NCBI GI	g2160156
BLAST score	660
E value	1.0e-69
Match length	122
% identity	100
NCBI Description	(AC000132) Strong similarity to S. pombe leucyl-tRNA synthetase (gb_Z73100). [Arabidopsis thaliana]

Seq. No.	138128
Seq. ID	LIB22-044-Q1-E1-H1
Method	BLASTN
NCBI GI	g2760829
BLAST score	245
E value	1.0e-135
Match length	349
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F18A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138129
Seq. ID	LIB22-044-Q1-E1-H10
Method	BLASTN
NCBI GI	g3241917
BLAST score	96
E value	1.0e-46
Match length	275
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19B1, complete sequence [Arabidopsis thaliana]

Seq. No.	138130
Seq. ID	LIB22-045-Q1-E1-A8
Method	BLASTX
NCBI GI	g4587547
BLAST score	243
E value	1.0e-20
Match length	86
% identity	53
NCBI Description	(AC006577) Contains similarity to DNA-binding protein Gt-2 gb_X68261 from Oryza sativa. [Arabidopsis thaliana]

Seq. No.	138131
Seq. ID	LIB22-045-Q1-E1-B2
Method	BLASTX
NCBI GI	g116923
BLAST score	143
E value	5.0e-09

Match length	48
% identity	54
NCBI Description	COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP) >gi_111414_pir__S13520 beta-COP protein - rat >gi_55819_emb_CAA40505_ (X57228) beta COP [Rattus norvegicus]

Seq. No.	138132
Seq. ID	LIB22-045-Q1-E1-B7
Method	BLASTX
NCBI GI	g1654140
BLAST score	200
E value	1.0e-15
Match length	85
% identity	54
NCBI Description	(U37840) lipoxygenase [Lycopersicon esculentum]

Seq. No.	138133
Seq. ID	LIB22-045-Q1-E1-B8
Method	BLASTN
NCBI GI	g3643588
BLAST score	230
E value	1.0e-126
Match length	365
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F17H15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138134
Seq. ID	LIB22-045-Q1-E1-D1
Method	BLASTX
NCBI GI	g2529229
BLAST score	549
E value	2.0e-56
Match length	117
% identity	90
NCBI Description	(AB007907) 6-phosphogluconate dehydrogenase [Glycine max]

Seq. No.	138135
Seq. ID	LIB22-045-Q1-E1-F5
Method	BLASTX
NCBI GI	g3360289
BLAST score	343
E value	3.0e-32
Match length	139
% identity	43
NCBI Description	(AF023164) leucine-rich repeat transmembrane protein kinase 1 [Zea mays]

Seq. No.	138136
Seq. ID	LIB22-045-Q1-E1-F7
Method	BLASTN
NCBI GI	g2072987
BLAST score	51
E value	1.0e-20
Match length	51
% identity	100

NCBI Description	Arabidopsis thaliana putative G-protein-coupled receptor (GCR1) mRNA, complete cds
Seq. No.	138137
Seq. ID	LIB22-045-Q1-E1-G6
Method	BLASTX
NCBI GI	g3935177
BLAST score	666
E value	4.0e-70
Match length	137
% identity	94
NCBI Description	(AC004557) F17L21.20 [Arabidopsis thaliana]
Seq. No.	138138
Seq. ID	LIB22-045-Q1-E1-H3
Method	BLASTN
NCBI GI	g3766106
BLAST score	338
E value	0.0e+00
Match length	338
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F9K20 sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	138139
Seq. ID	LIB22-046-Q1-E1-A1
Method	BLASTX
NCBI GI	g1076331
BLAST score	180
E value	2.0e-13
Match length	74
% identity	49
NCBI Description	histidine transport protein - Arabidopsis thaliana >gi_510238_emb_CAA54634_ (X77503) oligopeptide transporter 1-1 [Arabidopsis thaliana] >gi_744157_prf__2014244A His transporter [Arabidopsis thaliana]
Seq. No.	138140
Seq. ID	LIB22-046-Q1-E1-D3
Method	BLASTX
NCBI GI	g2674107
BLAST score	140
E value	1.0e-08
Match length	60
% identity	48
NCBI Description	(AF023451) guanine nucleotide-exchange protein [Bos taurus]
Seq. No.	138141
Seq. ID	LIB22-046-Q1-E1-D8
Method	BLASTX
NCBI GI	g1669387
BLAST score	537
E value	5.0e-55
Match length	99
% identity	100
NCBI Description	(U41998) actin 2 [Arabidopsis thaliana]

Seq. No.	138142
Seq. ID	LIB22-046-Q1-E1-E10
Method	BLASTX
NCBI GI	g4678337
BLAST score	612
E value	6.0e-64
Match length	120
% identity	100
NCBI Description	(AL049658) putative protein [Arabidopsis thaliana]

Seq. No.	138143
Seq. ID	LIB22-046-Q1-E1-E11
Method	BLASTX
NCBI GI	g3136336
BLAST score	344
E value	1.0e-32
Match length	81
% identity	44
NCBI Description	(AF064552) calmodulin; Cam [Apium graveolens]

Seq. No.	138144
Seq. ID	LIB22-046-Q1-E1-F5
Method	BLASTX
NCBI GI	g1170373
BLAST score	147
E value	3.0e-20
Match length	71
% identity	77
NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_1072473_pir__S46302 heat shock cognate protein 70-1 - Arabidopsis thaliana >gi_397482_emb_CAA52684_ (X74604) heat shock protein 70 cognate [Arabidopsis thaliana]

Seq. No.	138145
Seq. ID	LIB22-046-Q1-E1-G12
Method	BLASTN
NCBI GI	g2088638
BLAST score	344
E value	0.0e+00
Match length	356
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T28M21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138146
Seq. ID	LIB22-047-Q1-E1-A10
Method	BLASTN
NCBI GI	g1931636
BLAST score	119
E value	2.0e-60
Match length	191
% identity	98
NCBI Description	Arabidopsis thaliana BAC T19D16 genomic sequence

Seq. No.	138147
Seq. ID	LIB22-047-Q1-E1-B11
Method	BLASTX

NCBI GI	g3258572
BLAST score	215
E value	7.0e-22
Match length	71
% identity	79
NCBI Description	(U89959) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	138148
Seq. ID	LIB22-047-Q1-E1-C4
Method	BLASTX
NCBI GI	g267073
BLAST score	536
E value	5.0e-55
Match length	99
% identity	99
NCBI Description	TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin beta chain - Arabidopsis thaliana >gi_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701) beta-3 tubulin [Arabidopsis thaliana]

Seq. No.	138149
Seq. ID	LIB22-047-Q1-E1-D5
Method	BLASTX
NCBI GI	g1890352
BLAST score	435
E value	3.0e-43
Match length	81
% identity	55
NCBI Description	(X91398) transcription factor L2 [Arabidopsis thaliana]

Seq. No.	138150
Seq. ID	LIB22-047-Q1-E1-G2
Method	BLASTN
NCBI GI	g3449315
BLAST score	193
E value	1.0e-104
Match length	368
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K23L20, complete sequence [Arabidopsis thaliana]

Seq. No.	138151
Seq. ID	LIB22-048-Q1-E1-B3
Method	BLASTN
NCBI GI	g4455321
BLAST score	233
E value	1.0e-128
Match length	266
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4I10 (ESSAII project)

Seq. No.	138152
Seq. ID	LIB22-048-Q1-E1-C11
Method	BLASTX
NCBI GI	g166765
BLAST score	584

E value	1.0e-60
Match length	111
% identity	100
NCBI Description	(M23106) heat shock protein HSP70-1 [Arabidopsis thaliana]

Seq. No.	138153
Seq. ID	LIB22-048-Q1-E1-D11
Method	BLASTX
NCBI GI	g231536
BLAST score	620
E value	8.0e-65
Match length	124
% identity	100
NCBI Description	CYTOSOL AMINOPEPTIDASE (LEUCINE AMINOPEPTIDASE) (LAP) (LEUCYL AMINOPEPTIDASE) (PROLINE AMINOPEPTIDASE) (PROLYL AMINOPEPTIDASE) >gi_99683_pir__S22399 leucyl aminopeptidase (EC 3.4.11.1) - Arabidopsis thaliana >gi_16394_emb_CAA45040_ (X63444) leucine aminopeptidase [Arabidopsis thaliana] >gi_4115380 (AC005967) putative leucine aminopeptidase [Arabidopsis thaliana]

Seq. No.	138154
Seq. ID	LIB22-048-Q1-E1-D9
Method	BLASTX
NCBI GI	g4512615
BLAST score	686
E value	2.0e-72
Match length	133
% identity	100
NCBI Description	(AC004793) Strong similarity to gb_X59970 3-isopropylmalate dehydrogenase (IMDH) from Brassica napus. EST gb_F14478 comes from this gene. [Arabidopsis thaliana]

Seq. No.	138155
Seq. ID	LIB22-048-Q1-E1-E11
Method	BLASTX
NCBI GI	g4567286
BLAST score	322
E value	7.0e-30
Match length	59
% identity	60
NCBI Description	(AC006841) putative coatomer alpha subunit [Arabidopsis thaliana]

Seq. No.	138156
Seq. ID	LIB22-048-Q1-E1-G10
Method	BLASTX
NCBI GI	g2961390
BLAST score	600
E value	2.0e-62
Match length	111
% identity	100
NCBI Description	(AL022141) beta-galactosidase like protein [Arabidopsis thaliana]

Seq. No.	138157
Seq. ID	LIB22-048-Q1-E1-G3

Method	BLASTX
NCBI GI	g2995943
BLAST score	169
E value	6.0e-12
Match length	96
% identity	43
NCBI Description	(AF053560) cytochrome c oxidase subunit Vb precursor [Mesembryanthemum crystallinum]

Seq. No.	138158
Seq. ID	LIB22-049-Q1-E1-A7
Method	BLASTN
NCBI GI	g4519193
BLAST score	121
E value	2.0e-61
Match length	418
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC11, complete sequence

Seq. No.	138159
Seq. ID	LIB22-049-Q1-E1-B3
Method	BLASTN
NCBI GI	g3449316
BLAST score	277
E value	1.0e-154
Match length	417
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9D7, complete sequence [Arabidopsis thaliana]

Seq. No.	138160
Seq. ID	LIB22-049-Q1-E1-B5
Method	BLASTX
NCBI GI	g4191782
BLAST score	673
E value	5.0e-71
Match length	140
% identity	91
NCBI Description	(AC005917) WD-40 repeat protein [Arabidopsis thaliana]

Seq. No.	138161
Seq. ID	LIB22-049-Q1-E1-F3
Method	BLASTX
NCBI GI	g4586053
BLAST score	205
E value	2.0e-16
Match length	56
% identity	59
NCBI Description	(AC007020) putative lacasse [Arabidopsis thaliana]

Seq. No.	138162
Seq. ID	LIB22-050-Q1-E1-B4
Method	BLASTN
NCBI GI	g3668073
BLAST score	200
E value	1.0e-108

Match length	388
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T4C15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138163
Seq. ID	LIB22-050-Q1-E1-H2
Method	BLASTX
NCBI GI	g629669
BLAST score	142
E value	3.0e-09
Match length	74
% identity	41
NCBI Description	hypothetical protein - tomato

Seq. No.	138164
Seq. ID	LIB22-051-Q1-E1-B7
Method	BLASTX
NCBI GI	g1403134
BLAST score	413
E value	1.0e-40
Match length	83
% identity	98
NCBI Description	(X98453) peroxidase [Arabidopsis thaliana]

Seq. No.	138165
Seq. ID	LIB22-051-Q1-E1-C6
Method	BLASTN
NCBI GI	g4490324
BLAST score	93
E value	1.0e-44
Match length	219
% identity	88
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14 (ESSA project)

Seq. No.	138166
Seq. ID	LIB22-051-Q1-E1-E3
Method	BLASTN
NCBI GI	g4249393
BLAST score	211
E value	1.0e-115
Match length	419
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T9J23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138167
Seq. ID	LIB22-051-Q1-E1-F11
Method	BLASTN
NCBI GI	g3241927
BLAST score	35
E value	4.0e-10
Match length	88
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTE17, complete sequence [Arabidopsis thaliana]

Seq. No.	138168
Seq. ID	LIB22-051-Q1-E1-F3
Method	BLASTN
NCBI GI	g3449325
BLAST score	246
E value	1.0e-136
Match length	285
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K16H17, complete sequence [Arabidopsis thaliana]

Seq. No.	138169
Seq. ID	LIB22-051-Q1-E1-G9
Method	BLASTN
NCBI GI	g2584827
BLAST score	123
E value	3.0e-63
Match length	123
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F12F1 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138170
Seq. ID	LIB22-052-Q1-E1-A7
Method	BLASTN
NCBI GI	g2564044
BLAST score	279
E value	1.0e-155
Match length	407
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19P17, complete sequence [Arabidopsis thaliana]

Seq. No.	138171
Seq. ID	LIB22-052-Q1-E1-A8
Method	BLASTN
NCBI GI	g4490291
BLAST score	135
E value	3.0e-70
Match length	156
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17M5 (ESSA project)

Seq. No.	138172
Seq. ID	LIB22-052-Q1-E1-B11
Method	BLASTX
NCBI GI	g1702986
BLAST score	464
E value	2.0e-46
Match length	95
% identity	99
NCBI Description	14-3-3-LIKE PROTEIN GF14 CHI >gi_1255987 (U09377) GF14chi isoform [Arabidopsis thaliana] >gi_1256534 (L09112) GF14 chi chain [Arabidopsis thaliana]

Seq. No.	138173
Seq. ID	LIB22-052-Q1-E1-B4
Method	BLASTX
NCBI GI	g1550740
BLAST score	450
E value	6.0e-45
Match length	118
% identity	77
NCBI Description	(Y07961) GDP-associated inhibitor [Arabidopsis thaliana]

Seq. No.	138174
Seq. ID	LIB22-052-Q1-E1-C1
Method	BLASTN
NCBI GI	g3510343
BLAST score	350
E value	0.0e+00
Match length	380
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJC20, complete sequence [Arabidopsis thaliana]

Seq. No.	138175
Seq. ID	LIB22-052-Q1-E1-C4
Method	BLASTX
NCBI GI	g120675
BLAST score	486
E value	4.0e-49
Match length	110
% identity	85
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66011_pir__DEIS3C glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - white mustard >gi_21143_emb_CAA27844_ (X04301) GAPDH (aa 1-338) [Sinapis alba]

Seq. No.	138176
Seq. ID	LIB22-052-Q1-E1-C8
Method	BLASTX
NCBI GI	g3738309
BLAST score	493
E value	6.0e-50
Match length	120
% identity	79
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	138177
Seq. ID	LIB22-052-Q1-E1-C9
Method	BLASTX
NCBI GI	g3328101
BLAST score	299
E value	2.0e-27
Match length	85
% identity	61
NCBI Description	(AF073995) beta-galactosidase [synthetic construct]

Seq. No.	138178
Seq. ID	LIB22-052-Q1-E1-D6

Method	BLASTX
NCBI GI	g4539386
BLAST score	173
E value	2.0e-12
Match length	91
% identity	45
NCBI Description	(AL035526) extensin-like protein [Arabidopsis thaliana]

Seq. No.	138179
Seq. ID	LIB22-052-Q1-E1-E11
Method	BLASTX
NCBI GI	g2498943
BLAST score	215
E value	3.0e-17
Match length	91
% identity	42
NCBI Description	PUTATIVE SPERMIDINE SYNTHASE (PUTRESCINE AMINOPROPYLTRANSFERASE) (SPDSY) >gi_2129288_pir__B64339 spermidine synthase (EC 2.5.1.16) - Methanococcus jannaschii >gi_1591033 (U67486) spermidine synthase (speE) [Methanococcus jannaschii]

Seq. No.	138180
Seq. ID	LIB22-052-Q1-E1-E6
Method	BLASTX
NCBI GI	g2827559
BLAST score	326
E value	3.0e-30
Match length	76
% identity	80
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana] >gi_3292808_emb_CAA19798_ (AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	138181
Seq. ID	LIB22-052-Q1-E1-G6
Method	BLASTN
NCBI GI	g2828182
BLAST score	298
E value	1.0e-167
Match length	376
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOJ9, complete sequence [Arabidopsis thaliana]

Seq. No.	138182
Seq. ID	LIB22-053-Q1-E1-B4
Method	BLASTX
NCBI GI	g4586049
BLAST score	285
E value	1.0e-25
Match length	118
% identity	47
NCBI Description	(AC007020) hypothetical protein [Arabidopsis thaliana]

Seq. No.	138183
Seq. ID	LIB22-053-Q1-E1-F8

Method	BLASTX
NCBI GI	g3193302
BLAST score	139
E value	1.0e-08
Match length	60
% identity	48
NCBI Description	(AF069298) contains similarity to a protein kinase domain (Pfam: pkinase.hmm, score: 166.20) and to legume lectins beta domain (Pfam: lectin_legB.hmm, score: 139.32) [Arabidopsis thaliana]

Seq. No.	138184
Seq. ID	LIB22-053-Q1-E1-H12
Method	BLASTN
NCBI GI	g2959766
BLAST score	326
E value	0.0e+00
Match length	330
% identity	100
NCBI Description	Arabidopsis thaliana DNA for the glutathione-conjugate transporter AtMRP4

Seq. No.	138185
Seq. ID	LIB22-053-Q1-E1-H6
Method	BLASTX
NCBI GI	g3785972
BLAST score	385
E value	1.0e-37
Match length	85
% identity	89
NCBI Description	(AC005560) putative auxin transport protein [Arabidopsis thaliana] >gi_4262249_gb_AAD14542_ (AC006200) putative auxin transport protein [Arabidopsis thaliana]

Seq. No.	138186
Seq. ID	LIB22-054-Q1-E1-G6
Method	BLASTX
NCBI GI	g2262113
BLAST score	144
E value	2.0e-09
Match length	46
% identity	59
NCBI Description	(AC002343) unknown protein [Arabidopsis thaliana]

Seq. No.	138187
Seq. ID	LIB22-054-Q1-E2-A6
Method	BLASTN
NCBI GI	g3046850
BLAST score	99
E value	5.0e-49
Match length	99
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24G6, complete sequence [Arabidopsis thaliana]

Seq. No.	138188
Seq. ID	LIB22-054-Q1-E2-C12

Method	BLASTX
NCBI GI	g3757522
BLAST score	421
E value	1.0e-41
Match length	96
% identity	91
NCBI Description	(AC005167) putative splicing factor [Arabidopsis thaliana]

Seq. No.	138189
Seq. ID	LIB22-054-Q1-E2-C7
Method	BLASTX
NCBI GI	g4559339
BLAST score	200
E value	1.0e-15
Match length	56
% identity	79
NCBI Description	(AC007087) putative ATP-dependent RNA helicase [Arabidopsis thaliana]

Seq. No.	138190
Seq. ID	LIB22-054-Q1-E2-D12
Method	BLASTN
NCBI GI	g4415928
BLAST score	307
E value	1.0e-172
Match length	311
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F13A10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138191
Seq. ID	LIB22-054-Q1-E2-D7
Method	BLASTN
NCBI GI	g4589411
BLAST score	78
E value	2.0e-36
Match length	106
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F5H8, complete sequence

Seq. No.	138192
Seq. ID	LIB22-054-Q1-E2-E3
Method	BLASTN
NCBI GI	g4755185
BLAST score	260
E value	1.0e-144
Match length	272
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F5G3 genomic sequence, complete sequence

Seq. No.	138193
Seq. ID	LIB22-054-Q1-E2-F1
Method	BLASTN
NCBI GI	g2980787
BLAST score	84

E value	1.0e-39
Match length	196
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, P1 clone M7J2 (ESSAII project)

Seq. No.	138194
Seq. ID	LIB22-055-Q1-E1-A2
Method	BLASTN
NCBI GI	g3785992
BLAST score	331
E value	0.0e+00
Match length	331
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T6A23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138195
Seq. ID	LIB22-055-Q1-E1-B12
Method	BLASTN
NCBI GI	g3241939
BLAST score	156
E value	9.0e-83
Match length	164
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T26J13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138196
Seq. ID	LIB22-055-Q1-E1-B9
Method	BLASTX
NCBI GI	g4206155
BLAST score	228
E value	6.0e-19
Match length	78
% identity	56
NCBI Description	(AF109219) Mcd4p homolog [Homo sapiens]

Seq. No.	138197
Seq. ID	LIB22-055-Q1-E1-C8
Method	BLASTX
NCBI GI	g1773042
BLAST score	688
E value	9.0e-73
Match length	135
% identity	99
NCBI Description	(U82203) IDH-I [Arabidopsis thaliana]

Seq. No.	138198
Seq. ID	LIB22-055-Q1-E1-H1
Method	BLASTN
NCBI GI	g4756963
BLAST score	324
E value	0.0e+00
Match length	324
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23

(ESSA project)

Seq. No.	138199
Seq. ID	LIB22-056-Q1-E1-A6
Method	BLASTX
NCBI GI	g135433
BLAST score	730
E value	1.0e-77
Match length	138
% identity	99
NCBI Description	TUBULIN ALPHA CHAIN >gi_578450_emb_CAA77810_ (Z11763) alpha-Tubulin [Oxytricha granulifera]

Seq. No.	138200
Seq. ID	LIB22-056-Q1-E1-D4
Method	BLASTN
NCBI GI	g4582444
BLAST score	308
E value	1.0e-173
Match length	364
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T9H9 genomic sequence, complete sequence

Seq. No.	138201
Seq. ID	LIB22-056-Q1-E1-D6
Method	BLASTX
NCBI GI	g2117612
BLAST score	650
E value	3.0e-68
Match length	127
% identity	98
NCBI Description	catalase (EC 1.11.1.6) 3 - Arabidopsis thaliana

Seq. No.	138202
Seq. ID	LIB22-056-Q1-E1-D7
Method	BLASTX
NCBI GI	g3702336
BLAST score	280
E value	3.0e-25
Match length	91
% identity	60
NCBI Description	(AC005397) putative 3-methyl-2-oxobutanoate hydroxy-methyl-transferase [Arabidopsis thaliana]

Seq. No.	138203
Seq. ID	LIB22-056-Q1-E1-E12
Method	BLASTX
NCBI GI	g3834306
BLAST score	423
E value	9.0e-42
Match length	111
% identity	77
NCBI Description	(AC005679) EST gb_R65024 comes from this gene. [Arabidopsis thaliana]

Seq. No.	138204

Seq. ID	LIB22-056-Q1-E1-E9
Method	BLASTX
NCBI GI	g2146731
BLAST score	374
E value	5.0e-36
Match length	111
% identity	33
NCBI Description	FK506-binding protein - Arabidopsis thaliana >gi_1354207 (U49453) rof1 [Arabidopsis thaliana]

Seq. No.	138205
Seq. ID	LIB22-056-Q1-E1-F2
Method	BLASTN
NCBI GI	g3859658
BLAST score	352
E value	0.0e+00
Match length	425
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1 (ESSAII project)

Seq. No.	138206
Seq. ID	LIB22-056-Q1-E1-F7
Method	BLASTN
NCBI GI	g4415928
BLAST score	174
E value	4.0e-93
Match length	384
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F13A10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138207
Seq. ID	LIB22-056-Q1-E1-F9
Method	BLASTN
NCBI GI	g4662628
BLAST score	362
E value	0.0e+00
Match length	362
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F27O10 genomic sequence, complete sequence

Seq. No.	138208
Seq. ID	LIB22-056-Q1-E1-G4
Method	BLASTN
NCBI GI	g2351062
BLAST score	153
E value	6.0e-81
Match length	180
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAH20, complete sequence [Arabidopsis thaliana]

Seq. No.	138209
Seq. ID	LIB22-056-Q1-E1-H2
Method	BLASTN

NCBI GI	g2191157
BLAST score	129
E value	2.0e-66
Match length	203
% identity	94
NCBI Description	Arabidopsis thaliana BAC IG002P16

Seq. No.	138210
Seq. ID	LIB22-057-Q1-E1-H6
Method	BLASTX
NCBI GI	g4206209
BLAST score	322
E value	4.0e-42
Match length	97
% identity	82
NCBI Description	(AF071527) putative glucan synthase component [Arabidopsis thaliana] >gi_4263042_gb_AAD15311_ (AC005142) putative glucan synthase component [Arabidopsis thaliana]

Seq. No.	138211
Seq. ID	LIB22-058-Q1-E1-A9
Method	BLASTN
NCBI GI	g3449333
BLAST score	384
E value	0.0e+00
Match length	405
% identity	58
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXF12, complete sequence [Arabidopsis thaliana]

Seq. No.	138212
Seq. ID	LIB22-058-Q1-E1-B9
Method	BLASTN
NCBI GI	g3702315
BLAST score	174
E value	4.0e-93
Match length	295
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T3F17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138213
Seq. ID	LIB22-058-Q1-E1-C4
Method	BLASTN
NCBI GI	g3293582
BLAST score	384
E value	0.0e+00
Match length	411
% identity	100
NCBI Description	Arabidopsis thaliana BAC T15F16

Seq. No.	138214
Seq. ID	LIB22-058-Q1-E1-D2
Method	BLASTN
NCBI GI	g4159709
BLAST score	150
E value	6.0e-79

Match length	242
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLN21, complete sequence

Seq. No.	138215
Seq. ID	LIB22-058-Q1-E1-H5
Method	BLASTX
NCBI GI	g129809
BLAST score	603
E value	9.0e-63
Match length	125
% identity	94
NCBI Description	PEROXIDASE C2 PRECURSOR >gi_81665_pir__JH0149 peroxidase (EC 1.11.1.7) C2 precursor - horseradish >gi_217932_dbj_BAA14143_ (D90115) peroxidase isozyme [Armoracia rusticana]

Seq. No.	138216
Seq. ID	LIB22-059-Q1-E1-A5
Method	BLASTX
NCBI GI	g3193284
BLAST score	367
E value	5.0e-35
Match length	133
% identity	53
NCBI Description	(AF069298) No definition line found [Arabidopsis thaliana]

Seq. No.	138217
Seq. ID	LIB22-059-Q1-E1-C4
Method	BLASTN
NCBI GI	g4159705
BLAST score	137
E value	5.0e-71
Match length	372
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGD8, complete sequence

Seq. No.	138218
Seq. ID	LIB22-059-Q1-E1-D11
Method	BLASTX
NCBI GI	g1170089
BLAST score	535
E value	9.0e-55
Match length	106
% identity	100
NCBI Description	GLUTATHIONE S-TRANSFERASE ERD13 (CLASS PHI) >gi_481822_pir__S39542 probable glutathione transferase (EC 2.5.1.18) (clone ERD13) - Arabidopsis thaliana >gi_497789_dbj_BAA04554_ (D17673) glutathione S-transferase [Arabidopsis thaliana] >gi_3201614 (AC004669) glutathione S-transferase [Arabidopsis thaliana]

Seq. No.	138219
Seq. ID	LIB22-059-Q1-E1-D2
Method	BLASTX

NCBI GI	g4191791
BLAST score	173
E value	6.0e-16
Match length	65
% identity	72
NCBI Description	(AC005917) putative sf21 {Helianthus annuus} protein [Arabidopsis thaliana]

Seq. No.	138220
Seq. ID	LIB22-059-Q1-E1-D5
Method	BLASTX
NCBI GI	g2129549
BLAST score	473
E value	2.0e-47
Match length	88
% identity	99
NCBI Description	calcium-dependent protein kinase (EC 2.7.1.-) CDPK19 - Arabidopsis thaliana >gi_2129551_pir__S71778 calcium-dependent protein kinase 19 - Arabidopsis thaliana >gi_836942 (U20624) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_836948 (U20627) calcium-dependent protein kinase [Arabidopsis thaliana]

Seq. No.	138221
Seq. ID	LIB22-059-Q1-E1-F11
Method	BLASTX
NCBI GI	g2842469
BLAST score	146
E value	4.0e-09
Match length	68
% identity	43
NCBI Description	(AL021747) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	138222
Seq. ID	LIB22-059-Q1-E1-F6
Method	BLASTN
NCBI GI	g4756963
BLAST score	368
E value	0.0e+00
Match length	403
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23 (ESSA project)

Seq. No.	138223
Seq. ID	LIB22-059-Q1-E1-G3
Method	BLASTN
NCBI GI	g3241924
BLAST score	134
E value	3.0e-69
Match length	393
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNC6, complete sequence [Arabidopsis thaliana]

Seq. No.	138224
Seq. ID	LIB22-059-Q1-E1-G8

Method	BLASTX
NCBI GI	g2435522
BLAST score	276
E value	7.0e-30
Match length	136
% identity	51
NCBI Description	(AF024504) contains similarity to other AMP-binding enzymes [Arabidopsis thaliana]

Seq. No.	138225
Seq. ID	LIB22-059-Q1-E1-H4
Method	BLASTN
NCBI GI	g3128136
BLAST score	237
E value	1.0e-130
Match length	361
% identity	67
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1F13, complete sequence [Arabidopsis thaliana]

Seq. No.	138226
Seq. ID	LIB22-060-Q1-E1-A11
Method	BLASTN
NCBI GI	g2618605
BLAST score	167
E value	3.0e-89
Match length	183
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUK11, complete sequence [Arabidopsis thaliana]

Seq. No.	138227
Seq. ID	LIB22-060-Q1-E1-A12
Method	BLASTX
NCBI GI	g2492504
BLAST score	605
E value	4.0e-63
Match length	120
% identity	50
NCBI Description	CELL DIVISION CYCLE PROTEIN 48 HOMOLOG >gi_1669660_emb_CAA70565_ (Y09396) protein of AAA family [Capsicum annuum]

Seq. No.	138228
Seq. ID	LIB22-060-Q1-E1-B1
Method	BLASTX
NCBI GI	g2914700
BLAST score	347
E value	4.0e-33
Match length	88
% identity	83
NCBI Description	(AC003974) tRNA-processing protein SEN3-like [Arabidopsis thaliana]

Seq. No.	138229
Seq. ID	LIB22-060-Q1-E1-C11
Method	BLASTX

NCBI GI	g3080389
BLAST score	457
E value	8.0e-46
Match length	88
% identity	100
NCBI Description	(AL022603) putative membrane associated protein [Arabidopsis thaliana]

Seq. No.	138230
Seq. ID	LIB22-060-Q1-E1-D1
Method	BLASTN
NCBI GI	g3688169
BLAST score	81
E value	5.0e-38
Match length	169
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F26P21 (ESSAII project)

Seq. No.	138231
Seq. ID	LIB22-060-Q1-E1-H2
Method	BLASTN
NCBI GI	g2288979
BLAST score	346
E value	0.0e+00
Match length	346
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T01O24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138232
Seq. ID	LIB22-060-Q1-E1-H4
Method	BLASTN
NCBI GI	g3193311
BLAST score	143
E value	1.0e-74
Match length	278
% identity	98
NCBI Description	Arabidopsis thaliana BAC F6N15

Seq. No.	138233
Seq. ID	LIB22-060-Q1-E1-H6
Method	BLASTN
NCBI GI	g4199934
BLAST score	34
E value	1.0e-09
Match length	221
% identity	72
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T3P18, complete sequence [Arabidopsis thaliana]

Seq. No.	138234
Seq. ID	LIB22-061-Q1-E2-A7
Method	BLASTN
NCBI GI	g4519185
BLAST score	129
E value	2.0e-66

Match length	181
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15O15, complete sequence

Seq. No.	138235
Seq. ID	LIB22-061-Q1-E2-D10
Method	BLASTX
NCBI GI	g2506788
BLAST score	244
E value	1.0e-20
Match length	99
% identity	42
NCBI Description	GERANYLGERANYL TRANSFERASE TYPE II BETA SUBUNIT (RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT) (RAB GERANYL-GERANYLTRANSFERASE BETA SUBUNIT) (RAB GG TRANSFERASE) (RAB GGTASE) >gi_1332508_emb_CAA66638_ (X98001) geranylgeranyl transferase II [Homo sapiens]

Seq. No.	138236
Seq. ID	LIB22-061-Q1-E2-F6
Method	BLASTX
NCBI GI	g3868857
BLAST score	328
E value	1.0e-30
Match length	80
% identity	84
NCBI Description	(AB013886) RAV1 [Arabidopsis thaliana]

Seq. No.	138237
Seq. ID	LIB22-061-Q1-E2-G11
Method	BLASTN
NCBI GI	g3367567
BLAST score	290
E value	1.0e-162
Match length	294
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F8D20 (ESSAII project)

Seq. No.	138238
Seq. ID	LIB22-062-Q1-E1-A10
Method	BLASTX
NCBI GI	g3789911
BLAST score	253
E value	8.0e-22
Match length	95
% identity	52
NCBI Description	(AF081802) developmental protein DG1118 [Dictyostelium discoideum]

Seq. No.	138239
Seq. ID	LIB22-062-Q1-E1-A12
Method	BLASTN
NCBI GI	g469113
BLAST score	89
E value	9.0e-43

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Match length	177
% identity	100
NCBI Description	A.thaliana (Columbia) Dr4 mRNA

Seq. No.	138240
Seq. ID	LIB22-062-Q1-E1-A7
Method	BLASTN
NCBI GI	g2618600
BLAST score	212
E value	1.0e-116
Match length	304
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDC12, complete sequence [Arabidopsis thaliana]

Seq. No.	138241
Seq. ID	LIB22-062-Q1-E1-A8
Method	BLASTN
NCBI GI	g450242
BLAST score	39
E value	1.0e-12
Match length	59
% identity	92
NCBI Description	Actinidia deliciosa var. deliciosa (pKIWI505) mRNA, complete cds

Seq. No.	138242
Seq. ID	LIB22-062-Q1-E1-D6
Method	BLASTX
NCBI GI	g3264805
BLAST score	711
E value	2.0e-75
Match length	141
% identity	100
NCBI Description	(AF071788) phosphoenolpyruvate carboxylase [Arabidopsis thaliana] >gi_4079630_emb_CAA10486_ (AJ131710) phospho enole pyruvate carboxylase [Arabidopsis thaliana]

Seq. No.	138243
Seq. ID	LIB22-062-Q1-E1-E11
Method	BLASTN
NCBI GI	g2564044
BLAST score	130
E value	3.0e-67
Match length	146
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19P17, complete sequence [Arabidopsis thaliana]

Seq. No.	138244
Seq. ID	LIB22-062-Q1-E1-E7
Method	BLASTN
NCBI GI	g4314374
BLAST score	410
E value	0.0e+00
Match length	410
% identity	100

NCBI Description	Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	138245
Seq. ID	LIB22-062-Q1-E1-G6
Method	BLASTX
NCBI GI	g1370166
BLAST score	539
E value	3.0e-55
Match length	105
% identity	98
NCBI Description	(Z73932) RAB1C [Lotus japonicus]
Seq. No.	138246
Seq. ID	LIB22-062-Q1-E1-H10
Method	BLASTN
NCBI GI	g2109292
BLAST score	279
E value	1.0e-156
Match length	279
% identity	100
NCBI Description	Arabidopsis thaliana serine/threonine protein kinase mRNA, complete cds
Seq. No.	138247
Seq. ID	LIB22-062-Q1-E1-H7
Method	BLASTX
NCBI GI	g4263517
BLAST score	453
E value	3.0e-45
Match length	137
% identity	79
NCBI Description	(AC004044) similar to PHZF, catalyzing the hydroxylation of phenazine-1-carboxylic acid to 2-hydroxy-phenazine-1-carboxylic acid [Arabidopsis thaliana]
Seq. No.	138248
Seq. ID	LIB22-063-Q1-E1-A12
Method	BLASTN
NCBI GI	g1402874
BLAST score	347
E value	0.0e+00
Match length	355
% identity	100
NCBI Description	A.thaliana 81kb genomic sequence
Seq. No.	138249
Seq. ID	LIB22-063-Q1-E1-A2
Method	BLASTX
NCBI GI	g3915458
BLAST score	276
E value	2.0e-24
Match length	83
% identity	65
NCBI Description	PUTATIVE ABC TRANSPORTER C8C9.18 IN CHROMOSOME I

Seq. No.	138250
Seq. ID	LIB22-063-Q1-E1-A5
Method	BLASTN
NCBI GI	g2244788
BLAST score	93
E value	5.0e-45
Match length	183
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	138251
Seq. ID	LIB22-063-Q1-E1-B1
Method	BLASTX
NCBI GI	g4455276
BLAST score	554
E value	4.0e-57
Match length	107
% identity	100
NCBI Description	(AL035527) peptide transporter-like protein [Arabidopsis thaliana]

Seq. No.	138252
Seq. ID	LIB22-063-Q1-E1-B7
Method	BLASTN
NCBI GI	g3985957
BLAST score	329
E value	0.0e+00
Match length	329
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN8, complete sequence [Arabidopsis thaliana]

Seq. No.	138253
Seq. ID	LIB22-063-Q1-E1-B8
Method	BLASTN
NCBI GI	g4220641
BLAST score	79
E value	7.0e-37
Match length	104
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUL3, complete sequence [Arabidopsis thaliana]

Seq. No.	138254
Seq. ID	LIB22-063-Q1-E1-C11
Method	BLASTN
NCBI GI	g2459406
BLAST score	231
E value	1.0e-127
Match length	355
% identity	74
NCBI Description	Arabidopsis thaliana chromosome II BAC F4P9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138255
Seq. ID	LIB22-063-Q1-E1-C6

Method	BLASTX
NCBI GI	g1655932
BLAST score	284
E value	2.0e-25
Match length	133
% identity	48
NCBI Description	(U66565) RUSH-1beta [Oryctolagus cuniculus]

Seq. No.	138256
Seq. ID	LIB22-063-Q1-E1-C9
Method	BLASTN
NCBI GI	g2494106
BLAST score	166
E value	2.0e-88
Match length	340
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138257
Seq. ID	LIB22-063-Q1-E1-E2
Method	BLASTN
NCBI GI	g2252823
BLAST score	294
E value	1.0e-165
Match length	346
% identity	99
NCBI Description	Arabidopsis thaliana BAC IG005I10

Seq. No.	138258
Seq. ID	LIB22-063-Q1-E1-E3
Method	BLASTN
NCBI GI	g3264774
BLAST score	251
E value	1.0e-139
Match length	312
% identity	100
NCBI Description	Arabidopsis thaliana BAC T8A17 chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No.	138259
Seq. ID	LIB22-063-Q1-E1-E6
Method	BLASTX
NCBI GI	g4587987
BLAST score	614
E value	4.0e-64
Match length	137
% identity	80
NCBI Description	(AF085279) hypothetical Ser-Thr protein kinase [Arabidopsis thaliana]

Seq. No.	138260
Seq. ID	LIB22-063-Q1-E1-E9
Method	BLASTN
NCBI GI	g4733952
BLAST score	27
E value	1.0e-05

Match length	225
% identity	92
NCBI Description	Arabidopsis thaliana chromosome I BAC F23H11 genomic sequence, complete sequence

Seq. No.	138261
Seq. ID	LIB22-063-Q1-E1-F2
Method	BLASTX
NCBI GI	g3582329
BLAST score	488
E value	2.0e-49
Match length	95
% identity	100
NCBI Description	(AC005496) unknown protein [Arabidopsis thaliana]

Seq. No.	138262
Seq. ID	LIB22-063-Q1-E1-G8
Method	BLASTX
NCBI GI	g231587
BLAST score	530
E value	3.0e-54
Match length	133
% identity	77
NCBI Description	ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR >gi_283001_pir__S25304 H+-transporting ATP synthase (EC 3.6.1.34) beta chain precursor, mitochondrial - rice >gi_218147_dbj_BAA01372_ (D10491) mitochondrial F1-ATPase [Oryza sativa]

Seq. No.	138263
Seq. ID	LIB22-064-Q1-E1-A5
Method	BLASTN
NCBI GI	g3869068
BLAST score	106
E value	1.0e-52
Match length	206
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC16, complete sequence [Arabidopsis thaliana]

Seq. No.	138264
Seq. ID	LIB22-064-Q1-E1-B1
Method	BLASTN
NCBI GI	g4539290
BLAST score	276
E value	1.0e-154
Match length	348
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F14M19 (ESSA project)

Seq. No.	138265
Seq. ID	LIB22-064-Q1-E1-B2
Method	BLASTN
NCBI GI	g4220634
BLAST score	226
E value	1.0e-124

Match length	318
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9H21, complete sequence [Arabidopsis thaliana]

Seq. No.	138266
Seq. ID	LIB22-064-Q1-E1-B5
Method	BLASTN
NCBI GI	g2828278
BLAST score	336
E value	0.0e+00
Match length	398
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16 (ESSAII project)

Seq. No.	138267
Seq. ID	LIB22-064-Q1-E1-B8
Method	BLASTN
NCBI GI	g469113
BLAST score	384
E value	0.0e+00
Match length	384
% identity	100
NCBI Description	A.thaliana (Columbia) Dr4 mRNA

Seq. No.	138268
Seq. ID	LIB22-064-Q1-E1-C12
Method	BLASTN
NCBI GI	g2618599
BLAST score	57
E value	2.0e-23
Match length	272
% identity	82
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBD2, complete sequence [Arabidopsis thaliana]

Seq. No.	138269
Seq. ID	LIB22-064-Q1-E1-C2
Method	BLASTN
NCBI GI	g4220638
BLAST score	127
E value	5.0e-65
Match length	379
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIF21, complete sequence [Arabidopsis thaliana]

Seq. No.	138270
Seq. ID	LIB22-064-Q1-E1-C5
Method	BLASTX
NCBI GI	g3075399
BLAST score	161
E value	5.0e-11
Match length	73
% identity	51
NCBI Description	(AC004484) SF16-like protein [Arabidopsis thaliana]

Seq. No.	138271
Seq. ID	LIB22-064-Q1-E1-C9
Method	BLASTX
NCBI GI	g2980806
BLAST score	583
E value	2.0e-60
Match length	123
% identity	85
NCBI Description	(AL022197) putative protein [Arabidopsis thaliana]

Seq. No.	138272
Seq. ID	LIB22-064-Q1-E1-D2
Method	BLASTX
NCBI GI	g4680181
BLAST score	204
E value	4.0e-16
Match length	105
% identity	47
NCBI Description	(AF111709) unknown [Oryza sativa subsp. indica]

Seq. No.	138273
Seq. ID	LIB22-064-Q1-E1-D9
Method	BLASTX
NCBI GI	g3023216
BLAST score	166
E value	2.0e-53
Match length	127
% identity	76
NCBI Description	14-3-3-LIKE PROTEIN GF14 MU >gi_1531629 (U60444) GF14 mu [Arabidopsis thaliana]

Seq. No.	138274
Seq. ID	LIB22-064-Q1-E1-F12
Method	BLASTN
NCBI GI	g682727
BLAST score	57
E value	9.0e-24
Match length	77
% identity	95
NCBI Description	Arabidopsis thaliana S-adenosyl-L-methionine:trans-caffeoyl-Coenzyme A 3-O-methyltransferase homologue mRNA, complete cds

Seq. No.	138275
Seq. ID	LIB22-064-Q1-E1-G2
Method	BLASTN
NCBI GI	g2264306
BLAST score	42
E value	1.0e-14
Match length	208
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK5, complete sequence [Arabidopsis thaliana]

Seq. No.	138276
Seq. ID	LIB22-064-Q1-E1-G9

Method	BLASTN
NCBI GI	g4220643
BLAST score	290
E value	1.0e-162
Match length	375
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD22, complete sequence [Arabidopsis thaliana]

Seq. No.	138277
Seq. ID	LIB22-065-Q1-E1-A5
Method	BLASTX
NCBI GI	g2618723
BLAST score	595
E value	7.0e-62
Match length	132
% identity	89
NCBI Description	(U49073) IAA17 [Arabidopsis thaliana] >gi_2921756 (AF040631) IAA17/AXR3 protein [Arabidopsis thaliana] >gi_4389514_gb_AAB70451_ (AC000104) Identical to Arabidopsis gb_AF040632 and gb_U49073 IAA17/AXR3 gene. ESTs gb_H36782 and gb_F14074 come from this gene. [Arabidopsis thaliana]

Seq. No.	138278
Seq. ID	LIB22-065-Q1-E1-B10
Method	BLASTX
NCBI GI	g3450842
BLAST score	191
E value	1.0e-14
Match length	55
% identity	64
NCBI Description	(AF080436) mitogen activated protein kinase kinase [Oryza sativa]

Seq. No.	138279
Seq. ID	LIB22-065-Q1-E1-B4
Method	BLASTN
NCBI GI	g2645198
BLAST score	132
E value	5.0e-68
Match length	416
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC T26J12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138280
Seq. ID	LIB22-065-Q1-E1-B5
Method	BLASTN
NCBI GI	g2245031
BLAST score	70
E value	5.0e-31
Match length	419
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	138281
Seq. ID	LIB22-065-Q1-E1-B7
Method	BLASTN
NCBI GI	g4185128
BLAST score	143
E value	1.0e-74
Match length	421
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II P1 MSF3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138282
Seq. ID	LIB22-065-Q1-E1-C1
Method	BLASTX
NCBI GI	g2393724
BLAST score	144
E value	6.0e-09
Match length	70
% identity	41
NCBI Description	(U80819) glutathione-S-transferase homolog [Mus musculus]

Seq. No.	138283
Seq. ID	LIB22-065-Q1-E1-C10
Method	BLASTN
NCBI GI	g4589444
BLAST score	168
E value	6.0e-90
Match length	168
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWF20, complete sequence

Seq. No.	138284
Seq. ID	LIB22-065-Q1-E1-C3
Method	BLASTX
NCBI GI	g465702
BLAST score	218
E value	1.0e-17
Match length	134
% identity	33
NCBI Description	PROBABLE RIBOSOMAL PROTEIN B0303.15 IN CHROMOSOME III >gi_283555_pir__S27795 ribosomal protein L11 homolog - Caenorhabditis elegans >gi_156201 (M77697) ribosomal protein L11 [Caenorhabditis elegans]

Seq. No.	138285
Seq. ID	LIB22-065-Q1-E1-C5
Method	BLASTN
NCBI GI	g4589438
BLAST score	410
E value	0.0e+00
Match length	413
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQJ2, complete sequence

Seq. No.	138286

Seq. ID	LIB22-065-Q1-E1-C9
Method	BLASTN
NCBI GI	g3510343
BLAST score	393
E value	0.0e+00
Match length	393
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJC20, complete sequence [Arabidopsis thaliana]

Seq. No.	138287
Seq. ID	LIB22-065-Q1-E1-D3
Method	BLASTN
NCBI GI	g2358139
BLAST score	239
E value	1.0e-132
Match length	264
% identity	97
NCBI Description	Arabidopsis thaliana chromosome 1 YAC yUP8H12 complete sequence [Arabidopsis thaliana]

Seq. No.	138288
Seq. ID	LIB22-065-Q1-E1-D6
Method	BLASTX
NCBI GI	g3176874
BLAST score	204
E value	5.0e-16
Match length	93
% identity	42
NCBI Description	(AF065639) cucumisin-like serine protease [Arabidopsis thaliana]

Seq. No.	138289
Seq. ID	LIB22-065-Q1-E1-E10
Method	BLASTN
NCBI GI	g3785992
BLAST score	361
E value	0.0e+00
Match length	361
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T6A23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138290
Seq. ID	LIB22-065-Q1-E1-E3
Method	BLASTX
NCBI GI	g4220482
BLAST score	202
E value	9.0e-16
Match length	107
% identity	27
NCBI Description	(AC006069) hypothetical protein [Arabidopsis thaliana]

Seq. No.	138291
Seq. ID	LIB22-065-Q1-E1-E4
Method	BLASTN
NCBI GI	g2351066

BLAST score	168
E value	2.0e-89
Match length	409
% identity	64
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOP9, complete sequence [Arabidopsis thaliana]

Seq. No.	138292
Seq. ID	LIB22-065-Q1-E1-E5
Method	BLASTN
NCBI GI	g2924653
BLAST score	219
E value	1.0e-120
Match length	399
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDA7, complete sequence [Arabidopsis thaliana]

Seq. No.	138293
Seq. ID	LIB22-065-Q1-E1-F5
Method	BLASTX
NCBI GI	g3947448
BLAST score	301
E value	2.0e-27
Match length	135
% identity	46
NCBI Description	(AL033535) cDNA EST yk301f1.5 comes from this gene; cDNA EST yk475f6.3 comes from this gene; cDNA EST yk301f1.3 comes from this gene; cDNA EST yk475f6.5 comes from this gene; cDNA EST yk499g5.5 comes from this gene [Caenorhabdi... >gi_3947543_emb_CAA88952_ (Z49127) cDNA EST yk301f1.5 comes from this gene; cDNA EST yk475f6.3 comes from this gene; cDNA EST yk301f1.3 comes from this gene; cDNA EST yk475f6.5 comes from this gene; cDNA EST yk499g5.5 comes from this gene [Caenorhabditi

Seq. No.	138294
Seq. ID	LIB22-065-Q1-E1-F7
Method	BLASTX
NCBI GI	g3688799
BLAST score	555
E value	4.0e-57
Match length	111
% identity	99
NCBI Description	(AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis thaliana]

Seq. No.	138295
Seq. ID	LIB22-065-Q1-E1-G10
Method	BLASTX
NCBI GI	g1170840
BLAST score	323
E value	4.0e-30
Match length	115
% identity	89
NCBI Description	LOW-TEMPERATURE-INDUCED 78 KD PROTEIN (DESSICATION-RESPONSIVE PROTEIN 29B) >gi_419759_pir__S30154

	low-temperature-induced protein 78 - Arabidopsis thaliana >gi_16390_emb_CAA47903_ (X67671) lti78 [Arabidopsis thaliana] >gi_348692 (L22567) cor78 [Arabidopsis thaliana]
Seq. No.	138296
Seq. ID	LIB22-065-Q1-E1-G5
Method	BLASTX
NCBI GI	g2108252
BLAST score	396
E value	2.0e-38
Match length	108
% identity	38
NCBI Description	(Y10228) P-glycoprotein-2 [Arabidopsis thaliana] >gi_2108254_emb_CAA71276_ (Y10227) P-glycoprotein-2 [Arabidopsis thaliana] >gi_4538925_emb_CAB39661.1_ (AL049483) P-glycoprotein-2 (pgp2) [Arabidopsis thaliana]
Seq. No.	138297
Seq. ID	LIB22-065-Q1-E1-G7
Method	BLASTN
NCBI GI	g4713947
BLAST score	30
E value	3.0e-07
Match length	311
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC T16B23 genomic sequence, complete sequence
Seq. No.	138298
Seq. ID	LIB22-066-Q1-E1-B12
Method	BLASTN
NCBI GI	g4589419
BLAST score	306
E value	1.0e-172
Match length	328
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2I5, complete sequence
Seq. No.	138299
Seq. ID	LIB22-066-Q1-E1-B2
Method	BLASTX
NCBI GI	g2924509
BLAST score	229
E value	6.0e-19
Match length	100
% identity	46
NCBI Description	(AL022023) subtilisin proteinase-like [Arabidopsis thaliana]
Seq. No.	138300
Seq. ID	LIB22-066-Q1-E1-C4
Method	BLASTX
NCBI GI	g2244910
BLAST score	262
E value	8.0e-23
Match length	135

% identity	44
NCBI Description	(Z97339) unnamed protein product [Arabidopsis thaliana]

Seq. No.	138301
Seq. ID	LIB22-066-Q1-E1-D11
Method	BLASTN
NCBI GI	g4468801
BLAST score	183
E value	2.0e-98
Match length	357
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6G17 (ESSA project)

Seq. No.	138302
Seq. ID	LIB22-066-Q1-E1-D12
Method	BLASTN
NCBI GI	g2335089
BLAST score	310
E value	1.0e-174
Match length	355
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T11A7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138303
Seq. ID	LIB22-066-Q1-E1-E12
Method	BLASTX
NCBI GI	g2435519
BLAST score	228
E value	6.0e-19
Match length	102
% identity	54
NCBI Description	(AF024504) similar to mouse MEM3 (GB:U47024 and S. cerevisiae vacuolar sorting protein 35 (SW;P34110) [Arabidopsis thaliana]

Seq. No.	138304
Seq. ID	LIB22-066-Q1-E1-F12
Method	BLASTX
NCBI GI	g2642429
BLAST score	252
E value	9.0e-22
Match length	117
% identity	12
NCBI Description	(AC002391) putative poly(A)-binding protein [Arabidopsis thaliana]

Seq. No.	138305
Seq. ID	LIB22-066-Q1-E1-F9
Method	BLASTN
NCBI GI	g4544381
BLAST score	356
E value	0.0e+00
Match length	359
% identity	73
NCBI Description	Arabidopsis thaliana chromosome II BAC F16F14 genomic

sequence, complete sequence

Seq. No.	138306
Seq. ID	LIB22-066-Q1-E1-G12
Method	BLASTX
NCBI GI	g3599968
BLAST score	628
E value	9.0e-66
Match length	125
% identity	100
NCBI Description	(AF032123) clp protease [Arabidopsis thaliana]

Seq. No.	138307
Seq. ID	LIB22-066-Q1-E1-G3
Method	BLASTN
NCBI GI	g3869070
BLAST score	403
E value	0.0e+00
Match length	411
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MGO3, complete sequence [Arabidopsis thaliana]

Seq. No.	138308
Seq. ID	LIB22-066-Q1-E1-G6
Method	BLASTN
NCBI GI	g4757400
BLAST score	173
E value	1.0e-92
Match length	262
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MFJ20, complete sequence

Seq. No.	138309
Seq. ID	LIB22-066-Q1-E1-G9
Method	BLASTN
NCBI GI	g2191157
BLAST score	195
E value	1.0e-105
Match length	195
% identity	100
NCBI Description	Arabidopsis thaliana BAC IG002P16

Seq. No.	138310
Seq. ID	LIB22-066-Q1-E1-H2
Method	BLASTX
NCBI GI	g3327060
BLAST score	291
E value	2.0e-26
Match length	116
% identity	48
NCBI Description	(AB014523) KIAA0623 protein [Homo sapiens]

Seq. No.	138311
Seq. ID	LIB22-067-Q1-E1-A2
Method	BLASTN

NCBI GI	g4581103
BLAST score	153
E value	1.0e-80
Match length	349
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T24I21 genomic sequence, complete sequence

Seq. No.	138312
Seq. ID	LIB22-067-Q1-E1-B1
Method	BLASTX
NCBI GI	g3702121
BLAST score	296
E value	3.0e-27
Match length	83
% identity	69
NCBI Description	(AJ011681) retinoblastoma-related protein [Chenopodium rubrum]

Seq. No.	138313
Seq. ID	LIB22-067-Q1-E1-B2
Method	BLASTX
NCBI GI	g1449179
BLAST score	239
E value	1.0e-20
Match length	49
% identity	96
NCBI Description	(D86506) N-ethylmaleimide sensitive fusion protein [Nicotiana tabacum]

Seq. No.	138314
Seq. ID	LIB22-067-Q1-E1-C11
Method	BLASTX
NCBI GI	g1171993
BLAST score	409
E value	4.0e-40
Match length	92
% identity	89
NCBI Description	PHENYLALANINE AMMONIA-LYASE 2 >gi_1076370_pir__S52991 phenylalanine ammonia-lyase (EC 4.3.1.5) - Arabidopsis thaliana >gi_497421 (L33678) phenylalanine ammonia lyase [Arabidopsis thaliana]

Seq. No.	138315
Seq. ID	LIB22-067-Q1-E1-C9
Method	BLASTN
NCBI GI	g4490324
BLAST score	254
E value	1.0e-141
Match length	291
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14 (ESSA project)

Seq. No.	138316
Seq. ID	LIB22-067-Q1-E1-E1
Method	BLASTX

NCBI GI	g3193290
BLAST score	144
E value	4.0e-09
Match length	66
% identity	47
NCBI Description	(AF069298) contains similarity to a protein kinase domain (Pfam: pkinase.hmm, score: 165.48), to legume lectins beta domain (Pfam: lectin_legB.hmm, score: 125.64) and legume lectins alpha domain (Pfam: lectin_legA.hmm, score: 16.72) [Arabido

Seq. No.	138317
Seq. ID	LIB22-067-Q1-E1-E10
Method	BLASTN
NCBI GI	g2104523
BLAST score	212
E value	1.0e-116
Match length	364
% identity	98
NCBI Description	Arabidopsis thaliana BAC T10M13 from chromosome IV, from 10.8 cM to 11.6 cM, complete sequence

Seq. No.	138318
Seq. ID	LIB22-067-Q1-E1-E6
Method	BLASTX
NCBI GI	g1083160
BLAST score	211
E value	3.0e-17
Match length	70
% identity	56
NCBI Description	mannosyl-oligosaccharide 1,2-alpha-mannosidase (EC 3.2.1.113) - rabbit (fragment)

Seq. No.	138319
Seq. ID	LIB22-067-Q1-E1-F6
Method	BLASTX
NCBI GI	g2738248
BLAST score	527
E value	7.0e-54
Match length	103
% identity	98
NCBI Description	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No.	138320
Seq. ID	LIB22-067-Q1-E1-H12
Method	BLASTX
NCBI GI	g1402904
BLAST score	469
E value	3.0e-47
Match length	90
% identity	99
NCBI Description	(X98313) peroxidase [Arabidopsis thaliana]

Seq. No.	138321
Seq. ID	LIB22-068-Q1-E1-A10
Method	BLASTX

NCBI GI	g2738248
BLAST score	672
E value	7.0e-71
Match length	126
% identity	100
NCBI Description	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No.	138322
Seq. ID	LIB22-068-Q1-E1-B12
Method	BLASTX
NCBI GI	g4587584
BLAST score	366
E value	5.0e-35
Match length	130
% identity	52
NCBI Description	(AC007232) unknown protein [Arabidopsis thaliana]

Seq. No.	138323
Seq. ID	LIB22-068-Q1-E1-C12
Method	BLASTX
NCBI GI	g3641837
BLAST score	430
E value	5.0e-51
Match length	132
% identity	86
NCBI Description	(AL023094) Nonclathrin coat protein gamma - like protein [Arabidopsis thaliana]

Seq. No.	138324
Seq. ID	LIB22-068-Q1-E1-C6
Method	BLASTX
NCBI GI	g2252850
BLAST score	230
E value	4.0e-19
Match length	110
% identity	46
NCBI Description	(AF013294) contains region of similarity to DNA binding protein [Arabidopsis thaliana]

Seq. No.	138325
Seq. ID	LIB22-068-Q1-E1-C9
Method	BLASTX
NCBI GI	g3617741
BLAST score	709
E value	3.0e-75
Match length	138
% identity	99
NCBI Description	(AC005687) L3 cytoplasmic ribosomal protein [Arabidopsis thaliana]

Seq. No.	138326
Seq. ID	LIB22-068-Q1-E1-D1
Method	BLASTN
NCBI GI	g2618605
BLAST score	357
E value	0.0e+00

Match length	357
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUK11, complete sequence [Arabidopsis thaliana]

Seq. No.	138327
Seq. ID	LIB22-068-Q1-E1-D11
Method	BLASTX
NCBI GI	g3482975
BLAST score	168
E value	8.0e-12
Match length	107
% identity	35
NCBI Description	(AL031369) putative protein [Arabidopsis thaliana]

Seq. No.	138328
Seq. ID	LIB22-068-Q1-E1-D4
Method	BLASTX
NCBI GI	g2493318
BLAST score	221
E value	5.0e-18
Match length	110
% identity	44
NCBI Description	BLUE COPPER PROTEIN PRECURSOR >gi_562779_emb_CAA80963_ (Z25471) blue copper protein [Pisum sativum] >gi_1098264_prf__2115352A blue Cu protein [Pisum sativum]

Seq. No.	138329
Seq. ID	LIB22-068-Q1-E1-E4
Method	BLASTX
NCBI GI	g3522929
BLAST score	411
E value	3.0e-40
Match length	84
% identity	95
NCBI Description	(AC002535) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana] >gi_3738279 (AC005309) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No.	138330
Seq. ID	LIB22-068-Q1-E1-E9
Method	BLASTX
NCBI GI	g3386546
BLAST score	500
E value	1.0e-50
Match length	129
% identity	77
NCBI Description	(AF079503) H-protein promoter binding factor-2a [Arabidopsis thaliana]

Seq. No.	138331
Seq. ID	LIB22-068-Q1-E1-F8
Method	BLASTX
NCBI GI	g2129652
BLAST score	574
E value	2.0e-59
Match length	117

% identity	98
NCBI Description	myosin heavy chain homolog - Arabidopsis thaliana (fragment) >gi_699495 (U19616) myosin heavy chain homolog [Arabidopsis thaliana]
Seq. No.	138332
Seq. ID	LIB22-068-Q1-E1-G11
Method	BLASTN
NCBI GI	g2833627
BLAST score	85
E value	1.0e-40
Match length	85
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F17O7 complete sequence [Arabidopsis thaliana]
Seq. No.	138333
Seq. ID	LIB22-068-Q1-E1-G9
Method	BLASTX
NCBI GI	g2462836
BLAST score	527
E value	5.0e-54
Match length	116
% identity	88
NCBI Description	(AF000657) beta-glucanase [Arabidopsis thaliana]
Seq. No.	138334
Seq. ID	LIB22-068-Q1-E1-H11
Method	BLASTX
NCBI GI	g1172873
BLAST score	255
E value	5.0e-22
Match length	112
% identity	49
NCBI Description	CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_ (D13043) thiol protease [Arabidopsis thaliana]
Seq. No.	138335
Seq. ID	LIB22-068-Q1-E1-H2
Method	BLASTX
NCBI GI	g2580440
BLAST score	251
E value	2.0e-21
Match length	61
% identity	77
NCBI Description	(D87261) PCF2 [Oryza sativa]
Seq. No.	138336
Seq. ID	LIB22-069-Q1-E1-E5
Method	BLASTX
NCBI GI	g3860420
BLAST score	143
E value	7.0e-09
Match length	40
% identity	72

NCBI Description	(AJ011047) exo galactanase [Lupinus angustifolius]

Seq. No.	138337
Seq. ID	LIB22-069-Q1-E1-E8
Method	BLASTX
NCBI GI	g2352492
BLAST score	366
E value	5.0e-35
Match length	69
% identity	100
NCBI Description	(AF005047) transport inhibitor response 1 [Arabidopsis thaliana] >gi_2352494 (AF005048) transport inhibitor response 1 [Arabidopsis thaliana]

Seq. No.	138338
Seq. ID	LIB22-069-Q1-E1-F3
Method	BLASTN
NCBI GI	g3738275
BLAST score	69
E value	1.0e-30
Match length	177
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC F17A22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138339
Seq. ID	LIB22-069-Q1-E1-F6
Method	BLASTX
NCBI GI	g1708420
BLAST score	100
E value	5.0e-40
Match length	123
% identity	75
NCBI Description	ISOFLAVONE REDUCTASE HOMOLOG P3 >gi_1361992_pir__S57613 isoflavonoid reductase homolog - Arabidopsis thaliana >gi_886432_emb_CAA89859_ (Z49777) isoflavonoid reductase homologue [Arabidopsis thaliana]

Seq. No.	138340
Seq. ID	LIB22-069-Q1-E1-H3
Method	BLASTX
NCBI GI	g1084338
BLAST score	619
E value	1.0e-64
Match length	117
% identity	100
NCBI Description	drought-induced protein Dr4 - Arabidopsis thaliana >gi_469114_emb_CAA55323_ (X78586) Dr4 [Arabidopsis thaliana]

Seq. No.	138341
Seq. ID	LIB22-070-Q1-E1-A1
Method	BLASTN
NCBI GI	g4584519
BLAST score	217
E value	1.0e-119
Match length	337

% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F11C18 (ESSA project)

Seq. No.	138342
Seq. ID	LIB22-070-Q1-E1-A11
Method	BLASTN
NCBI GI	g4220631
BLAST score	393
E value	0.0e+00
Match length	397
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K5J14, complete sequence [Arabidopsis thaliana]

Seq. No.	138343
Seq. ID	LIB22-070-Q1-E1-C6
Method	BLASTN
NCBI GI	g3702731
BLAST score	176
E value	2.0e-94
Match length	244
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFC19, complete sequence [Arabidopsis thaliana]

Seq. No.	138344
Seq. ID	LIB22-070-Q1-E1-C8
Method	BLASTX
NCBI GI	g4678943
BLAST score	362
E value	1.0e-34
Match length	126
% identity	64
NCBI Description	(AL049711) putative protein [Arabidopsis thaliana]

Seq. No.	138345
Seq. ID	LIB22-070-Q1-E1-D6
Method	BLASTN
NCBI GI	g2880038
BLAST score	353
E value	0.0e+00
Match length	360
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T11J7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138346
Seq. ID	LIB22-070-Q1-E1-E1
Method	BLASTN
NCBI GI	g4454004
BLAST score	327
E value	0.0e+00
Match length	335
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F24A6 (ESSAII project)

Seq. No.	138347
Seq. ID	LIB22-070-Q1-E1-E5
Method	BLASTN
NCBI GI	g2815519
BLAST score	120
E value	6.0e-61
Match length	190
% identity	88
NCBI Description	Arabidopsis thaliana BAC T5J8 from chromosome IV, top arm, complete sequence [Arabidopsis thaliana]

Seq. No.	138348
Seq. ID	LIB22-070-Q1-E1-F11
Method	BLASTX
NCBI GI	g2335099
BLAST score	271
E value	7.0e-24
Match length	84
% identity	60
NCBI Description	(AC002339) unknown protein [Arabidopsis thaliana]

Seq. No.	138349
Seq. ID	LIB22-070-Q1-E1-F2
Method	BLASTN
NCBI GI	g2062153
BLAST score	104
E value	6.0e-52
Match length	108
% identity	99
NCBI Description	Arabidopsis thaliana chromosome III BAC T02O04 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138350
Seq. ID	LIB22-070-Q1-E1-F5
Method	BLASTN
NCBI GI	g2827513
BLAST score	58
E value	8.0e-25
Match length	58
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F8F16 (ESSAII project)

Seq. No.	138351
Seq. ID	LIB22-070-Q1-E1-G8
Method	BLASTX
NCBI GI	g3056591
BLAST score	229
E value	6.0e-19
Match length	130
% identity	44
NCBI Description	(AC004255) T1F9.12 [Arabidopsis thaliana]

Seq. No.	138352
Seq. ID	LIB22-070-Q1-E1-H10
Method	BLASTX

NCBI GI	g3876712
BLAST score	207
E value	2.0e-16
Match length	81
% identity	51
NCBI Description	(Z46242) similar to malonyl-COA decarboxylase [Caenorhabditis elegans]

Seq. No.	138353
Seq. ID	LIB22-071-Q1-E1-A2
Method	BLASTN
NCBI GI	g3702315
BLAST score	251
E value	1.0e-139
Match length	263
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T3F17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138354
Seq. ID	LIB22-071-Q1-E1-F1
Method	BLASTX
NCBI GI	g4678924
BLAST score	155
E value	3.0e-10
Match length	108
% identity	35
NCBI Description	(AL049711) putative protein [Arabidopsis thaliana]

Seq. No.	138355
Seq. ID	LIB22-071-Q1-E1-G3
Method	BLASTX
NCBI GI	g166765
BLAST score	591
E value	2.0e-61
Match length	114
% identity	99
NCBI Description	(M23106) heat shock protein HSP70-1 [Arabidopsis thaliana]

Seq. No.	138356
Seq. ID	LIB22-071-Q1-E1-H3
Method	BLASTN
NCBI GI	g4755185
BLAST score	338
E value	0.0e+00
Match length	338
% identity	50
NCBI Description	Arabidopsis thaliana chromosome II BAC F5G3 genomic sequence, complete sequence

Seq. No.	138357
Seq. ID	LIB22-073-Q1-E1-A1
Method	BLASTX
NCBI GI	g1864017
BLAST score	439
E value	1.0e-43
Match length	85

% identity	99
NCBI Description	(D63396) elongation factor-1 alpha [Nicotiana tabacum]
Seq. No.	138358
Seq. ID	LIB22-073-Q1-E1-B3
Method	BLASTX
NCBI GI	g2894574
BLAST score	427
E value	2.0e-42
Match length	81
% identity	100
NCBI Description	(AL021890) peroxidase prxr1 [Arabidopsis thaliana] >gi_2961341_emb_CAA18099.1_ (AL022140) peroxidase prxr1 [Arabidopsis thaliana]
Seq. No.	138359
Seq. ID	LIB22-073-Q1-E1-C8
Method	BLASTN
NCBI GI	g2760169
BLAST score	222
E value	1.0e-122
Match length	348
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFB13, complete sequence [Arabidopsis thaliana]
Seq. No.	138360
Seq. ID	LIB22-073-Q1-E1-F3
Method	BLASTX
NCBI GI	g3953458
BLAST score	564
E value	2.0e-58
Match length	110
% identity	98
NCBI Description	(AC002328) F20N2.3 [Arabidopsis thaliana]
Seq. No.	138361
Seq. ID	LIB22-073-Q1-E1-F5
Method	BLASTX
NCBI GI	g3212869
BLAST score	535
E value	6.0e-55
Match length	104
% identity	99
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]
Seq. No.	138362
Seq. ID	LIB22-073-Q1-E1-G2
Method	BLASTN
NCBI GI	g4220633
BLAST score	106
E value	5.0e-53
Match length	106
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K7J8, complete sequence [Arabidopsis thaliana]

Seq. No.	138363
Seq. ID	LIB22-073-Q1-E1-H5
Method	BLASTX
NCBI GI	g1170089
BLAST score	557
E value	2.0e-57
Match length	109
% identity	100
NCBI Description	GLUTATHIONE S-TRANSFERASE ERD13 (CLASS PHI) >gi_481822_pir__S39542 probable glutathione transferase (EC 2.5.1.18) (clone ERD13) - Arabidopsis thaliana >gi_497789_dbj_BAA04554_ (D17673) glutathione S-transferase [Arabidopsis thaliana] >gi_3201614 (AC004669) glutathione S-transferase [Arabidopsis thaliana]

Seq. No.	138364
Seq. ID	LIB22-074-Q1-E1-A5
Method	BLASTX
NCBI GI	g267073
BLAST score	577
E value	9.0e-60
Match length	107
% identity	98
NCBI Description	TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin beta chain - Arabidopsis thaliana >gi_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701) beta-3 tubulin [Arabidopsis thaliana]

Seq. No.	138365
Seq. ID	LIB22-074-Q1-E1-B10
Method	BLASTX
NCBI GI	g2827716
BLAST score	401
E value	3.0e-39
Match length	81
% identity	98
NCBI Description	(AL021684) predicted protein [Arabidopsis thaliana]

Seq. No.	138366
Seq. ID	LIB22-074-Q1-E1-B2
Method	BLASTX
NCBI GI	g4263718
BLAST score	673
E value	4.0e-71
Match length	120
% identity	100
NCBI Description	(AC006223) putative DNA topoisomerase III beta [Arabidopsis thaliana]

Seq. No.	138367
Seq. ID	LIB22-074-Q1-E1-B8
Method	BLASTX
NCBI GI	g3080415
BLAST score	493
E value	5.0e-50
Match length	113
% identity	84

NCBI Description	(AL022604) cysteine proteinase-like protein [Arabidopsis thaliana]
Seq. No.	138368
Seq. ID	LIB22-074-Q1-E1-D1
Method	BLASTX
NCBI GI	g2961284
BLAST score	229
E value	3.0e-37
Match length	88
% identity	91
NCBI Description	(Y16848) cinnamyl alcohol dehydrogenase-like protein, subunit a [Arabidopsis thaliana] >gi_4467103_emb_CAB37537_ (AL035538) cinnamyl alcohol dehydrogenase-like protein, LCADa [Arabidopsis thaliana]
Seq. No.	138369
Seq. ID	LIB22-074-Q1-E1-E11
Method	BLASTX
NCBI GI	g1076662
BLAST score	495
E value	3.0e-50
Match length	129
% identity	72
NCBI Description	H+-transporting ATPase (EC 3.6.1.35) (clone PHA1) - potato >gi_435003_emb_CAA54046_ (X76536) H(+)-transporting ATPase [Solanum tuberosum]
Seq. No.	138370
Seq. ID	LIB22-074-Q1-E1-E3
Method	BLASTX
NCBI GI	g2650102
BLAST score	161
E value	5.0e-11
Match length	126
% identity	36
NCBI Description	(AE001068) cell division control protein 21 (cdc21) [Archaeoglobus fulgidus]
Seq. No.	138371
Seq. ID	LIB22-074-Q1-E1-E5
Method	BLASTN
NCBI GI	g4159707
BLAST score	113
E value	8.0e-57
Match length	314
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJK13, complete sequence
Seq. No.	138372
Seq. ID	LIB22-074-Q1-E1-G10
Method	BLASTN
NCBI GI	g4263038
BLAST score	34
E value	4.0e-10
Match length	74

% identity	86
NCBI Description	Arabidopsis thaliana BAC T5L23 from chromosome IV, near 19 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	138373
Seq. ID	LIB22-074-Q1-E1-G12
Method	BLASTN
NCBI GI	g4733953
BLAST score	67
E value	2.0e-29
Match length	246
% identity	90
NCBI Description	Arabidopsis thaliana chromosome I BAC F13O11 genomic sequence, complete sequence

Seq. No.	138374
Seq. ID	LIB22-074-Q1-E1-H3
Method	BLASTN
NCBI GI	g4539448
BLAST score	155
E value	9.0e-82
Match length	392
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T5C23 (ESSA project)

Seq. No.	138375
Seq. ID	LIB22-075-Q1-E1-A4
Method	BLASTX
NCBI GI	g4522004
BLAST score	512
E value	3.0e-52
Match length	110
% identity	95
NCBI Description	(AC007069) putative histidine kinase, sensory transduction [Arabidopsis thaliana]

Seq. No.	138376
Seq. ID	LIB22-075-Q1-E1-A8
Method	BLASTN
NCBI GI	g3869073
BLAST score	346
E value	0.0e+00
Match length	346
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKN22, complete sequence [Arabidopsis thaliana]

Seq. No.	138377
Seq. ID	LIB22-075-Q1-E1-B4
Method	BLASTX
NCBI GI	g585453
BLAST score	267
E value	9.0e-24
Match length	85
% identity	66
NCBI Description	MALATE OXIDOREDUCTASE (MALIC ENZYME) (ME) (NADP-DEPENDENT

MALIC ENZYME) (NADP-ME) >gi_1084300_pir__S43718 malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) (EC 1.1.1.40) - common ice plant >gi_432380_emb_CAA45772_ (X64434) malate dehydrogenase (oxaloacetate decarboxylating) (NADP+) [Mesembryanthemum crystallinum]

Seq. No.	138378
Seq. ID	LIB22-075-Q1-E1-C7
Method	BLASTN
NCBI GI	g4210448
BLAST score	100
E value	3.0e-49
Match length	128
% identity	93
NCBI Description	Arabidopsis thaliana gene for ARR1 protein, complete cds

Seq. No.	138379
Seq. ID	LIB22-075-Q1-E1-D8
Method	BLASTN
NCBI GI	g3128142
BLAST score	206
E value	1.0e-112
Match length	403
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQN23, complete sequence [Arabidopsis thaliana]

Seq. No.	138380
Seq. ID	LIB22-075-Q1-E1-F4
Method	BLASTN
NCBI GI	g3241917
BLAST score	150
E value	3.0e-79
Match length	162
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19B1, complete sequence [Arabidopsis thaliana]

Seq. No.	138381
Seq. ID	LIB22-075-Q1-E1-H7
Method	BLASTX
NCBI GI	g2979554
BLAST score	491
E value	8.0e-50
Match length	108
% identity	86
NCBI Description	(AC003680) CDC4 like protein [Arabidopsis thaliana]

Seq. No.	138382
Seq. ID	LIB22-075-Q1-E1-H8
Method	BLASTX
NCBI GI	g3033379
BLAST score	189
E value	2.0e-14
Match length	55
% identity	65
NCBI Description	(AC004238) putative DNA-binding protein [Arabidopsis

thaliana]

Seq. No.	138383
Seq. ID	LIB22-076-Q1-E1-B7
Method	BLASTN
NCBI GI	g2264316
BLAST score	167
E value	4.0e-89
Match length	192
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRO11, complete sequence [Arabidopsis thaliana]

Seq. No.	138384
Seq. ID	LIB22-076-Q1-E1-D1
Method	BLASTN
NCBI GI	g2245031
BLAST score	148
E value	2.0e-77
Match length	434
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	138385
Seq. ID	LIB22-076-Q1-E1-E10
Method	BLASTX
NCBI GI	g4539004
BLAST score	245
E value	6.0e-21
Match length	61
% identity	72
NCBI Description	(AL049481) putative protein kinase [Arabidopsis thaliana]

Seq. No.	138386
Seq. ID	LIB22-076-Q1-E1-E11
Method	BLASTN
NCBI GI	g1946354
BLAST score	78
E value	7.0e-36
Match length	198
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T06B20 genomic sequence, complete sequence

Seq. No.	138387
Seq. ID	LIB22-076-Q1-E1-G8
Method	BLASTX
NCBI GI	g1531762
BLAST score	195
E value	7.0e-15
Match length	51
% identity	75
NCBI Description	(Y07765) S-adenosylmethionine decarboxylase [Arabidopsis thaliana]

Seq. No. 138388

Seq. ID	LIB22-076-Q1-E1-G9
Method	BLASTX
NCBI GI	g3080435
BLAST score	527
E value	5.0e-54
Match length	100
% identity	100
NCBI Description	(AL022605) putative protein [Arabidopsis thaliana]

Seq. No.	138389
Seq. ID	LIB22-077-Q1-E1-A11
Method	BLASTX
NCBI GI	g2738248
BLAST score	377
E value	2.0e-36
Match length	79
% identity	90
NCBI Description	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No.	138390
Seq. ID	LIB22-077-Q1-E1-D12
Method	BLASTN
NCBI GI	g3892698
BLAST score	201
E value	1.0e-109
Match length	201
% identity	45
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F7K2 (ESSAII project)

Seq. No.	138391
Seq. ID	LIB22-078-Q1-E1-A7
Method	BLASTX
NCBI GI	g99742
BLAST score	202
E value	8.0e-16
Match length	121
% identity	40
NCBI Description	2-dehydro-3-deoxyphosphoheptonate aldolase (EC 4.1.2.15) 1 - Arabidopsis thaliana

Seq. No.	138392
Seq. ID	LIB22-078-Q1-E1-C8
Method	BLASTX
NCBI GI	g3122753
BLAST score	504
E value	3.0e-51
Match length	92
% identity	100
NCBI Description	60S RIBOSOMAL PROTEIN L44 >gi_2244789_emb_CAB10211.1_ (Z97336) ribosomal protein [Arabidopsis thaliana]

Seq. No.	138393
Seq. ID	LIB22-078-Q1-E1-E2
Method	BLASTX
NCBI GI	g3434965

BLAST score	279
E value	7.0e-25
Match length	110
% identity	47
NCBI Description	(AB002530) mus-23 [Neurospora crassa]

Seq. No.	138394
Seq. ID	LIB22-078-Q1-E1-F5
Method	BLASTX
NCBI GI	g4588008
BLAST score	297
E value	2.0e-27
Match length	82
% identity	63
NCBI Description	(AF085279) hypothetical protein [Arabidopsis thaliana]

Seq. No.	138395
Seq. ID	LIB22-078-Q1-E1-G2
Method	BLASTX
NCBI GI	g3482978
BLAST score	598
E value	2.0e-62
Match length	114
% identity	100
NCBI Description	(AL031369) putative protein [Arabidopsis thaliana]

Seq. No.	138396
Seq. ID	LIB22-078-Q1-E1-G3
Method	BLASTN
NCBI GI	g3869074
BLAST score	245
E value	1.0e-135
Match length	396
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMI9, complete sequence [Arabidopsis thaliana]

Seq. No.	138397
Seq. ID	LIB22-078-Q1-E1-H7
Method	BLASTN
NCBI GI	g2618602
BLAST score	133
E value	9.0e-69
Match length	284
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	138398
Seq. ID	LIB22-078-Q1-E1-H9
Method	BLASTX
NCBI GI	g1652057
BLAST score	190
E value	1.0e-14
Match length	65
% identity	57
NCBI Description	(D90902) hypothetical protein [Synechocystis sp.]

Seq. No.	138399
Seq. ID	LIB22-079-Q1-E1-A3
Method	BLASTN
NCBI GI	g4235150
BLAST score	58
E value	2.0e-24
Match length	101
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC T25B24 genomic sequence, complete sequence

Seq. No.	138400
Seq. ID	LIB22-079-Q1-E1-A4
Method	BLASTN
NCBI GI	g3582315
BLAST score	346
E value	0.0e+00
Match length	346
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T27A16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138401
Seq. ID	LIB22-079-Q1-E1-B3
Method	BLASTN
NCBI GI	g1890129
BLAST score	217
E value	1.0e-119
Match length	228
% identity	99
NCBI Description	Arabidopsis thaliana valyl tRNA synthetase (valRS) mRNA, complete cds

Seq. No.	138402
Seq. ID	LIB22-079-Q1-E1-B8
Method	BLASTN
NCBI GI	g3702728
BLAST score	340
E value	0.0e+00
Match length	361
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M13, complete sequence [Arabidopsis thaliana]

Seq. No.	138403
Seq. ID	LIB22-079-Q1-E1-B9
Method	BLASTN
NCBI GI	g3687221
BLAST score	413
E value	0.0e+00
Match length	417
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F6F22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 138404

Seq. ID	LIB22-079-Q1-E1-F1
Method	BLASTN
NCBI GI	g2618683
BLAST score	56
E value	8.0e-23
Match length	184
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC T32G6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138405
Seq. ID	LIB22-080-Q1-E2-D10
Method	BLASTX
NCBI GI	g2244750
BLAST score	542
E value	1.0e-55
Match length	118
% identity	88
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	138406
Seq. ID	LIB22-080-Q1-E2-D5
Method	BLASTX
NCBI GI	g3335368
BLAST score	176
E value	7.0e-13
Match length	107
% identity	41
NCBI Description	(AC003028) hypothetical protein [Arabidopsis thaliana]

Seq. No.	138407
Seq. ID	LIB22-080-Q1-E2-D6
Method	BLASTX
NCBI GI	g4581205
BLAST score	128
E value	2.0e-07
Match length	82
% identity	93
NCBI Description	(Y17913) cyclic nucleotide and calmodulin-regulated ion channel [Arabidopsis thaliana]

Seq. No.	138408
Seq. ID	LIB22-080-Q1-E2-F12
Method	BLASTX
NCBI GI	g4512653
BLAST score	603
E value	7.0e-63
Match length	122
% identity	100
NCBI Description	(AC007048) unknown protein [Arabidopsis thaliana]

Seq. No.	138409
Seq. ID	LIB22-080-Q1-E2-G2
Method	BLASTN
NCBI GI	g3184270

BLAST score	162
E value	6.0e-86
Match length	365
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T8K22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138410
Seq. ID	LIB22-081-Q1-E1-C8
Method	BLASTX
NCBI GI	g4033469
BLAST score	199
E value	2.0e-15
Match length	40
% identity	93
NCBI Description	ARGININE/SERINE-RICH SPLICING FACTOR RSP41 >gi_1707370_emb_CAA67799_ (X99436) splicing factor [Arabidopsis thaliana]

Seq. No.	138411
Seq. ID	LIB22-081-Q1-E1-D1
Method	BLASTX
NCBI GI	g1175011
BLAST score	406
E value	6.0e-40
Match length	76
% identity	100
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 1B (TRANSMEMBRANE PROTEIN A) (TMP-A) >gi_296085_emb_CAA48356_ (X68293) transmembrane protein [Arabidopsis thaliana] >gi_3386599 (AC004665) plasma membrane intrinsic protein 1B [Arabidopsis thaliana]

Seq. No.	138412
Seq. ID	LIB22-081-Q1-E2-A2
Method	BLASTN
NCBI GI	g4490734
BLAST score	105
E value	3.0e-52
Match length	194
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	138413
Seq. ID	LIB22-081-Q1-E2-A6
Method	BLASTN
NCBI GI	g2337888
BLAST score	196
E value	1.0e-106
Match length	421
% identity	98
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14J16, complete sequence [Arabidopsis thaliana]

Seq. No.	138414
Seq. ID	LIB22-081-Q1-E2-D5
Method	BLASTN

NCBI GI	g2462780
BLAST score	325
E value	0.0e+00
Match length	333
% identity	100
NCBI Description	Arabidopsis thaliana carbamoyl phosphate synthetase small subunit mRNA (carA), complete cds

Seq. No.	138415
Seq. ID	LIB22-081-Q1-E2-D7
Method	BLASTX
NCBI GI	g4454048
BLAST score	585
E value	1.0e-60
Match length	119
% identity	90
NCBI Description	(AL035394) putative protein [Arabidopsis thaliana]

Seq. No.	138416
Seq. ID	LIB22-081-Q1-E2-E4
Method	BLASTN
NCBI GI	g2244829
BLAST score	143
E value	4.0e-75
Match length	143
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	138417
Seq. ID	LIB22-081-Q1-E2-E6
Method	BLASTN
NCBI GI	g2244829
BLAST score	143
E value	5.0e-75
Match length	143
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	138418
Seq. ID	LIB22-081-Q1-E2-G12
Method	BLASTN
NCBI GI	g3212846
BLAST score	107
E value	1.0e-53
Match length	115
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138419
Seq. ID	LIB22-082-Q1-E1-A8
Method	BLASTX
NCBI GI	g4455342
BLAST score	678
E value	1.0e-71

Match length	135
% identity	99
NCBI Description	(AL035522) O-methyltransferase-like protein [Arabidopsis thaliana]

Seq. No.	138420
Seq. ID	LIB22-082-Q1-E1-B6
Method	BLASTX
NCBI GI	g2623962
BLAST score	427
E value	4.0e-42
Match length	91
% identity	91
NCBI Description	(Y12540) isocitrate dehydrogenase (NADP+) [Apium graveolens]

Seq. No.	138421
Seq. ID	LIB22-082-Q1-E1-G5
Method	BLASTX
NCBI GI	g3212877
BLAST score	509
E value	8.0e-52
Match length	116
% identity	89
NCBI Description	(AC004005) Lea-like protein [Arabidopsis thaliana]

Seq. No.	138422
Seq. ID	LIB22-082-Q1-E1-G7
Method	BLASTX
NCBI GI	g2760330
BLAST score	340
E value	5.0e-32
Match length	85
% identity	74
NCBI Description	(AC002130) F1N21.15 [Arabidopsis thaliana]

Seq. No.	138423
Seq. ID	LIB22-082-Q1-E2-C8
Method	BLASTX
NCBI GI	g4262225
BLAST score	339
E value	9.0e-32
Match length	116
% identity	54
NCBI Description	(AC006200) putative phosphatidic acid phosphatase [Arabidopsis thaliana]

Seq. No.	138424
Seq. ID	LIB22-082-Q1-E2-E10
Method	BLASTN
NCBI GI	g2618720
BLAST score	46
E value	8.0e-17
Match length	85
% identity	98
NCBI Description	Arabidopsis thaliana early auxin-induced (IAA16) mRNA, complete cds

Seq. No.	138425
Seq. ID	LIB22-082-Q1-E2-E12
Method	BLASTX
NCBI GI	g3738339
BLAST score	331
E value	7.0e-31
Match length	136
% identity	51
NCBI Description	(AC005170) putative kinase [Arabidopsis thaliana]

Seq. No.	138426
Seq. ID	LIB22-082-Q1-E2-H1
Method	BLASTN
NCBI GI	g4589426
BLAST score	250
E value	1.0e-138
Match length	339
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDE13, complete sequence

Seq. No.	138427
Seq. ID	LIB22-083-Q1-E2-C11
Method	BLASTX
NCBI GI	g4033365
BLAST score	763
E value	2.0e-81
Match length	148
% identity	96
NCBI Description	(AJ223499) ATP sulfurylase [Brassica juncea]

Seq. No.	138428
Seq. ID	LIB22-083-Q1-E2-D9
Method	BLASTN
NCBI GI	g2245031
BLAST score	85
E value	3.0e-40
Match length	217
% identity	86
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	138429
Seq. ID	LIB22-083-Q1-E2-E12
Method	BLASTX
NCBI GI	g3785981
BLAST score	776
E value	5.0e-83
Match length	142
% identity	100
NCBI Description	(AC005560) putative major latex protein [Arabidopsis thaliana]

Seq. No.	138430
Seq. ID	LIB22-083-Q1-E2-G11
Method	BLASTN

NCBI GI	g3004543
BLAST score	115
E value	8.0e-58
Match length	457
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F19F24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138431
Seq. ID	LIB22-083-Q1-E2-H1
Method	BLASTN
NCBI GI	g4589430
BLAST score	103
E value	6.0e-51
Match length	235
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLD14, complete sequence

Seq. No.	138432
Seq. ID	LIB22-084-Q1-E1-B3
Method	BLASTX
NCBI GI	g3776578
BLAST score	238
E value	5.0e-20
Match length	94
% identity	50
NCBI Description	(AC005388) ESTs gb_F13915 and gb_F13916 come from this gene. [Arabidopsis thaliana]

Seq. No.	138433
Seq. ID	LIB22-084-Q1-E1-C11
Method	BLASTX
NCBI GI	g1709698
BLAST score	143
E value	7.0e-09
Match length	55
% identity	49
NCBI Description	POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (POLYNUCLEOTIDE PHOSPHORYLASE) (PNPASE) (VEGETATIVE PROTEIN 15) (VEG15) >gi_2127172_pir__S70691 polynucleotide phosphorylase - Bacillus subtilis >gi_1184680 (U29668) polynucleotide phosphorylase [Bacillus subtilis] >gi_2634041_emb_CAB13542_ (Z99112) polynucleotide phosphorylase (PNPase) [Bacillus subtilis] >gi_1589234_prf__2210369A polynucleotide phosphorylase [Bacillus subtilis]

Seq. No.	138434
Seq. ID	LIB22-084-Q1-E1-D7
Method	BLASTN
NCBI GI	g2564050
BLAST score	141
E value	2.0e-73
Match length	312
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUA22, complete sequence [Arabidopsis thaliana]

Seq. No.	138435
Seq. ID	LIB22-084-Q1-E1-E10
Method	BLASTX
NCBI GI	g4454051
BLAST score	237
E value	2.0e-20
Match length	74
% identity	58
NCBI Description	(AL035394) putative polygalacturonase [Arabidopsis thaliana]

Seq. No.	138436
Seq. ID	LIB22-084-Q1-E1-F10
Method	BLASTN
NCBI GI	g1871502
BLAST score	297
E value	1.0e-166
Match length	305
% identity	99
NCBI Description	A.thaliana bfruct4 gene

Seq. No.	138437
Seq. ID	LIB22-084-Q1-E1-F12
Method	BLASTX
NCBI GI	g1483177
BLAST score	328
E value	1.0e-30
Match length	114
% identity	53
NCBI Description	(D86598) antifreeze-like protein (af70) [Picea abies]

Seq. No.	138438
Seq. ID	LIB22-085-Q1-E1-C11
Method	BLASTX
NCBI GI	g2895510
BLAST score	495
E value	4.0e-50
Match length	132
% identity	77
NCBI Description	(AF033204) putative pectin methylesterase [Arabidopsis thaliana]

Seq. No.	138439
Seq. ID	LIB22-085-Q1-E1-F11
Method	BLASTX
NCBI GI	g3329368
BLAST score	162
E value	2.0e-11
Match length	37
% identity	78
NCBI Description	(AF031244) nodulin-like protein [Arabidopsis thaliana]

Seq. No.	138440
Seq. ID	LIB22-085-Q1-E2-A6
Method	BLASTX
NCBI GI	g1943751

BLAST score	246
E value	2.0e-21
Match length	62
% identity	76
NCBI Description	(U93845) Arabidopsis thaliana ER-type calcium pump protein, complete sequence >gi_2078292 (U96455) ER-type Ca2+-pumping ATPase; ECA1p [Arabidopsis thaliana]

Seq. No.	138441
Seq. ID	LIB22-085-Q1-E2-C4
Method	BLASTX
NCBI GI	g135535
BLAST score	455
E value	2.0e-45
Match length	94
% identity	98
NCBI Description	T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA) (CCT-ALPHA) >gi_322602_pir__JN0448 t-complex polypeptide Tcp-1 - Arabidopsis thaliana >gi_217871_dbj_BAA01955_ (D11351) t-complex polypeptide 1 homologue [Arabidopsis thaliana] >gi_2326265_dbj_BAA21772_ (D11352) CCT alpha/TCP-1 [Arabidopsis thaliana]

Seq. No.	138442
Seq. ID	LIB22-085-Q1-E2-G12
Method	BLASTX
NCBI GI	g4587685
BLAST score	677
E value	2.0e-71
Match length	132
% identity	99
NCBI Description	(AC007197) putative methylmalonate semi-aldehyde dehydrogenase [Arabidopsis thaliana]

Seq. No.	138443
Seq. ID	LIB22-086-Q1-E1-A10
Method	BLASTX
NCBI GI	g2462746
BLAST score	212
E value	4.0e-17
Match length	91
% identity	93
NCBI Description	(AC002292) Similar to ATP-citrate-lyase [Arabidopsis thaliana]

Seq. No.	138444
Seq. ID	LIB22-086-Q1-E1-B2
Method	BLASTN
NCBI GI	g3985934
BLAST score	243
E value	1.0e-134
Match length	372
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJE7, complete sequence [Arabidopsis thaliana]

Seq. No.	138445

Seq. ID	LIB22-086-Q1-E1-C9
Method	BLASTN
NCBI GI	g1490552
BLAST score	206
E value	1.0e-112
Match length	206
% identity	100
NCBI Description	Arabidopsis thaliana S-adenosylmethionine decarboxylase (SAMdc) mRNA, complete cds

Seq. No.	138446
Seq. ID	LIB22-086-Q1-E1-D3
Method	BLASTN
NCBI GI	g2275194
BLAST score	231
E value	1.0e-127
Match length	312
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T08I13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138447
Seq. ID	LIB22-086-Q1-E1-E1
Method	BLASTX
NCBI GI	g1402908
BLAST score	444
E value	3.0e-44
Match length	101
% identity	85
NCBI Description	(X98315) peroxidase [Arabidopsis thaliana] >gi_1429221_emb_CAA67313_ (X98777) peroxidase ATP16a [Arabidopsis thaliana] >gi_4455802_emb_CAB37193_ (AJ133036) peroxidase [Arabidopsis thaliana]

Seq. No.	138448
Seq. ID	LIB22-086-Q1-E1-E12
Method	BLASTN
NCBI GI	g2477521
BLAST score	122
E value	1.0e-62
Match length	122
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC F22K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138449
Seq. ID	LIB22-086-Q1-E1-E8
Method	BLASTN
NCBI GI	g2564050
BLAST score	223
E value	1.0e-122
Match length	307
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUA22, complete sequence [Arabidopsis thaliana]

Seq. No.	138450

Seq. ID	LIB22-086-Q1-E1-F6
Method	BLASTX
NCBI GI	g4713953
BLAST score	638
E value	7.0e-67
Match length	129
% identity	94
NCBI Description	(AC007293) subtilisin-like protease, 3' partial [Arabidopsis thaliana]

Seq. No.	138451
Seq. ID	LIB22-086-Q1-E1-G5
Method	BLASTN
NCBI GI	g4753645
BLAST score	360
E value	0.0e+00
Match length	360
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17N18 (ESSA project)

Seq. No.	138452
Seq. ID	LIB22-086-Q1-E1-G6
Method	BLASTN
NCBI GI	g2618602
BLAST score	420
E value	0.0e+00
Match length	420
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	138453
Seq. ID	LIB22-086-Q1-E1-H1
Method	BLASTX
NCBI GI	g4455342
BLAST score	354
E value	9.0e-34
Match length	64
% identity	100
NCBI Description	(AL035522) O-methyltransferase-like protein [Arabidopsis thaliana]

Seq. No.	138454
Seq. ID	LIB22-086-Q1-E1-H10
Method	BLASTN
NCBI GI	g3063690
BLAST score	215
E value	1.0e-117
Match length	343
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11 (ESSAII project)

Seq. No.	138455
Seq. ID	LIB22-086-Q1-E1-H7
Method	BLASTX

NCBI GI	g3063445
BLAST score	182
E value	2.0e-13
Match length	118
% identity	4
NCBI Description	(AC003981) F22O13.7 [Arabidopsis thaliana]

Seq. No.	138456
Seq. ID	LIB22-087-Q1-E1-A1
Method	BLASTN
NCBI GI	g3242970
BLAST score	164
E value	2.0e-87
Match length	164
% identity	100
NCBI Description	Arabidopsis thaliana BAC T4I9, chromosome IV, near 17 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	138457
Seq. ID	LIB22-087-Q1-E1-A11
Method	BLASTN
NCBI GI	g3860243
BLAST score	61
E value	4.0e-26
Match length	145
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC F15K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138458
Seq. ID	LIB22-087-Q1-E1-A6
Method	BLASTX
NCBI GI	g4680643
BLAST score	161
E value	6.0e-11
Match length	101
% identity	36
NCBI Description	(AF132936) CGI-01 protein [Homo sapiens]

Seq. No.	138459
Seq. ID	LIB22-087-Q1-E1-B6
Method	BLASTX
NCBI GI	g4454032
BLAST score	381
E value	9.0e-37
Match length	118
% identity	64
NCBI Description	(AL035394) putative protein [Arabidopsis thaliana]

Seq. No.	138460
Seq. ID	LIB22-087-Q1-E1-C5
Method	BLASTX
NCBI GI	g1707011
BLAST score	564
E value	3.0e-58
Match length	106
% identity	100

NCBI Description	(U78721) auxin-repressed protein isolog [Arabidopsis thaliana]

Seq. No.	138461
Seq. ID	LIB22-087-Q1-E1-C7
Method	BLASTX
NCBI GI	g2323410
BLAST score	292
E value	2.0e-26
Match length	138
% identity	46
NCBI Description	(AF015913) Skb1Hs [Homo sapiens]

Seq. No.	138462
Seq. ID	LIB22-087-Q1-E1-D2
Method	BLASTX
NCBI GI	g2462746
BLAST score	602
E value	1.0e-62
Match length	123
% identity	94
NCBI Description	(AC002292) Similar to ATP-citrate-lyase [Arabidopsis thaliana]

Seq. No.	138463
Seq. ID	LIB22-087-Q1-E1-D6
Method	BLASTN
NCBI GI	g4185128
BLAST score	295
E value	1.0e-165
Match length	405
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II P1 MSF3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138464
Seq. ID	LIB22-087-Q1-E1-E2
Method	BLASTX
NCBI GI	g4585980
BLAST score	423
E value	1.0e-41
Match length	138
% identity	68
NCBI Description	(AC005287) Very similar to TATA binding protein-associated factor [Arabidopsis thaliana]

Seq. No.	138465
Seq. ID	LIB22-087-Q1-E1-E6
Method	BLASTX
NCBI GI	g2130080
BLAST score	319
E value	2.0e-29
Match length	94
% identity	60
NCBI Description	Nramp1 protein - rice >gi_1470320_bbs_177441 (S81897) OsNramp1=Nramp1 homolog/Bcg product homolog [Oryza sativa, indica, cv. IR 36, etiolated shoots, Peptide, 517 aa]

[Oryza sativa] >gi_2231132 (L41217) integral membrane protein [Oryza sativa]

Seq. No.	138466
Seq. ID	LIB22-087-Q1-E1-F7
Method	BLASTX
NCBI GI	g2291190
BLAST score	164
E value	3.0e-11
Match length	97
% identity	25
NCBI Description	(AF016422) contains similarity to TPR domains [Caenorhabditis elegans]

Seq. No.	138467
Seq. ID	LIB22-087-Q1-E1-G5
Method	BLASTX
NCBI GI	g4417280
BLAST score	523
E value	2.0e-53
Match length	118
% identity	90
NCBI Description	(AC007019) putative ATP synthase [Arabidopsis thaliana]

Seq. No.	138468
Seq. ID	LIB22-087-Q1-E1-H10
Method	BLASTN
NCBI GI	g4371278
BLAST score	219
E value	1.0e-120
Match length	243
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T2N18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138469
Seq. ID	LIB22-087-Q1-E1-H2
Method	BLASTN
NCBI GI	g4581204
BLAST score	67
E value	7.0e-30
Match length	91
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for putative ion channel, cngc5

Seq. No.	138470
Seq. ID	LIB22-087-Q1-E1-H8
Method	BLASTN
NCBI GI	g2264367
BLAST score	281
E value	1.0e-157
Match length	341
% identity	98
NCBI Description	Arabidopsis thaliana BAC F6P23 from chromosome IV, top arm, complete sequence [Arabidopsis thaliana]

Seq. No.	138471

Seq. ID	LIB22-088-Q1-E1-A3
Method	BLASTN
NCBI GI	g3522932
BLAST score	286
E value	1.0e-160
Match length	290
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138472
Seq. ID	LIB22-088-Q1-E1-A8
Method	BLASTX
NCBI GI	g2352492
BLAST score	293
E value	1.0e-26
Match length	103
% identity	54
NCBI Description	(AF005047) transport inhibitor response 1 [Arabidopsis thaliana] >gi_2352494 (AF005048) transport inhibitor response 1 [Arabidopsis thaliana]

Seq. No.	138473
Seq. ID	LIB22-088-Q1-E1-B10
Method	BLASTN
NCBI GI	g4056429
BLAST score	373
E value	0.0e+00
Match length	373
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F5O8 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138474
Seq. ID	LIB22-088-Q1-E1-C3
Method	BLASTN
NCBI GI	g4455168
BLAST score	224
E value	1.0e-123
Match length	252
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)

Seq. No.	138475
Seq. ID	LIB22-088-Q1-E1-F12
Method	BLASTX
NCBI GI	g2118220
BLAST score	337
E value	1.0e-31
Match length	98
% identity	71
NCBI Description	H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P1) - Arabidopsis thaliana >gi_926929 (L44581) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana] >gi_926933 (L44583) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]

>gi_3096941_emb_CAA18851.1_ (AL023094) vacuolar H+-transporting ATPase 16K chain [Arabidopsis thaliana]
>gi_4539311_emb_CAB38812.1_ (AL035679) H+-transporting ATPase 16K chain P2, vacuolar [Arabidopsis thaliana]
>gi_4589976_gb_AAD26493.1_AC007195_7 (AC007195) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]

Seq. No.	138476
Seq. ID	LIB22-088-Q1-E1-F3
Method	BLASTX
NCBI GI	g730544
BLAST score	162
E value	1.0e-11
Match length	64
% identity	66
NCBI Description	60S RIBOSOMAL PROTEIN L24

Seq. No.	138477
Seq. ID	LIB22-088-Q1-E1-G11
Method	BLASTX
NCBI GI	g2924777
BLAST score	123
E value	5.0e-29
Match length	91
% identity	77
NCBI Description	(AC002334) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	138478
Seq. ID	LIB22-088-Q1-E1-G2
Method	BLASTN
NCBI GI	g4678266
BLAST score	205
E value	1.0e-111
Match length	366
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F15B8 (ESSA project)

Seq. No.	138479
Seq. ID	LIB22-088-Q1-E1-G9
Method	BLASTX
NCBI GI	g1350680
BLAST score	589
E value	3.0e-61
Match length	121
% identity	94
NCBI Description	60S RIBOSOMAL PROTEIN L1

Seq. No.	138480
Seq. ID	LIB22-088-Q1-E1-H12
Method	BLASTN
NCBI GI	g4559375
BLAST score	237
E value	1.0e-131
Match length	306
% identity	98

NCBI Description	Arabidopsis thaliana chromosome II BAC F11C10 genomic sequence, complete sequence
Seq. No.	138481
Seq. ID	LIB22-089-Q1-E1-A8
Method	BLASTN
NCBI GI	g488786
BLAST score	65
E value	4.0e-28
Match length	169
% identity	85
NCBI Description	B.oleracea putative imbibition protein mRNA
Seq. No.	138482
Seq. ID	LIB22-089-Q1-E1-C12
Method	BLASTX
NCBI GI	g4006829
BLAST score	722
E value	9.0e-77
Match length	139
% identity	100
NCBI Description	(AC005970) putative protein kinase [Arabidopsis thaliana]
Seq. No.	138483
Seq. ID	LIB22-089-Q1-E1-E8
Method	BLASTN
NCBI GI	g2618602
BLAST score	213
E value	1.0e-116
Match length	213
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]
Seq. No.	138484
Seq. ID	LIB22-089-Q1-E1-F2
Method	BLASTN
NCBI GI	g3250673
BLAST score	125
E value	3.0e-64
Match length	133
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T16H5 (ESSAII project)
Seq. No.	138485
Seq. ID	LIB22-089-Q1-E1-F7
Method	BLASTN
NCBI GI	g3004543
BLAST score	227
E value	1.0e-125
Match length	355
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F19F24 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	138486

Seq. ID	LIB22-089-Q1-E1-G10
Method	BLASTX
NCBI GI	g4096693
BLAST score	221
E value	5.0e-18
Match length	65
% identity	100
NCBI Description	(U37235) cinnamate 4-hydroxylase [Arabidopsis thaliana]

Seq. No.	138487
Seq. ID	LIB22-089-Q1-E1-H10
Method	BLASTN
NCBI GI	g3212102
BLAST score	174
E value	5.0e-93
Match length	419
% identity	100
NCBI Description	Arabidopsis Thaliana BAC F6A4, Chromosome IV, near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	138488
Seq. ID	LIB22-089-Q1-E1-H2
Method	BLASTX
NCBI GI	g1480078
BLAST score	444
E value	3.0e-44
Match length	88
% identity	100
NCBI Description	(X99696) shaggy-like protein kinase iota [Arabidopsis thaliana] >gi_2444277_gb_AAB71545.1_ (AF019927) GSK3/shaggy-like protein kinase [Arabidopsis thaliana]

Seq. No.	138489
Seq. ID	LIB22-089-Q1-E1-H9
Method	BLASTX
NCBI GI	g3386604
BLAST score	202
E value	7.0e-16
Match length	107
% identity	36
NCBI Description	(AC004665) putative protein kinase [Arabidopsis thaliana]

Seq. No.	138490
Seq. ID	LIB23-001-Q1-E1-A5
Method	BLASTX
NCBI GI	g3445209
BLAST score	126
E value	3.0e-38
Match length	99
% identity	76
NCBI Description	(AC004786) putative serine carboxypeptidase I [Arabidopsis thaliana]

Seq. No.	138491
Seq. ID	LIB23-001-Q1-E1-C2
Method	BLASTN
NCBI GI	g3176693

BLAST score	45
E value	2.0e-16
Match length	141
% identity	83
NCBI Description	Arabidopsis thaliana chromosome I BAC T27I1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138492
Seq. ID	LIB23-001-Q1-E1-C8
Method	BLASTN
NCBI GI	g3449320
BLAST score	396
E value	0.0e+00
Match length	400
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRB17, complete sequence [Arabidopsis thaliana]

Seq. No.	138493
Seq. ID	LIB23-001-Q1-E1-C9
Method	BLASTN
NCBI GI	g516042
BLAST score	60
E value	1.0e-25
Match length	92
% identity	91
NCBI Description	Arabidopsis thaliana Columbia Dwarf1 (DWF1) mRNA, complete cds

Seq. No.	138494
Seq. ID	LIB23-001-Q1-E1-E4
Method	BLASTN
NCBI GI	g217842
BLAST score	33
E value	7.0e-09
Match length	61
% identity	89
NCBI Description	A.thaliana mRNA for protein kinase

Seq. No.	138495
Seq. ID	LIB23-001-Q1-E1-F4
Method	BLASTX
NCBI GI	g399013
BLAST score	476
E value	5.0e-48
Match length	96
% identity	98
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549) adenylate translocator [Arabidopsis thaliana] >gi_445607_prf__1909354A adenylate translocator [Arabidopsis thaliana]

Seq. No.	138496
Seq. ID	LIB23-001-Q1-E1-H3

Method	BLASTX
NCBI GI	g2244827
BLAST score	403
E value	2.0e-39
Match length	119
% identity	74
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	138497
Seq. ID	LIB23-002-Q1-E1-B3
Method	BLASTX
NCBI GI	g4512660
BLAST score	343
E value	2.0e-32
Match length	106
% identity	59
NCBI Description	(AC006931) hypothetical protein [Arabidopsis thaliana] >gi_4544467_gb_AAD22374.1_AC006580_6 (AC006580) hypothetical protein [Arabidopsis thaliana]

Seq. No.	138498
Seq. ID	LIB23-002-Q1-E1-E1
Method	BLASTX
NCBI GI	g4538943
BLAST score	475
E value	6.0e-48
Match length	102
% identity	84
NCBI Description	(AL049483) putative beta-galactosidase [Arabidopsis thaliana]

Seq. No.	138499
Seq. ID	LIB23-002-Q1-E1-E4
Method	BLASTN
NCBI GI	g4587986
BLAST score	43
E value	5.0e-15
Match length	131
% identity	83
NCBI Description	Arabidopsis thaliana ABA-regulated gene cluster, complete sequence

Seq. No.	138500
Seq. ID	LIB23-002-Q1-E1-G11
Method	BLASTN
NCBI GI	g3046856
BLAST score	74
E value	6.0e-34
Match length	74
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXI22, complete sequence [Arabidopsis thaliana]

Seq. No.	138501
Seq. ID	LIB23-002-Q1-E1-G12
Method	BLASTN
NCBI GI	g4580530

BLAST score	256
E value	1.0e-142
Match length	256
% identity	100
NCBI Description	Arabidopsis thaliana scarecrow-like 14 (SCL14) mRNA, partial cds

Seq. No.	138502
Seq. ID	LIB23-003-Q1-E1-A11
Method	BLASTX
NCBI GI	g115783
BLAST score	101
E value	2.0e-22
Match length	68
% identity	81
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	138503
Seq. ID	LIB23-003-Q1-E1-C10
Method	BLASTX
NCBI GI	g3941436
BLAST score	275
E value	6.0e-25
Match length	57
% identity	86
NCBI Description	(AF062872) putative transcription factor [Arabidopsis thaliana]

Seq. No.	138504
Seq. ID	LIB23-003-Q1-E1-D7
Method	BLASTX
NCBI GI	g3183454
BLAST score	172
E value	2.0e-12
Match length	98
% identity	38
NCBI Description	HYPOTHETICAL 30.7 KD PROTEIN IN MCPC-KINA INTERGENIC REGION >gi_2632217_emb_CAA10859_ (AJ222587) YkwC protein [Bacillus subtilis] >gi_2633767_emb_CAB13269_ (Z99111) similar to 3-hydroxyisobutyrate dehydrogenase [Bacillus subtilis]

Seq. No.	138505
Seq. ID	LIB23-003-Q1-E1-H2
Method	BLASTX
NCBI GI	g2335096
BLAST score	589
E value	4.0e-61
Match length	116
% identity	100
NCBI Description	(AC002339) hypothetical protein [Arabidopsis thaliana]

Seq. No.	138506
Seq. ID	LIB23-004-Q1-E1-B6
Method	BLASTN

NCBI GI	g3212846
BLAST score	252
E value	1.0e-139
Match length	416
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138507
Seq. ID	LIB23-004-Q1-E1-B8
Method	BLASTN
NCBI GI	g3096946
BLAST score	419
E value	0.0e+00
Match length	434
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for putative cyclic nucleotide-regulated ion channel, cngc1

Seq. No.	138508
Seq. ID	LIB23-004-Q1-E1-E10
Method	BLASTX
NCBI GI	g3461817
BLAST score	173
E value	1.0e-12
Match length	64
% identity	55
NCBI Description	(AC004138) unknown protein [Arabidopsis thaliana]

Seq. No.	138509
Seq. ID	LIB23-004-Q1-E1-E2
Method	BLASTN
NCBI GI	g4220643
BLAST score	435
E value	0.0e+00
Match length	435
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD22, complete sequence [Arabidopsis thaliana]

Seq. No.	138510
Seq. ID	LIB23-004-Q1-E1-E9
Method	BLASTX
NCBI GI	g4633087
BLAST score	433
E value	3.0e-43
Match length	88
% identity	93
NCBI Description	(AF102508) fizzy-related protein [Homo sapiens]

Seq. No.	138511
Seq. ID	LIB23-004-Q1-E1-G1
Method	BLASTX
NCBI GI	g2651314
BLAST score	372
E value	1.0e-35
Match length	108

% identity	69
NCBI Description	(AC002336) putative ribosomal protein S26 [Arabidopsis thaliana]

Seq. No.	138512
Seq. ID	LIB23-005-Q1-E1-D6
Method	BLASTN
NCBI GI	g259446
BLAST score	89
E value	2.0e-42
Match length	244
% identity	71
NCBI Description	glycine-rich protein {clone atGRP-3} [Arabidopsis thaliana, C24, mRNA, 680 nt]

Seq. No.	138513
Seq. ID	LIB23-005-Q1-E1-E11
Method	BLASTX
NCBI GI	g445612
BLAST score	578
E value	7.0e-60
Match length	121
% identity	91
NCBI Description	ribosomal protein S19 [Solanum tuberosum]

Seq. No.	138514
Seq. ID	LIB23-005-Q1-E1-E2
Method	BLASTN
NCBI GI	g3047100
BLAST score	323
E value	0.0e+00
Match length	364
% identity	66
NCBI Description	Arabidopsis thaliana BAC F6N23

Seq. No.	138515
Seq. ID	LIB23-005-Q1-E1-E4
Method	BLASTN
NCBI GI	g4455168
BLAST score	348
E value	0.0e+00
Match length	348
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)

Seq. No.	138516
Seq. ID	LIB23-005-Q1-E1-F4
Method	BLASTN
NCBI GI	g2828185
BLAST score	322
E value	0.0e+00
Match length	322
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUD21, complete sequence [Arabidopsis thaliana]

Seq. No.	138517
Seq. ID	LIB23-005-Q1-E1-G5
Method	BLASTX
NCBI GI	g4204270
BLAST score	274
E value	3.0e-24
Match length	91
% identity	64
NCBI Description	(AC005223) branched-chain alpha-keto acid decarboxylase E1 beta subunit [Arabidopsis thaliana]

Seq. No.	138518
Seq. ID	LIB23-005-Q1-E1-H9
Method	BLASTX
NCBI GI	g4100433
BLAST score	321
E value	1.0e-29
Match length	107
% identity	62
NCBI Description	(AF000378) beta-glucosidase [Glycine max]

Seq. No.	138519
Seq. ID	LIB23-006-Q1-E1-B5
Method	BLASTX
NCBI GI	g115783
BLAST score	512
E value	4.0e-52
Match length	96
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	138520
Seq. ID	LIB23-006-Q1-E1-B8
Method	BLASTX
NCBI GI	g3287679
BLAST score	675
E value	3.0e-71
Match length	137
% identity	99
NCBI Description	(AC003979) T22J18.6 [Arabidopsis thaliana]

Seq. No.	138521
Seq. ID	LIB23-006-Q1-E1-D6
Method	BLASTX
NCBI GI	g4544402
BLAST score	190
E value	2.0e-14
Match length	137
% identity	31
NCBI Description	(AC007047) putative leucine rich repeat protein [Arabidopsis thaliana]

Seq. No.	138522
Seq. ID	LIB23-006-Q1-E1-E7

Method	BLASTX
NCBI GI	g4504909
BLAST score	250
E value	2.0e-21
Match length	119
% identity	45
NCBI Description	karyopherin (importin) beta 3 >gi_2102696 (U72761) karyopherin beta 3 [Homo sapiens]

Seq. No.	138523
Seq. ID	LIB23-006-Q1-E1-F3
Method	BLASTX
NCBI GI	g2911067
BLAST score	516
E value	9.0e-53
Match length	111
% identity	94
NCBI Description	(AL021960) UV-damaged DNA-binding protein-like [Arabidopsis thaliana]

Seq. No.	138524
Seq. ID	LIB23-006-Q1-E1-G10
Method	BLASTN
NCBI GI	g4006885
BLAST score	261
E value	1.0e-145
Match length	309
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	138525
Seq. ID	LIB23-006-Q1-E1-G3
Method	BLASTX
NCBI GI	g2738248
BLAST score	440
E value	9.0e-44
Match length	120
% identity	77
NCBI Description	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No.	138526
Seq. ID	LIB23-006-Q1-E1-H12
Method	BLASTN
NCBI GI	g3449317
BLAST score	185
E value	1.0e-100
Match length	185
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKM21, complete sequence [Arabidopsis thaliana]

Seq. No.	138527
Seq. ID	LIB23-007-Q1-E1-B10
Method	BLASTN
NCBI GI	g4325323

BLAST score	218
E value	1.0e-119
Match length	248
% identity	96
NCBI Description	Arabidopsis thaliana lysyl-tRNA synthetase mRNA, complete cds

Seq. No.	138528
Seq. ID	LIB23-007-Q1-E1-B11
Method	BLASTN
NCBI GI	g3075383
BLAST score	137
E value	5.0e-71
Match length	353
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T1D16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138529
Seq. ID	LIB23-007-Q1-E1-B3
Method	BLASTN
NCBI GI	g4589438
BLAST score	336
E value	0.0e+00
Match length	336
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQJ2, complete sequence

Seq. No.	138530
Seq. ID	LIB23-007-Q1-E1-B4
Method	BLASTX
NCBI GI	g1853966
BLAST score	484
E value	6.0e-49
Match length	111
% identity	86
NCBI Description	(D83511) ATMYC1 [Arabidopsis thaliana]

Seq. No.	138531
Seq. ID	LIB23-007-Q1-E1-C1
Method	BLASTN
NCBI GI	g2244747
BLAST score	301
E value	1.0e-169
Match length	354
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	138532
Seq. ID	LIB23-007-Q1-E1-C3
Method	BLASTX
NCBI GI	g4753658
BLAST score	163
E value	2.0e-11
Match length	80

% identity	39
NCBI Description	(AL049751) putative protein [Arabidopsis thaliana]

Seq. No.	138533
Seq. ID	LIB23-007-Q1-E1-D12
Method	BLASTN
NCBI GI	g3252804
BLAST score	263
E value	1.0e-146
Match length	346
% identity	69
NCBI Description	Arabidopsis thaliana chromosome II BAC F26C24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138534
Seq. ID	LIB23-007-Q1-E1-D3
Method	BLASTN
NCBI GI	g3451055
BLAST score	312
E value	1.0e-175
Match length	350
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F16G20 (ESSAII project)

Seq. No.	138535
Seq. ID	LIB23-007-Q1-E1-D5
Method	BLASTX
NCBI GI	g99741
BLAST score	372
E value	8.0e-36
Match length	114
% identity	46
NCBI Description	P-glycoprotein pgp1 - Arabidopsis thaliana

Seq. No.	138536
Seq. ID	LIB23-007-Q1-E1-D7
Method	BLASTX
NCBI GI	g2281697
BLAST score	169
E value	6.0e-12
Match length	96
% identity	41
NCBI Description	(AF010138) transcription factor [Mus musculus]

Seq. No.	138537
Seq. ID	LIB23-007-Q1-E1-E8
Method	BLASTN
NCBI GI	g3128136
BLAST score	424
E value	0.0e+00
Match length	427
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1F13, complete sequence [Arabidopsis thaliana]

Seq. No.	138538

Seq. ID	LIB23-007-Q1-E1-F3
Method	BLASTX
NCBI GI	g4522012
BLAST score	251
E value	1.0e-21
Match length	95
% identity	49
NCBI Description	(AC007069) hypothetical protein [Arabidopsis thaliana]

Seq. No.	138539
Seq. ID	LIB23-007-Q1-E1-F9
Method	BLASTN
NCBI GI	g2760165
BLAST score	298
E value	1.0e-167
Match length	330
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC9, complete sequence [Arabidopsis thaliana]

Seq. No.	138540
Seq. ID	LIB23-007-Q1-E1-H10
Method	BLASTN
NCBI GI	g2245073
BLAST score	103
E value	3.0e-51
Match length	124
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	138541
Seq. ID	LIB23-007-Q1-E1-H12
Method	BLASTN
NCBI GI	g2656025
BLAST score	320
E value	1.0e-180
Match length	389
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCD7

Seq. No.	138542
Seq. ID	LIB23-007-Q1-E1-H7
Method	BLASTX
NCBI GI	g2673920
BLAST score	425
E value	4.0e-42
Match length	83
% identity	100
NCBI Description	(AC002561) similar to Drosophila couch potato protein [Arabidopsis thaliana]

Seq. No.	138543
Seq. ID	LIB23-008-Q1-E1-A12
Method	BLASTX
NCBI GI	g3219858

BLAST score	389
E value	9.0e-38
Match length	105
% identity	84
NCBI Description	DNA-DIRECTED RNA POLYMERASE II 13.6 KD POLYPEPTIDE >gi_2129724_pir__S71204 RNA polymerase II 13.6 kDa chain - Arabidopsis thaliana >gi_881501 (U28048) RNA polymerase II 13.6 kDa subunit [Arabidopsis thaliana] >gi_4678938_emb_CAB41329.1_ (AL049711) DNA-directed RNA polymerase II 13.6K chain [Arabidopsis thaliana]

Seq. No.	138544
Seq. ID	LIB23-008-Q1-E1-A3
Method	BLASTX
NCBI GI	g2129727
BLAST score	195
E value	6.0e-15
Match length	75
% identity	60
NCBI Description	RNA-binding protein 37 - Arabidopsis thaliana >gi_1174153 (U44134) RNA-binding protein [Arabidopsis thaliana]

Seq. No.	138545
Seq. ID	LIB23-008-Q1-E1-A7
Method	BLASTX
NCBI GI	g1854445
BLAST score	499
E value	1.0e-50
Match length	117
% identity	78
NCBI Description	(D83971) CPRD14 protein [Vigna unguiculata]

Seq. No.	138546
Seq. ID	LIB23-008-Q1-E1-C2
Method	BLASTN
NCBI GI	g2252848
BLAST score	277
E value	1.0e-154
Match length	415
% identity	60
NCBI Description	Arabidopsis thaliana BAC TM018A10

Seq. No.	138547
Seq. ID	LIB23-008-Q1-E1-C4
Method	BLASTN
NCBI GI	g4159709
BLAST score	426
E value	0.0e+00
Match length	429
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLN21, complete sequence

Seq. No.	138548
Seq. ID	LIB23-008-Q1-E1-C5
Method	BLASTN
NCBI GI	g2980787

BLAST score	354
E value	0.0e+00
Match length	424
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, P1 clone M7J2 (ESSAII project)

Seq. No.	138549
Seq. ID	LIB23-008-Q1-E1-D5
Method	BLASTN
NCBI GI	g3168605
BLAST score	80
E value	6.0e-37
Match length	376
% identity	83
NCBI Description	Arabidopsis thaliana catalase 3 (CAT3) and catalase 1 (CAT1) genes, complete cds

Seq. No.	138550
Seq. ID	LIB23-008-Q1-E1-E2
Method	BLASTN
NCBI GI	g4249393
BLAST score	184
E value	4.0e-99
Match length	354
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T9J23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138551
Seq. ID	LIB23-008-Q1-E1-F9
Method	BLASTX
NCBI GI	g2760839
BLAST score	186
E value	6.0e-14
Match length	129
% identity	35
NCBI Description	(AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq. No.	138552
Seq. ID	LIB23-008-Q1-E1-G4
Method	BLASTX
NCBI GI	g3540185
BLAST score	355
E value	1.0e-33
Match length	119
% identity	50
NCBI Description	(AC004122) Highly Similar to branched-chain amino acid aminotransferase [Arabidopsis thaliana]

Seq. No.	138553
Seq. ID	LIB23-008-Q1-E1-G6
Method	BLASTX
NCBI GI	g4467128
BLAST score	743
E value	3.0e-79
Match length	141

% identity	100
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]

Seq. No.	138554
Seq. ID	LIB23-008-Q1-E1-H11
Method	BLASTN
NCBI GI	g4199934
BLAST score	191
E value	1.0e-103
Match length	277
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T3P18, complete sequence [Arabidopsis thaliana]

Seq. No.	138555
Seq. ID	LIB23-008-Q1-E1-H7
Method	BLASTN
NCBI GI	g472870
BLAST score	114
E value	3.0e-57
Match length	286
% identity	94
NCBI Description	A.thaliana gene for methyltransferase

Seq. No.	138556
Seq. ID	LIB23-009-Q1-E1-F2
Method	BLASTX
NCBI GI	g4678301
BLAST score	276
E value	2.0e-24
Match length	87
% identity	62
NCBI Description	(AL049655) pectate lyase-like protein [Arabidopsis thaliana]

Seq. No.	138557
Seq. ID	LIB23-009-Q1-E1-F8
Method	BLASTN
NCBI GI	g4115352
BLAST score	189
E value	1.0e-102
Match length	306
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T15J14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138558
Seq. ID	LIB23-009-Q1-E1-G3
Method	BLASTN
NCBI GI	g2618602
BLAST score	283
E value	1.0e-158
Match length	379
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	138559
Seq. ID	LIB23-009-Q1-E1-H8
Method	BLASTX
NCBI GI	g2894574
BLAST score	314
E value	2.0e-29
Match length	61
% identity	98
NCBI Description	(AL021890) peroxidase prxr1 [Arabidopsis thaliana] >gi_2961341_emb_CAA18099.1_ (AL022140) peroxidase prxr1 [Arabidopsis thaliana]

Seq. No.	138560
Seq. ID	LIB23-009-Q1-E2-A7
Method	BLASTN
NCBI GI	g3297806
BLAST score	131
E value	8.0e-68
Match length	171
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17I5 (ESSA project)

Seq. No.	138561
Seq. ID	LIB23-009-Q1-E2-C5
Method	BLASTN
NCBI GI	g2924733
BLAST score	66
E value	3.0e-29
Match length	122
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]

Seq. No.	138562
Seq. ID	LIB23-009-Q1-E2-D2
Method	BLASTN
NCBI GI	g3128143
BLAST score	65
E value	3.0e-28
Match length	197
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTI20, complete sequence [Arabidopsis thaliana]

Seq. No.	138563
Seq. ID	LIB23-009-Q1-E2-D7
Method	BLASTN
NCBI GI	g4159706
BLAST score	53
E value	2.0e-21
Match length	105
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGL6, complete sequence

Seq. No. 138564

Seq. ID	LIB23-009-Q1-E2-E6
Method	BLASTN
NCBI GI	g2618683
BLAST score	130
E value	8.0e-67
Match length	274
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC T32G6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138565
Seq. ID	LIB23-009-Q1-E2-G10
Method	BLASTN
NCBI GI	g1490552
BLAST score	118
E value	4.0e-60
Match length	142
% identity	96
NCBI Description	Arabidopsis thaliana S-adenosylmethionine decarboxylase (SAMdc) mRNA, complete cds

Seq. No.	138566
Seq. ID	LIB23-010-Q1-E1-A8
Method	BLASTX
NCBI GI	g4104058
BLAST score	248
E value	4.0e-21
Match length	106
% identity	47
NCBI Description	(AF031195) blue copper-binding protein homolog [Triticum aestivum]

Seq. No.	138567
Seq. ID	LIB23-010-Q1-E1-B7
Method	BLASTN
NCBI GI	g3046855
BLAST score	182
E value	8.0e-98
Match length	374
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSL1, complete sequence [Arabidopsis thaliana]

Seq. No.	138568
Seq. ID	LIB23-010-Q1-E2-A11
Method	BLASTX
NCBI GI	g2921158
BLAST score	591
E value	2.0e-61
Match length	142
% identity	61
NCBI Description	(AF022909) ClpC [Arabidopsis thaliana]

Seq. No.	138569
Seq. ID	LIB23-010-Q1-E2-C12
Method	BLASTN
NCBI GI	g4760411

BLAST score	364
E value	0.0e+00
Match length	368
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F25C20 sequence, complete sequence

Seq. No.	138570
Seq. ID	LIB23-010-Q1-E2-D12
Method	BLASTN
NCBI GI	g2828278
BLAST score	346
E value	0.0e+00
Match length	349
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16 (ESSAII project)

Seq. No.	138571
Seq. ID	LIB23-010-Q1-E2-G5
Method	BLASTX
NCBI GI	g2341034
BLAST score	619
E value	1.0e-64
Match length	124
% identity	100
NCBI Description	(AC000104) F19P19.13 [Arabidopsis thaliana]

Seq. No.	138572
Seq. ID	LIB23-010-Q1-E2-H2
Method	BLASTX
NCBI GI	g1944575
BLAST score	360
E value	2.0e-34
Match length	72
% identity	86
NCBI Description	(Z94058) pectinesterase [Lycopersicon esculentum]

Seq. No.	138573
Seq. ID	LIB23-010-Q1-E2-H9
Method	BLASTX
NCBI GI	g1168529
BLAST score	760
E value	4.0e-81
Match length	149
% identity	96
NCBI Description	SERINE/THREONINE-PROTEIN KINASE ASK1 >gi_541890_pir__S36944 probable serine/threonine-specific protein kinase (EC 2.7.1.-) (clone ASK1) - Arabidopsis thaliana >gi_166882 (M91548) serine/threonine kinase [Arabidopsis thaliana] >gi_1931648 (U95973) Ser/Thr kinase [Arabidopsis thaliana]

Seq. No.	138574
Seq. ID	LIB23-011-Q1-E1-A9
Method	BLASTX
NCBI GI	g3152558
BLAST score	424

E value	4.0e-42
Match length	80
% identity	96
NCBI Description	(AC002986) Similar to M. tuberculosis gene gb_Z96072 and M. leprae gene gb_400019. [Arabidopsis thaliana]

Seq. No.	138575
Seq. ID	LIB23-011-Q1-E1-B1
Method	BLASTN
NCBI GI	g4757410
BLAST score	108
E value	5.0e-54
Match length	203
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MVE11, complete sequence

Seq. No.	138576
Seq. ID	LIB23-011-Q1-E1-B4
Method	BLASTX
NCBI GI	g1663724
BLAST score	359
E value	3.0e-34
Match length	115
% identity	57
NCBI Description	(U50846) 4-coumarate:coenzyme A ligase [Nicotiana tabacum]

Seq. No.	138577
Seq. ID	LIB23-011-Q1-E1-D2
Method	BLASTN
NCBI GI	g4337186
BLAST score	333
E value	0.0e+00
Match length	368
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T28I24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138578
Seq. ID	LIB23-011-Q1-E1-F4
Method	BLASTX
NCBI GI	g2708750
BLAST score	341
E value	4.0e-32
Match length	101
% identity	64
NCBI Description	(AC003952) putative physical impedence protein [Arabidopsis thaliana]

Seq. No.	138579
Seq. ID	LIB23-011-Q1-E1-G2
Method	BLASTX
NCBI GI	g4538923
BLAST score	430
E value	1.0e-42
Match length	89
% identity	98

NCBI Description	(AL049483) predicted protein destination factor [Arabidopsis thaliana]
Seq. No.	138580
Seq. ID	LIB23-011-Q1-E1-H7
Method	BLASTX
NCBI GI	g421826
BLAST score	574
E value	2.0e-59
Match length	133
% identity	81
NCBI Description	chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis thaliana]
Seq. No.	138581
Seq. ID	LIB23-012-Q1-E1-A10
Method	BLASTX
NCBI GI	g267073
BLAST score	463
E value	2.0e-46
Match length	85
% identity	100
NCBI Description	TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin beta chain - Arabidopsis thaliana >gi_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701) beta-3 tubulin [Arabidopsis thaliana]
Seq. No.	138582
Seq. ID	LIB23-012-Q1-E1-A3
Method	BLASTN
NCBI GI	g4185120
BLAST score	81
E value	1.0e-37
Match length	370
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F5F19 sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	138583
Seq. ID	LIB23-012-Q1-E1-A6
Method	BLASTN
NCBI GI	g3420042
BLAST score	68
E value	8.0e-30
Match length	167
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC T13E15 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	138584
Seq. ID	LIB23-012-Q1-E1-A7
Method	BLASTN
NCBI GI	g2252639
BLAST score	244
E value	1.0e-135
Match length	340

% identity	99
NCBI Description	Genomic sequence of Arabidopsis BAC F8A5, complete sequence [Arabidopsis thaliana]

Seq. No.	138585
Seq. ID	LIB23-012-Q1-E1-C11
Method	BLASTN
NCBI GI	g2924732
BLAST score	96
E value	9.0e-47
Match length	217
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUA2, complete sequence [Arabidopsis thaliana]

Seq. No.	138586
Seq. ID	LIB23-012-Q1-E1-C6
Method	BLASTN
NCBI GI	g3241926
BLAST score	372
E value	0.0e+00
Match length	404
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSG15, complete sequence [Arabidopsis thaliana]

Seq. No.	138587
Seq. ID	LIB23-012-Q1-E1-D9
Method	BLASTN
NCBI GI	g4733952
BLAST score	127
E value	4.0e-65
Match length	298
% identity	95
NCBI Description	Arabidopsis thaliana chromosome I BAC F23H11 genomic sequence, complete sequence

Seq. No.	138588
Seq. ID	LIB23-012-Q1-E1-E8
Method	BLASTX
NCBI GI	g4559366
BLAST score	508
E value	9.0e-52
Match length	106
% identity	91
NCBI Description	(AC006585) putative tyrosine transaminase [Arabidopsis thaliana]

Seq. No.	138589
Seq. ID	LIB23-012-Q1-E1-G1
Method	BLASTX
NCBI GI	g3063446
BLAST score	449
E value	5.0e-45
Match length	89
% identity	98
NCBI Description	(AC003981) F22O13.8 [Arabidopsis thaliana]

Seq. No.	138590
Seq. ID	LIB23-012-Q1-E1-H6
Method	BLASTN
NCBI GI	g3337347
BLAST score	35
E value	3.0e-10
Match length	203
% identity	83
NCBI Description	Arabidopsis thaliana chromosome II BAC F13P17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138591
Seq. ID	LIB23-013-Q1-E1-B10
Method	BLASTX
NCBI GI	g2832625
BLAST score	193
E value	1.0e-14
Match length	74
% identity	45
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	138592
Seq. ID	LIB23-013-Q1-E1-D6
Method	BLASTX
NCBI GI	g531829
BLAST score	172
E value	2.0e-12
Match length	77
% identity	48
NCBI Description	(U12390) beta-galactosidase alpha peptide [cloning vector pSport1]

Seq. No.	138593
Seq. ID	LIB23-013-Q1-E1-D8
Method	BLASTX
NCBI GI	g1711572
BLAST score	141
E value	2.0e-51
Match length	129
% identity	83
NCBI Description	SUCCINYL-COA LIGASE (GDP-FORMING), ALPHA-CHAIN PRECURSOR (SUCCINYL-COA SYNTHETASE, ALPHA CHAIN) (SCS-ALPHA) >gi_1076415_pir__S30579 succinate--CoA ligase (GDP-forming) (EC 6.2.1.4) alpha chain - Arabidopsis thaliana (fragment) >gi_16510_emb_CAA48891_ (X69138) succinate--CoA ligase (GDP-forming) [Arabidopsis thaliana]

Seq. No.	138594
Seq. ID	LIB23-013-Q1-E1-F4
Method	BLASTX
NCBI GI	g4220514
BLAST score	296
E value	7.0e-27
Match length	71
% identity	79
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	138595
Seq. ID	LIB23-013-Q1-E1-F8
Method	BLASTX
NCBI GI	g1174498
BLAST score	482
E value	1.0e-48
Match length	94
% identity	98
NCBI Description	SYNAPTOBREVIN-RELATED PROTEIN >gi_600710 (M90418) formerly called HAT24; synaptobrevin-related protein [Arabidopsis thaliana]

Seq. No.	138596
Seq. ID	LIB23-013-Q1-E1-H5
Method	BLASTN
NCBI GI	g2828182
BLAST score	418
E value	0.0e+00
Match length	422
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOJ9, complete sequence [Arabidopsis thaliana]

Seq. No.	138597
Seq. ID	LIB23-014-Q1-E1-A1
Method	BLASTN
NCBI GI	g4092471
BLAST score	71
E value	6.0e-32
Match length	79
% identity	97
NCBI Description	Arabidopsis thaliana BAC F9M13 from chromosome IV near 21.5 cM, complete sequence

Seq. No.	138598
Seq. ID	LIB23-014-Q1-E1-B6
Method	BLASTN
NCBI GI	g4455321
BLAST score	161
E value	1.0e-85
Match length	172
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4I10 (ESSAII project)

Seq. No.	138599
Seq. ID	LIB23-014-Q1-E1-C10
Method	BLASTX
NCBI GI	g2911049
BLAST score	312
E value	8.0e-29
Match length	104
% identity	57
NCBI Description	(AL021961) glucosyltransferase -like protein [Arabidopsis thaliana]

Seq. No.	138600
Seq. ID	LIB23-014-Q1-E1-C6
Method	BLASTX
NCBI GI	g2961388
BLAST score	416
E value	6.0e-41
Match length	104
% identity	81
NCBI Description	(AL022141) putative protein [Arabidopsis thaliana]

Seq. No.	138601
Seq. ID	LIB23-014-Q1-E1-D2
Method	BLASTN
NCBI GI	g4490291
BLAST score	147
E value	5.0e-77
Match length	295
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17M5 (ESSA project)

Seq. No.	138602
Seq. ID	LIB23-014-Q1-E1-D3
Method	BLASTX
NCBI GI	g2924781
BLAST score	143
E value	2.0e-09
Match length	34
% identity	76
NCBI Description	(AC002334) putative cellulose synthase [Arabidopsis thaliana]

Seq. No.	138603
Seq. ID	LIB23-014-Q1-E1-D9
Method	BLASTX
NCBI GI	g2335108
BLAST score	428
E value	2.0e-42
Match length	97
% identity	81
NCBI Description	(AC002339) putative isulinase [Arabidopsis thaliana]

Seq. No.	138604
Seq. ID	LIB23-014-Q1-E1-E5
Method	BLASTX
NCBI GI	g4512620
BLAST score	206
E value	1.0e-16
Match length	47
% identity	91
NCBI Description	(AC004793) Identical to gb_X71364 gene for aspartate kinase homoserine dehydrogenase from Arabidopsis thaliana

Seq. No.	138605
Seq. ID	LIB23-014-Q1-E1-G8
Method	BLASTX
NCBI GI	g3170230

BLAST score	439
E value	1.0e-43
Match length	137
% identity	62
NCBI Description	(AF041848) fructose-6-phosphate 2-kinase /fructose-2,6-bisphosphatase [Spinacia oleracea]

Seq. No.	138606
Seq. ID	LIB23-015-Q1-E1-A5
Method	BLASTX
NCBI GI	g2492519
BLAST score	215
E value	1.0e-17
Match length	44
% identity	95
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT 7) >gi_1395191_dbj_BAA13021_ (D86121) 26S proteasome ATPase subunit [Spinacia oleracea]

Seq. No.	138607
Seq. ID	LIB23-015-Q1-E1-B2
Method	BLASTX
NCBI GI	g3928543
BLAST score	581
E value	3.0e-60
Match length	128
% identity	84
NCBI Description	(AB016819) UDP-glucose glucosyltransferase [Arabidopsis thaliana]

Seq. No.	138608
Seq. ID	LIB23-015-Q1-E1-B5
Method	BLASTN
NCBI GI	g3420043
BLAST score	43
E value	4.0e-15
Match length	71
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC F23F1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138609
Seq. ID	LIB23-015-Q1-E1-B8
Method	BLASTX
NCBI GI	g2738248
BLAST score	639
E value	5.0e-67
Match length	120
% identity	100
NCBI Description	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No.	138610
Seq. ID	LIB23-015-Q1-E1-B9
Method	BLASTX
NCBI GI	g115783
BLAST score	409

E value	3.0e-40
Match length	79
% identity	97
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	138611
Seq. ID	LIB23-015-Q1-E1-C3
Method	BLASTN
NCBI GI	g3293582
BLAST score	125
E value	6.0e-64
Match length	226
% identity	100
NCBI Description	Arabidopsis thaliana BAC T15F16

Seq. No.	138612
Seq. ID	LIB23-015-Q1-E1-C4
Method	BLASTX
NCBI GI	g2829899
BLAST score	676
E value	2.0e-71
Match length	132
% identity	100
NCBI Description	(AC002311) similar to ripening-induced protein, gp_AJ001449_2465015 and major#latex protein, gp_X91961_1107495 [Arabidopsis thaliana]

Seq. No.	138613
Seq. ID	LIB23-015-Q1-E1-C6
Method	BLASTX
NCBI GI	g3004551
BLAST score	170
E value	5.0e-12
Match length	98
% identity	44
NCBI Description	(AC003673) hypothetical protein [Arabidopsis thaliana]

Seq. No.	138614
Seq. ID	LIB23-015-Q1-E1-D6
Method	BLASTX
NCBI GI	g3461818
BLAST score	187
E value	2.0e-14
Match length	54
% identity	70
NCBI Description	(AC004138) putative glutathione S-transferase [Arabidopsis thaliana]

Seq. No.	138615
Seq. ID	LIB23-015-Q1-E1-E4
Method	BLASTX
NCBI GI	g170354
BLAST score	606
E value	4.0e-63

Match length	122
% identity	22
NCBI Description	(M74156) pentameric polyubiquitin [Nicotiana sylvestris]

Seq. No.	138616
Seq. ID	LIB23-015-Q1-E1-E8
Method	BLASTX
NCBI GI	g2462929
BLAST score	661
E value	1.0e-69
Match length	127
% identity	100
NCBI Description	(Y12295) glutathione transferase [Arabidopsis thaliana]

Seq. No.	138617
Seq. ID	LIB23-015-Q1-E1-F1
Method	BLASTX
NCBI GI	g4099090
BLAST score	482
E value	1.0e-48
Match length	138
% identity	74
NCBI Description	(U83178) unknown [Arabidopsis thaliana]

Seq. No.	138618
Seq. ID	LIB23-015-Q1-E1-G8
Method	BLASTX
NCBI GI	g115767
BLAST score	156
E value	6.0e-11
Match length	34
% identity	97
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	138619
Seq. ID	LIB23-015-Q1-E1-H3
Method	BLASTX
NCBI GI	g3096947
BLAST score	708
E value	4.0e-75
Match length	137
% identity	99
NCBI Description	(Y16327) putative cyclic nucleotide-regulated ion channel [Arabidopsis thaliana]

Seq. No.	138620
Seq. ID	LIB23-016-Q1-E1-B5
Method	BLASTX
NCBI GI	g166867
BLAST score	649
E value	4.0e-68

Match length	141
% identity	88
NCBI Description	(J05216) ribosomal protein S11 (probable start codon at bp 67) [Arabidopsis thaliana]

Seq. No.	138621
Seq. ID	LIB23-016-Q1-E1-B7
Method	BLASTN
NCBI GI	g2088638
BLAST score	303
E value	1.0e-170
Match length	355
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T28M21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138622
Seq. ID	LIB23-016-Q1-E1-D11
Method	BLASTX
NCBI GI	g1841355
BLAST score	261
E value	7.0e-23
Match length	66
% identity	65
NCBI Description	(D85381) cytochrome c oxidase subunit Vb precursor [Oryza sativa]

Seq. No.	138623
Seq. ID	LIB23-016-Q1-E1-E11
Method	BLASTN
NCBI GI	g3327922
BLAST score	286
E value	1.0e-160
Match length	286
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T31E10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138624
Seq. ID	LIB23-016-Q1-E1-E12
Method	BLASTX
NCBI GI	g4757796
BLAST score	251
E value	1.0e-21
Match length	106
% identity	46
NCBI Description	arsA (bacterial) arsenite transporter, ATP-binding, homolog 1 >gi_1616741 (U60276) hASNA-I [Homo sapiens]

Seq. No.	138625
Seq. ID	LIB23-016-Q1-E1-E2
Method	BLASTX
NCBI GI	g2506276
BLAST score	313
E value	8.0e-29
Match length	76
% identity	84

NCBI Description	RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60 KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA) >gi_2129561_pir__S71235 chaperonin-60 alpha chain - Arabidopsis thaliana >gi_1223910 (U49357) chaperonin-60 alpha subunit [Arabidopsis thaliana] >gi_4510416_gb_AAD21502.1_ (AC006929) putative rubisco binding protein alpha subunit [Arabidopsis thaliana]
Seq. No.	138626
Seq. ID	LIB23-016-Q1-E1-F10
Method	BLASTN
NCBI GI	g4757678
BLAST score	162
E value	6.0e-86
Match length	370
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC F9H16 genomic sequence, complete sequence
Seq. No.	138627
Seq. ID	LIB23-016-Q1-E1-F4
Method	BLASTN
NCBI GI	g4589445
BLAST score	288
E value	1.0e-161
Match length	288
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWL2, complete sequence
Seq. No.	138628
Seq. ID	LIB23-016-Q1-E1-H1
Method	BLASTX
NCBI GI	g4249386
BLAST score	498
E value	2.0e-50
Match length	97
% identity	100
NCBI Description	(AC005966) Strong similarity to gb_AF061286 gamma-adaptin 1 from Arabidopsis thaliana. EST gb_H37393 comes from this gene. [Arabidopsis thaliana]
Seq. No.	138629
Seq. ID	LIB23-016-Q1-E1-H2
Method	BLASTN
NCBI GI	g402903
BLAST score	38
E value	2.0e-12
Match length	158
% identity	94
NCBI Description	Arabidopsis thaliana Columbia laminin receptor-like protein mRNA, complete cds
Seq. No.	138630
Seq. ID	LIB23-017-Q1-E1-A7
Method	BLASTX
NCBI GI	g2894574

BLAST score	485
E value	4.0e-49
Match length	93
% identity	99
NCBI Description	(AL021890) peroxidase prxr1 [Arabidopsis thaliana] >gi_2961341_emb_CAA18099.1_ (AL022140) peroxidase prxr1 [Arabidopsis thaliana]

Seq. No.	138631
Seq. ID	LIB23-017-Q1-E1-B11
Method	BLASTX
NCBI GI	g300264
BLAST score	198
E value	2.0e-15
Match length	73
% identity	58
NCBI Description	(S59747) HSP68=68 kda heat-stress DnaK homolog [Solanum tuberosum=potatoes, Peptide Mitochondrial, 682 aa] [Solanum tuberosum]

Seq. No.	138632
Seq. ID	LIB23-017-Q1-E1-B9
Method	BLASTX
NCBI GI	g2494116
BLAST score	322
E value	6.0e-30
Match length	57
% identity	98
NCBI Description	(AC002376) Similar to Synechocystis hypothetical protein (gb_D90915). [Arabidopsis thaliana]

Seq. No.	138633
Seq. ID	LIB23-017-Q1-E1-C12
Method	BLASTN
NCBI GI	g2564047
BLAST score	377
E value	0.0e+00
Match length	377
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJB21, complete sequence [Arabidopsis thaliana]

Seq. No.	138634
Seq. ID	LIB23-017-Q1-E1-D5
Method	BLASTX
NCBI GI	g3695385
BLAST score	390
E value	8.0e-38
Match length	104
% identity	80
NCBI Description	(AF096370) similar to Medicago truncatula MtN21 (GB:Y15293) [Arabidopsis thaliana]

Seq. No.	138635
Seq. ID	LIB23-017-Q1-E1-E3
Method	BLASTN
NCBI GI	g4159704

BLAST score	394
E value	0.0e+00
Match length	394
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MCB17, complete sequence

Seq. No.	138636
Seq. ID	LIB23-017-Q1-E1-F6
Method	BLASTX
NCBI GI	g115783
BLAST score	231
E value	1.0e-19
Match length	58
% identity	79
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	138637
Seq. ID	LIB23-017-Q1-E1-F7
Method	BLASTX
NCBI GI	g3834328
BLAST score	487
E value	2.0e-49
Match length	105
% identity	100
NCBI Description	(AC005679) Strong similarity to glycoprotein EP1 gb_L16983 Daucus carota and a member of S locus glycoprotein family PF_00954. [Arabidopsis thaliana]

Seq. No.	138638
Seq. ID	LIB23-017-Q1-E1-G8
Method	BLASTN
NCBI GI	g2980757
BLAST score	197
E value	1.0e-107
Match length	284
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18 (ESSAII project)

Seq. No.	138639
Seq. ID	LIB23-017-Q1-E1-H12
Method	BLASTX
NCBI GI	g1352243
BLAST score	596
E value	4.0e-62
Match length	118
% identity	99
NCBI Description	LIGHT-MEDIATED DEVELOPMENT PROTEIN DET1 >gi_625972_pir__A54841 DET1 protein - Arabidopsis thaliana >gi_510275 (L33695) DET1 [Arabidopsis thaliana] >gi_3695414 (AF096373) Arabidopsis thaliana light-mediated development protein DET1 (SP:P48732) [Arabidopsis thaliana] >gi_4538982_emb_CAB39770.1_ (AL049487) Deetiolated1 (DET1)

light signal transduction protein [Arabidopsis thaliana]

Seq. No.	138640
Seq. ID	LIB23-018-Q1-E1-B10
Method	BLASTX
NCBI GI	g1170555
BLAST score	218
E value	1.0e-17
Match length	121
% identity	44
NCBI Description	MYO-INOSITOL 4-O-METHYLTRANSFERASE >gi_282822_pir__S22696 methyltransferase - common ice plant >gi_167262 (M87340) myo-inositol O-methyl transferase [Mesembryanthemum crystallinum] >gi_1488237 (U63634) inositol methyltransferase [Mesembryanthemum crystallinum]

Seq. No.	138641
Seq. ID	LIB23-018-Q1-E1-E10
Method	BLASTX
NCBI GI	g2864623
BLAST score	548
E value	2.0e-56
Match length	124
% identity	90
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana]

Seq. No.	138642
Seq. ID	LIB23-018-Q1-E1-E7
Method	BLASTX
NCBI GI	g259447
BLAST score	178
E value	2.0e-13
Match length	30
% identity	93
NCBI Description	(S47409) glycine-rich protein, atGRP {clone atGRP-3} [Arabidopsis thaliana, C24, Peptide, 145 aa] [Arabidopsis thaliana]

Seq. No.	138643
Seq. ID	LIB23-018-Q1-E1-F12
Method	BLASTX
NCBI GI	g3600058
BLAST score	548
E value	2.0e-56
Match length	112
% identity	100
NCBI Description	(AF080120) similar to vacuolar ATPases [Arabidopsis thaliana]

Seq. No.	138644
Seq. ID	LIB23-018-Q1-E1-F2
Method	BLASTX
NCBI GI	g2459445
BLAST score	283
E value	2.0e-25
Match length	80
% identity	30

NCBI Description	(AC002332) putative ribonucleoprotein [Arabidopsis thaliana]
Seq. No.	138645
Seq. ID	LIB23-018-Q1-E1-G1
Method	BLASTX
NCBI GI	g3047104
BLAST score	374
E value	4.0e-36
Match length	109
% identity	67
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]
Seq. No.	138646
Seq. ID	LIB23-018-Q1-E1-H1
Method	BLASTN
NCBI GI	g4589421
BLAST score	132
E value	3.0e-68
Match length	228
% identity	55
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K5K13, complete sequence
Seq. No.	138647
Seq. ID	LIB23-018-Q1-E1-H9
Method	BLASTN
NCBI GI	g2618599
BLAST score	164
E value	2.0e-87
Match length	172
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBD2, complete sequence [Arabidopsis thaliana]
Seq. No.	138648
Seq. ID	LIB23-019-Q1-E1-A1
Method	BLASTX
NCBI GI	g1707011
BLAST score	208
E value	2.0e-16
Match length	37
% identity	100
NCBI Description	(U78721) auxin-repressed protein isolog [Arabidopsis thaliana]
Seq. No.	138649
Seq. ID	LIB23-019-Q1-E1-A2
Method	BLASTX
NCBI GI	g2746341
BLAST score	360
E value	2.0e-34
Match length	74
% identity	85
NCBI Description	(AF037590) ATA27 [Arabidopsis thaliana]
Seq. No.	138650

Seq. ID	LIB23-019-Q1-E1-B6
Method	BLASTN
NCBI GI	g3985957
BLAST score	321
E value	0.0e+00
Match length	365
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN8, complete sequence [Arabidopsis thaliana]

Seq. No.	138651
Seq. ID	LIB23-019-Q1-E1-D3
Method	BLASTX
NCBI GI	g2832642
BLAST score	144
E value	6.0e-09
Match length	84
% identity	20
NCBI Description	(AL021710) putative protein [Arabidopsis thaliana]

Seq. No.	138652
Seq. ID	LIB23-019-Q1-E1-E6
Method	BLASTX
NCBI GI	g1432083
BLAST score	546
E value	4.0e-56
Match length	124
% identity	88
NCBI Description	(U60981) homolog to Skp1p, an evolutionarily conserved kinetochore protein in budding yeast [Arabidopsis thaliana] >gi_3068807 (AF059294) Skp1 homolog [Arabidopsis thaliana] >gi_3719209 (U97020) UIP1 [Arabidopsis thaliana]

Seq. No.	138653
Seq. ID	LIB23-019-Q1-E1-E7
Method	BLASTN
NCBI GI	g4678371
BLAST score	444
E value	0.0e+00
Match length	444
% identity	72
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T6G15 (ESSA project)

Seq. No.	138654
Seq. ID	LIB23-019-Q1-E1-F10
Method	BLASTN
NCBI GI	g3869075
BLAST score	351
E value	0.0e+00
Match length	406
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence [Arabidopsis thaliana]

Seq. No.	138655
Seq. ID	LIB23-019-Q1-E1-G4

Method	BLASTN
NCBI GI	g3046855
BLAST score	46
E value	1.0e-16
Match length	110
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSL1, complete sequence [Arabidopsis thaliana]

Seq. No.	138656
Seq. ID	LIB23-019-Q1-E1-H10
Method	BLASTX
NCBI GI	g2462929
BLAST score	673
E value	6.0e-71
Match length	131
% identity	99
NCBI Description	(Y12295) glutathione transferase [Arabidopsis thaliana]

Seq. No.	138657
Seq. ID	LIB23-019-Q1-E1-H4
Method	BLASTN
NCBI GI	g2833627
BLAST score	251
E value	1.0e-139
Match length	263
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F17O7 complete sequence [Arabidopsis thaliana]

Seq. No.	138658
Seq. ID	LIB23-020-Q1-E1-B5
Method	BLASTN
NCBI GI	g2749918
BLAST score	236
E value	1.0e-130
Match length	240
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC F3I6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138659
Seq. ID	LIB23-020-Q1-E1-C4
Method	BLASTN
NCBI GI	g2244991
BLAST score	340
E value	0.0e+00
Match length	340
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	138660
Seq. ID	LIB23-020-Q1-E1-D6
Method	BLASTX
NCBI GI	g1518540
BLAST score	530

E value	3.0e-54
Match length	110
% identity	91
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	138661
Seq. ID	LIB23-020-Q1-E1-E10
Method	BLASTN
NCBI GI	g3738088
BLAST score	92
E value	2.0e-44
Match length	217
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T30L20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138662
Seq. ID	LIB23-020-Q1-E1-E4
Method	BLASTN
NCBI GI	g3449313
BLAST score	348
E value	0.0e+00
Match length	348
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21P3, complete sequence [Arabidopsis thaliana]

Seq. No.	138663
Seq. ID	LIB23-020-Q1-E1-E5
Method	BLASTX
NCBI GI	g2497886
BLAST score	300
E value	3.0e-27
Match length	54
% identity	100
NCBI Description	METALLOTHIONEIN-LIKE PROTEIN 2B (MT-2B) >gi_1361999_pir__S57862 metallothionein 2b - Arabidopsis thaliana >gi_1086463 (U11256) metallothionein [Arabidopsis thaliana]

Seq. No.	138664
Seq. ID	LIB23-021-Q2-E1-C12
Method	BLASTX
NCBI GI	g3935138
BLAST score	540
E value	2.0e-55
Match length	123
% identity	85
NCBI Description	(AC005106) T25N20.2 [Arabidopsis thaliana]

Seq. No.	138665
Seq. ID	LIB23-021-Q2-E1-D1
Method	BLASTX
NCBI GI	g3402751
BLAST score	701
E value	3.0e-74
Match length	129

% identity	51
NCBI Description	(AL031187) putative protein [Arabidopsis thaliana]

Seq. No.	138666
Seq. ID	LIB23-021-Q2-E1-E1
Method	BLASTN
NCBI GI	g4206766
BLAST score	58
E value	7.0e-24
Match length	58
% identity	100
NCBI Description	Arabidopsis thaliana glycine-rich protein 3 short isoform (GRP3S) mRNA, complete cds

Seq. No.	138667
Seq. ID	LIB23-021-Q2-E1-E5
Method	BLASTX
NCBI GI	g3342802
BLAST score	440
E value	1.0e-43
Match length	113
% identity	76
NCBI Description	(AF061838) putative cytosolic 6-phosphogluconate dehydrogenase [Zea mays]

Seq. No.	138668
Seq. ID	LIB23-021-Q2-E1-F1
Method	BLASTX
NCBI GI	g2623962
BLAST score	593
E value	1.0e-61
Match length	137
% identity	80
NCBI Description	(Y12540) isocitrate dehydrogenase (NADP+) [Apium graveolens]

Seq. No.	138669
Seq. ID	LIB23-021-Q2-E1-F12
Method	BLASTX
NCBI GI	g2262167
BLAST score	595
E value	7.0e-62
Match length	114
% identity	99
NCBI Description	(AC002329) cytosolic ribosomal protein S4 [Arabidopsis thaliana]

Seq. No.	138670
Seq. ID	LIB23-021-Q2-E1-G10
Method	BLASTN
NCBI GI	g2281081
BLAST score	343
E value	0.0e+00
Match length	367
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F18O19 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138671
Seq. ID	LIB23-021-Q2-E1-H3
Method	BLASTN
NCBI GI	g2760167
BLAST score	195
E value	1.0e-105
Match length	378
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCO15, complete sequence [Arabidopsis thaliana]

Seq. No.	138672
Seq. ID	LIB23-022-Q2-E1-C11
Method	BLASTX
NCBI GI	g4757880
BLAST score	153
E value	5.0e-10
Match length	113
% identity	28
NCBI Description	BUB3 (budding uninhibited by benzimidazoles 3, yeast) homolog >gi_2921873 (AF047472) spleen mitotic checkpoint BUB3 [Homo sapiens] >gi_2981231_gb_AAC06258_ (AF053304) mitotic checkpoint component Bub3 [Homo sapiens] >gi_3639060 (AF081496) kinetochore protein BUB3 [Homo sapiens]

Seq. No.	138673
Seq. ID	LIB23-022-Q2-E1-C6
Method	BLASTN
NCBI GI	g4580454
BLAST score	297
E value	1.0e-166
Match length	373
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T2G17 genomic sequence, complete sequence

Seq. No.	138674
Seq. ID	LIB23-022-Q2-E1-C7
Method	BLASTN
NCBI GI	g3426033
BLAST score	144
E value	1.0e-75
Match length	168
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F12C20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138675
Seq. ID	LIB23-022-Q2-E1-E1
Method	BLASTX
NCBI GI	g1888357
BLAST score	244
E value	8.0e-21
Match length	66
% identity	71

NCBI Description	(X98130) alpha-mannosidase [Arabidopsis thaliana] >gi_1890154_emb_CAA72432_ (Y11767) alpha-mannosidase precursor [Arabidopsis thaliana]
Seq. No.	138676
Seq. ID	LIB23-022-Q2-E1-F10
Method	BLASTX
NCBI GI	g2924786
BLAST score	689
E value	7.0e-73
Match length	134
% identity	99
NCBI Description	(AC002334) similar to disease resistance protein [Arabidopsis thaliana]
Seq. No.	138677
Seq. ID	LIB23-022-Q2-E1-F5
Method	BLASTN
NCBI GI	g560770
BLAST score	249
E value	1.0e-138
Match length	310
% identity	85
NCBI Description	Arabidopsis thaliana rd22 gene, complete cds
Seq. No.	138678
Seq. ID	LIB23-022-Q2-E1-G9
Method	BLASTX
NCBI GI	g3859592
BLAST score	667
E value	2.0e-70
Match length	119
% identity	100
NCBI Description	(AF104919) contains similarity to expansins [Arabidopsis thaliana]
Seq. No.	138679
Seq. ID	LIB23-022-Q2-E1-H2
Method	BLASTN
NCBI GI	g2564050
BLAST score	280
E value	1.0e-156
Match length	375
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUA22, complete sequence [Arabidopsis thaliana]
Seq. No.	138680
Seq. ID	LIB23-022-Q2-E1-H3
Method	BLASTX
NCBI GI	g4063734
BLAST score	285
E value	1.0e-25
Match length	107
% identity	55
NCBI Description	(AC006259) putative P450 [Arabidopsis thaliana]

Seq. No.	138681
Seq. ID	LIB23-022-Q2-E1-H7
Method	BLASTX
NCBI GI	g4415942
BLAST score	568
E value	9.0e-59
Match length	110
% identity	100
NCBI Description	(AC006418) hypothetical protein [Arabidopsis thaliana]

Seq. No.	138682
Seq. ID	LIB23-023-Q1-E1-A4
Method	BLASTX
NCBI GI	g3850621
BLAST score	531
E value	1.0e-54
Match length	105
% identity	100
NCBI Description	(Y15382) putative RNA binding protein [Arabidopsis thaliana]

Seq. No.	138683
Seq. ID	LIB23-023-Q1-E1-B4
Method	BLASTX
NCBI GI	g2464901
BLAST score	181
E value	2.0e-13
Match length	76
% identity	51
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	138684
Seq. ID	LIB23-023-Q1-E1-C2
Method	BLASTN
NCBI GI	g2656032
BLAST score	219
E value	1.0e-120
Match length	219
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZF18

Seq. No.	138685
Seq. ID	LIB23-023-Q1-E1-E1
Method	BLASTX
NCBI GI	g120667
BLAST score	145
E value	3.0e-09
Match length	27
% identity	100
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis thaliana >gi_166706 (M64116) cystolic glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No.	138686
Seq. ID	LIB23-023-Q1-E1-E3
Method	BLASTX
NCBI GI	g2894600
BLAST score	156
E value	1.0e-10
Match length	79
% identity	37
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	138687
Seq. ID	LIB23-023-Q1-E1-F1
Method	BLASTX
NCBI GI	g1684857
BLAST score	447
E value	1.0e-44
Match length	90
% identity	37
NCBI Description	(U77940) polyubiquitin [Phaseolus vulgaris]

Seq. No.	138688
Seq. ID	LIB23-023-Q1-E1-F10
Method	BLASTN
NCBI GI	g2160155
BLAST score	352
E value	0.0e+00
Match length	364
% identity	99
NCBI Description	Sequence of BAC F21M12 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	138689
Seq. ID	LIB23-023-Q1-E1-F9
Method	BLASTN
NCBI GI	g4589437
BLAST score	99
E value	2.0e-48
Match length	181
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPN9, complete sequence

Seq. No.	138690
Seq. ID	LIB23-023-Q1-E1-H9
Method	BLASTX
NCBI GI	g2980774
BLAST score	213
E value	3.0e-17
Match length	41
% identity	100
NCBI Description	(AL022198) leucyl aminopeptidase - like protein [Arabidopsis thaliana]

Seq. No.	138691
Seq. ID	LIB23-025-Q1-E1-A1
Method	BLASTN

NCBI GI	g3449316
BLAST score	47
E value	2.0e-17
Match length	63
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9D7, complete sequence [Arabidopsis thaliana]

Seq. No.	138692
Seq. ID	LIB23-025-Q1-E1-A6
Method	BLASTX
NCBI GI	g4704613
BLAST score	445
E value	2.0e-44
Match length	101
% identity	88
NCBI Description	(AF109695) monodehydroascorbate reductase [Brassica juncea]

Seq. No.	138693
Seq. ID	LIB23-025-Q1-E1-A8
Method	BLASTX
NCBI GI	g1076763
BLAST score	88
E value	1.0e-02
Match length	80
% identity	9
NCBI Description	AWJL218 protein - wheat >gi_551212_emb_CAA57134_ (X81369) AWJL218 [Triticum aestivum]

Seq. No.	138694
Seq. ID	LIB23-025-Q1-E1-B10
Method	BLASTN
NCBI GI	g2351069
BLAST score	306
E value	1.0e-172
Match length	310
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSH12, complete sequence [Arabidopsis thaliana]

Seq. No.	138695
Seq. ID	LIB23-025-Q1-E1-C2
Method	BLASTX
NCBI GI	g4567271
BLAST score	420
E value	2.0e-41
Match length	126
% identity	71
NCBI Description	(AC006841) putative kinesin protein [Arabidopsis thaliana]

Seq. No.	138696
Seq. ID	LIB23-025-Q1-E1-C4
Method	BLASTX
NCBI GI	g3928103
BLAST score	411
E value	2.0e-40
Match length	93

% identity	87
NCBI Description	(AC005770) putative water channel protein [Arabidopsis thaliana]

Seq. No.	138697
Seq. ID	LIB23-025-Q1-E1-D11
Method	BLASTN
NCBI GI	g2182289
BLAST score	387
E value	0.0e+00
Match length	387
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC F11P17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138698
Seq. ID	LIB23-025-Q1-E1-D3
Method	BLASTX
NCBI GI	g3831452
BLAST score	680
E value	7.0e-72
Match length	123
% identity	100
NCBI Description	(AC005700) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	138699
Seq. ID	LIB23-025-Q1-E1-D6
Method	BLASTX
NCBI GI	g3785991
BLAST score	407
E value	3.0e-40
Match length	81
% identity	86
NCBI Description	(AC005560) putative MAP kinase [Arabidopsis thaliana]

Seq. No.	138700
Seq. ID	LIB23-025-Q1-E1-D7
Method	BLASTX
NCBI GI	g4558549
BLAST score	445
E value	1.0e-44
Match length	87
% identity	100
NCBI Description	(AC007138) putative SecA-type chloroplast protein transport factor [Arabidopsis thaliana]

Seq. No.	138701
Seq. ID	LIB23-025-Q1-E1-E4
Method	BLASTN
NCBI GI	g2623294
BLAST score	91
E value	9.0e-44
Match length	248
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T20B5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138702
Seq. ID	LIB23-025-Q1-E1-F4
Method	BLASTN
NCBI GI	g3319339
BLAST score	57
E value	3.0e-23
Match length	69
% identity	96
NCBI Description	Arabidopsis thaliana BAC F9D12

Seq. No.	138703
Seq. ID	LIB23-025-Q1-E1-F5
Method	BLASTX
NCBI GI	g2315362
BLAST score	153
E value	8.0e-38
Match length	120
% identity	33
NCBI Description	(AF016441) contains similarity to multiple TPR domains [Caenorhabditis elegans]

Seq. No.	138704
Seq. ID	LIB23-025-Q1-E1-H8
Method	BLASTN
NCBI GI	g2104523
BLAST score	221
E value	1.0e-121
Match length	281
% identity	95
NCBI Description	Arabidopsis thaliana BAC T10M13 from chromosome IV, from 10.8 cM to 11.6 cM, complete sequence

Seq. No.	138705
Seq. ID	LIB23-026-Q1-E1-A11
Method	BLASTN
NCBI GI	g2564048
BLAST score	126
E value	1.0e-64
Match length	294
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKD15, complete sequence [Arabidopsis thaliana]

Seq. No.	138706
Seq. ID	LIB23-026-Q1-E1-A12
Method	BLASTN
NCBI GI	g16228
BLAST score	66
E value	7.0e-29
Match length	98
% identity	92
NCBI Description	A.thaliana cor47 mRNA

Seq. No.	138707
Seq. ID	LIB23-026-Q1-E1-A2
Method	BLASTX
NCBI GI	g2914706

BLAST score 486
E value 4.0e-49
Match length 125
% identity 73
NCBI Description (AC003974) putative homeobox protein [Arabidopsis thaliana]

Seq. No. 138708
Seq. ID LIB23-026-Q1-E1-B8
Method BLASTX
NCBI GI g4455199
BLAST score 534
E value 9.0e-55
Match length 118
% identity 89
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 138709
Seq. ID LIB23-026-Q1-E1-C10
Method BLASTX
NCBI GI g2739386
BLAST score 253
E value 4.0e-22
Match length 87
% identity 61
NCBI Description (AC002505) unknown protein [Arabidopsis thaliana]

Seq. No. 138710
Seq. ID LIB23-026-Q1-E1-D1
Method BLASTX
NCBI GI g4539460
BLAST score 222
E value 3.0e-18
Match length 116
% identity 5
NCBI Description (AL049500) putative protein [Arabidopsis thaliana]

Seq. No. 138711
Seq. ID LIB23-026-Q1-E1-D8
Method BLASTX
NCBI GI g419760
BLAST score 476
E value 3.0e-48
Match length 94
% identity 50
NCBI Description P-glycoprotein atpgp1 - Arabidopsis thaliana
>gi_3849833_emb_CAA43646_ (X61370) P-glycoprotein
[Arabidopsis thaliana]

Seq. No. 138712
Seq. ID LIB23-026-Q1-E1-E9
Method BLASTX
NCBI GI g730456
BLAST score 332
E value 3.0e-31
Match length 79
% identity 75
NCBI Description 40S RIBOSOMAL PROTEIN S19

Seq. No.	138713
Seq. ID	LIB23-026-Q1-E1-F6
Method	BLASTN
NCBI GI	g2618602
BLAST score	331
E value	0.0e+00
Match length	335
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	138714
Seq. ID	LIB23-026-Q1-E1-G1
Method	BLASTX
NCBI GI	g3287693
BLAST score	550
E value	1.0e-56
Match length	117
% identity	86
NCBI Description	(AC003979) Similar to LIM17 gene product gb_1653769 from the genome of Synechocystis sp. gb_D90916. [Arabidopsis thaliana]

Seq. No.	138715
Seq. ID	LIB23-026-Q1-E1-H2
Method	BLASTX
NCBI GI	g2317911
BLAST score	442
E value	5.0e-44
Match length	105
% identity	85
NCBI Description	(U89959) similar to GTP-binding protein [Arabidopsis thaliana]

Seq. No.	138716
Seq. ID	LIB23-026-Q1-E1-H3
Method	BLASTN
NCBI GI	g4678291
BLAST score	233
E value	1.0e-128
Match length	346
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F28P10 (ESSA project)

Seq. No.	138717
Seq. ID	LIB23-026-Q1-E1-H9
Method	BLASTN
NCBI GI	g4733952
BLAST score	223
E value	1.0e-122
Match length	251
% identity	97
NCBI Description	Arabidopsis thaliana chromosome I BAC F23H11 genomic sequence, complete sequence

Seq. No.	138718
Seq. ID	LIB23-027-Q1-E1-A12
Method	BLASTN
NCBI GI	g4757401
BLAST score	86
E value	1.0e-40
Match length	183
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGH6, complete sequence

Seq. No.	138719
Seq. ID	LIB23-027-Q1-E1-A3
Method	BLASTN
NCBI GI	g2062705
BLAST score	20
E value	1.8e-01
Match length	48
% identity	31
NCBI Description	Human butyrophilin (BTF5) mRNA, complete cds

Seq. No.	138720
Seq. ID	LIB23-027-Q1-E1-A8
Method	BLASTN
NCBI GI	g3402745
BLAST score	260
E value	1.0e-144
Match length	374
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F18E5 (ESSAII project)

Seq. No.	138721
Seq. ID	LIB23-027-Q1-E1-A9
Method	BLASTX
NCBI GI	g3021270
BLAST score	471
E value	2.0e-47
Match length	104
% identity	87
NCBI Description	(AL022347) serine/threonine kinase -like protein [Arabidopsis thaliana]

Seq. No.	138722
Seq. ID	LIB23-027-Q1-E1-B8
Method	BLASTX
NCBI GI	g1170203
BLAST score	647
E value	6.0e-68
Match length	128
% identity	99
NCBI Description	GLUTAMYL-TRNA REDUCTASE 1 PRECURSOR (GLUTR) >gi_454359 (U03774) glutamyl-tRNA reductase [Arabidopsis thaliana]

Seq. No.	138723
Seq. ID	LIB23-027-Q1-E1-C10
Method	BLASTX

NCBI GI	g2435514
BLAST score	550
E value	1.0e-56
Match length	123
% identity	84
NCBI Description	(AF024504) Similar to serine/threonine protein kinase; coded for by A. thaliana cDNA T20930; coded for by A. thaliana cDNA T43472 [Arabidopsis thaliana]

Seq. No.	138724
Seq. ID	LIB23-027-Q1-E1-C2
Method	BLASTX
NCBI GI	g4220527
BLAST score	481
E value	1.0e-48
Match length	122
% identity	66
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	138725
Seq. ID	LIB23-027-Q1-E1-C3
Method	BLASTN
NCBI GI	g2564046
BLAST score	148
E value	1.0e-77
Match length	281
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MGI19, complete sequence [Arabidopsis thaliana]

Seq. No.	138726
Seq. ID	LIB23-027-Q1-E1-C9
Method	BLASTX
NCBI GI	g2895510
BLAST score	451
E value	5.0e-45
Match length	121
% identity	77
NCBI Description	(AF033204) putative pectin methylesterase [Arabidopsis thaliana]

Seq. No.	138727
Seq. ID	LIB23-027-Q1-E1-D8
Method	BLASTX
NCBI GI	g541816
BLAST score	525
E value	1.0e-53
Match length	125
% identity	74
NCBI Description	protein kinase - common ice plant >gi_457689_emb_CAA82990_ (Z30329) protein kinase [Mesembryanthemum crystallinum]

Seq. No.	138728
Seq. ID	LIB23-027-Q1-E1-E11
Method	BLASTX
NCBI GI	g4309697
BLAST score	482

E value	1.0e-48
Match length	95
% identity	94
NCBI Description	(AC006266) putative DNA-directed RNA polymerase subunit [Arabidopsis thaliana]

Seq. No.	138729
Seq. ID	LIB23-027-Q1-E1-E6
Method	BLASTX
NCBI GI	g1931647
BLAST score	473
E value	1.0e-47
Match length	88
% identity	98
NCBI Description	(U95973) endomembrane protein EMP70 precusor isolog [Arabidopsis thaliana]

Seq. No.	138730
Seq. ID	LIB23-027-Q1-E1-F10
Method	BLASTX
NCBI GI	g4455160
BLAST score	316
E value	4.0e-29
Match length	92
% identity	77
NCBI Description	(AL031187) kinesin-related protein katA (fragment) [Arabidopsis thaliana]

Seq. No.	138731
Seq. ID	LIB23-027-Q1-E1-F3
Method	BLASTX
NCBI GI	g2894607
BLAST score	194
E value	7.0e-15
Match length	60
% identity	60
NCBI Description	(AL021889) NAM (no apical meristem) - like protein [Arabidopsis thaliana]

Seq. No.	138732
Seq. ID	LIB23-027-Q1-E1-G6
Method	BLASTX
NCBI GI	g1170089
BLAST score	651
E value	2.0e-68
Match length	128
% identity	100
NCBI Description	GLUTATHIONE S-TRANSFERASE ERD13 (CLASS PHI) >gi_481822_pir__S39542 probable glutathione transferase (EC 2.5.1.18) (clone ERD13) - Arabidopsis thaliana >gi_497789_dbj_BAA04554_ (D17673) glutathione S-transferase [Arabidopsis thaliana] >gi_3201614 (AC004669) glutathione S-transferase [Arabidopsis thaliana]

Seq. No.	138733
Seq. ID	LIB23-027-Q1-E1-H9
Method	BLASTN

NCBI GI	g3046854
BLAST score	202
E value	1.0e-110
Match length	369
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRG7, complete sequence [Arabidopsis thaliana]

Seq. No.	138734
Seq. ID	LIB23-028-Q1-E1-A3
Method	BLASTN
NCBI GI	g2264310
BLAST score	267
E value	1.0e-148
Match length	312
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKP11, complete sequence [Arabidopsis thaliana]

Seq. No.	138735
Seq. ID	LIB23-028-Q1-E1-A8
Method	BLASTN
NCBI GI	g3241923
BLAST score	269
E value	1.0e-150
Match length	373
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMN10, complete sequence [Arabidopsis thaliana]

Seq. No.	138736
Seq. ID	LIB23-028-Q1-E1-C9
Method	BLASTN
NCBI GI	g4753645
BLAST score	50
E value	1.0e-19
Match length	135
% identity	90
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17N18 (ESSA project)

Seq. No.	138737
Seq. ID	LIB23-028-Q1-E1-E6
Method	BLASTX
NCBI GI	g3036819
BLAST score	575
E value	1.0e-59
Match length	111
% identity	100
NCBI Description	(AJ000058) MCM3 homolog [Arabidopsis thaliana]

Seq. No.	138738
Seq. ID	LIB23-028-Q1-E1-E8
Method	BLASTX
NCBI GI	g1169422
BLAST score	210
E value	9.0e-17

Match length	52
% identity	79
NCBI Description	DIHYDROFOLATE REDUCTASE 1 / THYMIDYLATE SYNTHASE 1 (DHFR-TS) >gi_289193 (L08593) dihydrofolate reductase-thymidylate synthase [Arabidopsis thaliana]

Seq. No.	138739
Seq. ID	LIB23-028-Q1-E1-F12
Method	BLASTN
NCBI GI	g2098816
BLAST score	350
E value	0.0e+00
Match length	350
% identity	100
NCBI Description	Arabidopsis thaliana BAC F19G10, complete sequence

Seq. No.	138740
Seq. ID	LIB23-028-Q1-E1-F3
Method	BLASTX
NCBI GI	g4455209
BLAST score	421
E value	1.0e-41
Match length	84
% identity	98
NCBI Description	(AL035440) putative Proline synthetase associated protein [Arabidopsis thaliana]

Seq. No.	138741
Seq. ID	LIB23-028-Q1-E1-G10
Method	BLASTX
NCBI GI	g1531762
BLAST score	195
E value	5.0e-15
Match length	51
% identity	75
NCBI Description	(Y07765) S-adenosylmethionine decarboxylase [Arabidopsis thaliana]

Seq. No.	138742
Seq. ID	LIB23-029-Q1-E1-A8
Method	BLASTX
NCBI GI	g2454184
BLAST score	484
E value	1.0e-64
Match length	129
% identity	92
NCBI Description	(U80186) pyruvate dehydrogenase E1 beta subunit [Arabidopsis thaliana]

Seq. No.	138743
Seq. ID	LIB23-029-Q1-E1-B11
Method	BLASTX
NCBI GI	g4455273
BLAST score	334
E value	1.0e-31
Match length	81
% identity	80

NCBI Description	(AL035527) subtilisin proteinase-like [Arabidopsis thaliana]
Seq. No.	138744
Seq. ID	LIB23-029-Q1-E1-B9
Method	BLASTX
NCBI GI	g2494175
BLAST score	596
E value	5.0e-62
Match length	114
% identity	100
NCBI Description	GLUTAMATE DECARBOXYLASE 2 (GAD 2) >gi_1184960 (U46665) glutamate decarboxylase 2 [Arabidopsis thaliana] >gi_1236619 (U49937) glutamate decarboxylase [Arabidopsis thaliana]
Seq. No.	138745
Seq. ID	LIB23-029-Q1-E1-C5
Method	BLASTN
NCBI GI	g2281081
BLAST score	65
E value	3.0e-28
Match length	187
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC F18O19 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	138746
Seq. ID	LIB23-029-Q1-E1-D2
Method	BLASTN
NCBI GI	g3176695
BLAST score	285
E value	1.0e-159
Match length	285
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC F14J9 genomic sequence contains phyA marker, complete sequence [Arabidopsis thaliana]
Seq. No.	138747
Seq. ID	LIB23-029-Q1-E1-D8
Method	BLASTN
NCBI GI	g2738757
BLAST score	199
E value	1.0e-108
Match length	199
% identity	100
NCBI Description	Arabidopsis thaliana 5'-adenylylsulfate reductase (APR2) gene, complete cds
Seq. No.	138748
Seq. ID	LIB23-029-Q1-E1-E1
Method	BLASTN
NCBI GI	g3869065
BLAST score	87
E value	2.0e-41
Match length	253

% identity	72
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24M7, complete sequence [Arabidopsis thaliana]

Seq. No.	138749
Seq. ID	LIB23-029-Q1-E1-E2
Method	BLASTN
NCBI GI	g2828278
BLAST score	51
E value	2.0e-20
Match length	51
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16 (ESSAII project)

Seq. No.	138750
Seq. ID	LIB23-029-Q1-E1-F3
Method	BLASTX
NCBI GI	g2702276
BLAST score	514
E value	1.0e-52
Match length	97
% identity	99
NCBI Description	(AC003033) putative beta-glucosidase [Arabidopsis thaliana]

Seq. No.	138751
Seq. ID	LIB23-029-Q1-E1-G1
Method	BLASTX
NCBI GI	g1076366
BLAST score	587
E value	5.0e-61
Match length	113
% identity	97
NCBI Description	peptidylprolyl isomerase (EC 5.2.1.8) - Arabidopsis thaliana >gi_460968 (U07276) peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana] >gi_992643 (U32186) cyclophilin [Arabidopsis thaliana] >gi_1091580_prf__2021266A peptidyl-Pro cis-trans isomerase [Arabidopsis thaliana]

Seq. No.	138752
Seq. ID	LIB23-030-Q1-E1-A11
Method	BLASTN
NCBI GI	g4218109
BLAST score	124
E value	2.0e-63
Match length	274
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F16A16 (ESSAII project)

Seq. No.	138753
Seq. ID	LIB23-030-Q1-E1-A3
Method	BLASTN
NCBI GI	g2924651
BLAST score	129
E value	1.0e-66

Match length	129
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana]

Seq. No.	138754
Seq. ID	LIB23-030-Q1-E1-A5
Method	BLASTN
NCBI GI	g3821780
BLAST score	34
E value	1.0e-09
Match length	34
% identity	59
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	138755
Seq. ID	LIB23-030-Q1-E1-B7
Method	BLASTN
NCBI GI	g2702261
BLAST score	356
E value	0.0e+00
Match length	356
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T21L14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138756
Seq. ID	LIB23-030-Q1-E1-D5
Method	BLASTX
NCBI GI	g4415933
BLAST score	610
E value	1.0e-63
Match length	117
% identity	98
NCBI Description	(AC006418) putative cellular apoptosis susceptibility protein [Arabidopsis thaliana] >gi_4559390_gb_AAD23050.1_AC006526_15 (AC006526) putative cellular apoptosis susceptibility protein [Arabidopsis thaliana]

Seq. No.	138757
Seq. ID	LIB23-030-Q1-E1-F3
Method	BLASTN
NCBI GI	g4220468
BLAST score	141
E value	8.0e-74
Match length	157
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T8O11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138758
Seq. ID	LIB23-031-Q1-E1-B3
Method	BLASTN
NCBI GI	g2832639
BLAST score	219
E value	1.0e-120

Match length	275
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28J12 (ESSAII project)

Seq. No.	138759
Seq. ID	LIB23-031-Q1-E1-B4
Method	BLASTX
NCBI GI	g4455351
BLAST score	362
E value	1.0e-34
Match length	94
% identity	71
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	138760
Seq. ID	LIB23-031-Q1-E1-C6
Method	BLASTX
NCBI GI	g115783
BLAST score	512
E value	3.0e-52
Match length	96
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	138761
Seq. ID	LIB23-031-Q1-E1-C8
Method	BLASTN
NCBI GI	g4220628
BLAST score	323
E value	0.0e+00
Match length	344
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24C1, complete sequence [Arabidopsis thaliana]

Seq. No.	138762
Seq. ID	LIB23-031-Q1-E1-D10
Method	BLASTN
NCBI GI	g2979540
BLAST score	200
E value	1.0e-108
Match length	306
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F17K2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138763
Seq. ID	LIB23-031-Q1-E1-E10
Method	BLASTN
NCBI GI	g4510392
BLAST score	346
E value	0.0e+00
Match length	350

% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T17D12 genomic sequence, complete sequence

Seq. No.	138764
Seq. ID	LIB23-031-Q1-E1-F1
Method	BLASTX
NCBI GI	g2244750
BLAST score	484
E value	6.0e-49
Match length	106
% identity	90
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	138765
Seq. ID	LIB23-031-Q1-E1-F3
Method	BLASTN
NCBI GI	g3980374
BLAST score	41
E value	6.0e-14
Match length	41
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F16P2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138766
Seq. ID	LIB23-031-Q1-E1-F5
Method	BLASTX
NCBI GI	g115767
BLAST score	499
E value	9.0e-51
Match length	95
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	138767
Seq. ID	LIB23-031-Q1-E1-F7
Method	BLASTN
NCBI GI	g2828186
BLAST score	398
E value	0.0e+00
Match length	398
% identity	77
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18I23, complete sequence [Arabidopsis thaliana]

Seq. No.	138768
Seq. ID	LIB23-031-Q1-E1-G11
Method	BLASTX

NCBI GI	g4678939
BLAST score	172
E value	3.0e-12
Match length	61
% identity	56
NCBI Description	(AL049711) putative protein [Arabidopsis thaliana]

Seq. No.	138769
Seq. ID	LIB23-031-Q1-E1-G7
Method	BLASTX
NCBI GI	g4218535
BLAST score	335
E value	2.0e-31
Match length	88
% identity	65
NCBI Description	(AJ010829) GRAB1 protein [Triticum sp.]

Seq. No.	138770
Seq. ID	LIB23-032-Q1-E1-F1
Method	BLASTN
NCBI GI	g2564046
BLAST score	261
E value	1.0e-145
Match length	261
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MGI19, complete sequence [Arabidopsis thaliana]

Seq. No.	138771
Seq. ID	LIB23-032-Q1-E1-F11
Method	BLASTX
NCBI GI	g1699023
BLAST score	455
E value	2.0e-45
Match length	84
% identity	100
NCBI Description	(U78866) putative arginine-aspartate-rich RNA binding protein [Arabidopsis thaliana] >gi_1699051 (U78867) putative aspartate-arginine-rich mRNA binding protein [Arabidopsis thaliana]

Seq. No.	138772
Seq. ID	LIB23-032-Q1-E1-H12
Method	BLASTX
NCBI GI	g4689473
BLAST score	263
E value	6.0e-23
Match length	133
% identity	48
NCBI Description	(AC007213) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	138773
Seq. ID	LIB23-032-Q1-E1-H5
Method	BLASTX
NCBI GI	g4417296
BLAST score	151

E value	2.0e-36
Match length	92
% identity	59
NCBI Description	(AC007019) unknown protein [Arabidopsis thaliana] >gi_4587592_gb_AAD25820.1_AC007232_10 (AC007232) unknown protein [Arabidopsis thaliana]

Seq. No.	138774
Seq. ID	LIB23-033-Q1-E1-B5
Method	BLASTN
NCBI GI	g3763915
BLAST score	192
E value	1.0e-104
Match length	404
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F14B2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138775
Seq. ID	LIB23-033-Q1-E1-C4
Method	BLASTX
NCBI GI	g1171978
BLAST score	369
E value	2.0e-35
Match length	91
% identity	35
NCBI Description	POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2) (PABP 2) >gi_304109 (L19418) poly(A)-binding protein [Arabidopsis thaliana] >gi_2911051_emb_CAA17561_ (AL021961) poly(A)-binding protein [Arabidopsis thaliana]

Seq. No.	138776
Seq. ID	LIB23-033-Q1-E1-D8
Method	BLASTX
NCBI GI	g4176545
BLAST score	256
E value	4.0e-22
Match length	114
% identity	43
NCBI Description	(AL035259) strong similarity to human leukotriene a-4 hydrolase [Schizosaccharomyces pombe]

Seq. No.	138777
Seq. ID	LIB23-033-Q1-E1-E4
Method	BLASTX
NCBI GI	g115783
BLAST score	479
E value	2.0e-48
Match length	90
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	138778
Seq. ID	LIB23-033-Q1-E1-E6

Method	BLASTX
NCBI GI	g1903021
BLAST score	630
E value	6.0e-66
Match length	125
% identity	100
NCBI Description	(Y10216) hypothetical 3-isopropylmalate dehydrogenase [Arabidopsis thaliana]

Seq. No.	138779
Seq. ID	LIB23-033-Q1-E1-F6
Method	BLASTX
NCBI GI	g115783
BLAST score	479
E value	3.0e-48
Match length	90
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	138780
Seq. ID	LIB23-033-Q1-E1-G1
Method	BLASTX
NCBI GI	g2244852
BLAST score	121
E value	1.0e-43
Match length	91
% identity	99
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	138781
Seq. ID	LIB23-033-Q1-E1-G10
Method	BLASTN
NCBI GI	g3449329
BLAST score	292
E value	1.0e-163
Match length	448
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDH9, complete sequence [Arabidopsis thaliana]

Seq. No.	138782
Seq. ID	LIB23-034-Q1-E1-D2
Method	BLASTX
NCBI GI	g4049344
BLAST score	365
E value	5.0e-35
Match length	71
% identity	97
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	138783
Seq. ID	LIB23-034-Q1-E1-D6
Method	BLASTX
NCBI GI	g4049344

BLAST score	286
E value	6.0e-26
Match length	69
% identity	84
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	138784
Seq. ID	LIB23-034-Q1-E1-F10
Method	BLASTX
NCBI GI	g2262113
BLAST score	789
E value	2.0e-84
Match length	150
% identity	99
NCBI Description	(AC002343) unknown protein [Arabidopsis thaliana]

Seq. No.	138785
Seq. ID	LIB23-034-Q1-E1-F8
Method	BLASTX
NCBI GI	g3757518
BLAST score	750
E value	5.0e-80
Match length	142
% identity	100
NCBI Description	(AC005167) putative immediate-early salicylate-induced glucosyltransferase [Arabidopsis thaliana]

Seq. No.	138786
Seq. ID	LIB23-034-Q1-E1-G4
Method	BLASTX
NCBI GI	g2499616
BLAST score	491
E value	9.0e-50
Match length	117
% identity	77
NCBI Description	MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG NTF6 (P43) >gi_1076639_pir__S51320 mitogen-activated protein kinase 6 (EC 2.7.1.-) - common tobacco >gi_2129967_pir__S68189 serine/threonine protein kinase p43 - common tobacco >gi_634068_emb_CAA58760_ (X83879) p43Nft6 serine/threonine protein kinase [Nicotiana tabacum]

Seq. No.	138787
Seq. ID	LIB23-034-Q1-E1-H7
Method	BLASTX
NCBI GI	g2118045
BLAST score	352
E value	2.0e-33
Match length	59
% identity	97
NCBI Description	beta-fructofuranosidase (EC 3.2.1.26) - Arabidopsis thaliana (fragment) >gi_899153_emb_CAA61624_ (X89454) beta-fructofuranosidase [Arabidopsis thaliana]

Seq. No.	138788
Seq. ID	LIB23-034-Q1-E1-H8
Method	BLASTN

NCBI GI	g3335356
BLAST score	305
E value	1.0e-171
Match length	490
% identity	60
NCBI Description	Arabidopsis thaliana chromosome II BAC F16M14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138789
Seq. ID	LIB23-035-Q1-E1-D9
Method	BLASTX
NCBI GI	g1351014
BLAST score	193
E value	7.0e-15
Match length	78
% identity	54
NCBI Description	40S RIBOSOMAL PROTEIN S8 >gi_968902_dbj_BAA07207_ (D38010) ribosomal protein S8 [Oryza sativa]

Seq. No.	138790
Seq. ID	LIB23-035-Q1-E1-H9
Method	BLASTX
NCBI GI	g4455223
BLAST score	275
E value	8.0e-26
Match length	109
% identity	27
NCBI Description	(AL035440) putative DNA binding protein [Arabidopsis thaliana]

Seq. No.	138791
Seq. ID	LIB23-035-Q1-E112-A1
Method	BLASTN
NCBI GI	g4519194
BLAST score	90
E value	2.0e-43
Match length	185
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHM17, complete sequence

Seq. No.	138792
Seq. ID	LIB23-035-Q1-E112-A5
Method	BLASTX
NCBI GI	g2464913
BLAST score	648
E value	4.0e-68
Match length	126
% identity	100
NCBI Description	(Z99708) sugar transporter like protein [Arabidopsis thaliana]

Seq. No.	138793
Seq. ID	LIB23-035-Q1-E112-A7
Method	BLASTX
NCBI GI	g2688299
BLAST score	321

E value	9.0e-30
Match length	117
% identity	51
NCBI Description	(AE001145) prolyl-tRNA synthetase (proS) [Borrelia burgdorferi]

Seq. No.	138794
Seq. ID	LIB23-035-Q1-E112-B8
Method	BLASTX
NCBI GI	g1175467
BLAST score	153
E value	4.0e-10
Match length	86
% identity	38
NCBI Description	HYPOTHETICAL 69.5 KD PROTEIN C22G7.05 IN CHROMOSOME I >gi_2130326_pir__S62449 hypothetical protein SPAC22G7.05 - fission yeast (Schizosaccharomyces pombe) >gi_1009455_emb_CAA91129.1_ (Z54328) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	138795
Seq. ID	LIB23-035-Q1-E112-D4
Method	BLASTX
NCBI GI	g2506139
BLAST score	385
E value	3.0e-37
Match length	92
% identity	83
NCBI Description	COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP) (ARCHAIN) >gi_1314049_emb_CAA91901_ (Z67962) archain/delta-COP [Oryza sativa]

Seq. No.	138796
Seq. ID	LIB23-035-Q1-E112-D7
Method	BLASTN
NCBI GI	g2262135
BLAST score	166
E value	3.0e-88
Match length	426
% identity	99
NCBI Description	Arabidopsis thaliana BAC T10P11 from chromosome IV, near 15 cM, complete sequence

Seq. No.	138797
Seq. ID	LIB23-035-Q1-E112-E5
Method	BLASTX
NCBI GI	g4581146
BLAST score	425
E value	6.0e-42
Match length	88
% identity	93
NCBI Description	(AC006919) putative fructose-bisphosphate aldolase, cytoplasmic [Arabidopsis thaliana]

Seq. No.	138798
Seq. ID	LIB23-035-Q1-E112-G5
Method	BLASTX

NCBI GI	g166834
BLAST score	150
E value	1.0e-29
Match length	68
% identity	100
NCBI Description	(M86720) ribulose bisphosphate carboxylase/oxygenase activase [Arabidopsis thaliana] >gi_2642155 (AC003000) Rubisco activase [Arabidopsis thaliana]

Seq. No.	138799
Seq. ID	LIB23-036-Q1-E1-B12
Method	BLASTX
NCBI GI	g99696
BLAST score	295
E value	9.0e-27
Match length	81
% identity	75
NCBI Description	glutamate--ammonia ligase (EC 6.3.1.2) precursor, chloroplast (clone lambdaAtgsl1) - Arabidopsis thaliana >gi_240070_bbs_69728 (S69727) light-regulated glutamine synthetase isoenzyme [Arabidopsis thaliana, Peptide, 430 aa] [Arabidopsis thaliana] >gi_228453_prf__1804333A Gln synthetase [Arabidopsis thaliana]

Seq. No.	138800
Seq. ID	LIB23-036-Q1-E1-C1
Method	BLASTN
NCBI GI	g4490717
BLAST score	200
E value	1.0e-108
Match length	269
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	138801
Seq. ID	LIB23-036-Q1-E1-C6
Method	BLASTX
NCBI GI	g1173218
BLAST score	471
E value	2.0e-47
Match length	92
% identity	100
NCBI Description	40S RIBOSOMAL PROTEIN S15A >gi_440824 (L27461) ribosomal protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]

Seq. No.	138802
Seq. ID	LIB23-036-Q1-E1-D12
Method	BLASTX
NCBI GI	g3850569
BLAST score	273
E value	4.0e-24
Match length	112
% identity	44
NCBI Description	(AC005278) ESTs gb_T21276, gb_T45403, and gb_AA586113 come from this gene. [Arabidopsis thaliana]

Seq. No.	138803
Seq. ID	LIB23-036-Q1-E1-E6
Method	BLASTN
NCBI GI	g2252823
BLAST score	204
E value	1.0e-111
Match length	290
% identity	96
NCBI Description	Arabidopsis thaliana BAC IG005I10

Seq. No.	138804
Seq. ID	LIB23-036-Q1-E1-E9
Method	BLASTX
NCBI GI	g2827537
BLAST score	413
E value	1.0e-40
Match length	125
% identity	66
NCBI Description	(AL021633) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	138805
Seq. ID	LIB23-036-Q1-E1-F1
Method	BLASTX
NCBI GI	g4204849
BLAST score	316
E value	3.0e-29
Match length	80
% identity	75
NCBI Description	(U55875) protein kinase [Arabidopsis thaliana]

Seq. No.	138806
Seq. ID	LIB23-036-Q1-E1-F3
Method	BLASTX
NCBI GI	g3335337
BLAST score	545
E value	5.0e-56
Match length	110
% identity	99
NCBI Description	(AC004512) Similar to acyl carrier protein, mitochondrial precursor (ACP) NADH-ubiquinone oxidoreductase 9.6 KD subunit (MYACP-1), gb_L23574 from A. thaliana. ESTs gb_Z30712, gb_Z30713, gb_Z26204, gb_N37975 and gb_N96330 come from this gene

Seq. No.	138807
Seq. ID	LIB23-036-Q1-E1-F5
Method	BLASTX
NCBI GI	g461550
BLAST score	393
E value	3.0e-38
Match length	113
% identity	73
NCBI Description	ATP SYNTHASE GAMMA CHAIN 1, CHLOROPLAST PRECURSOR >gi_81635_pir__B39732 H+-transporting ATP synthase (EC 3.6.1.34) gamma-1 chain precursor, chloroplast -

Arabidopsis thaliana >gi_166632 (M61741) ATP synthase gamma-subunit [Arabidopsis thaliana]

Seq. No.	138808
Seq. ID	LIB23-036-Q1-E1-G1
Method	BLASTX
NCBI GI	g4467099
BLAST score	461
E value	3.0e-46
Match length	90
% identity	100
NCBI Description	(AL035538) glycine hydroxymethyltransferase like protein [Arabidopsis thaliana]

Seq. No.	138809
Seq. ID	LIB23-036-Q1-E1-H2
Method	BLASTX
NCBI GI	g3142303
BLAST score	428
E value	3.0e-42
Match length	126
% identity	33
NCBI Description	(AC002411) Strong similarity to MRP-like ABC transporter gb_U92650 from A. thaliana and canalicular multi-drug resistance protein gb_L49379 from Rattus norvegicus. [Arabidopsis thaliana]

Seq. No.	138810
Seq. ID	LIB23-036-Q1-E1-H8
Method	BLASTX
NCBI GI	g2344890
BLAST score	153
E value	4.0e-10
Match length	41
% identity	71
NCBI Description	(AC002388) TINY transcription factor isolog [Arabidopsis thaliana]

Seq. No.	138811
Seq. ID	LIB23-037-Q1-E1-A10
Method	BLASTX
NCBI GI	g4586021
BLAST score	509
E value	7.0e-52
Match length	112
% identity	90
NCBI Description	(AC007170) putative cytoplasmic aconitate hydratase [Arabidopsis thaliana]

Seq. No.	138812
Seq. ID	LIB23-037-Q1-E1-A12
Method	BLASTX
NCBI GI	g115783
BLAST score	512
E value	3.0e-52
Match length	96
% identity	100

NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]
Seq. No.	138813
Seq. ID	LIB23-037-Q1-E1-A6
Method	BLASTN
NCBI GI	g4159708
BLAST score	374
E value	0.0e+00
Match length	374
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MKP6, complete sequence
Seq. No.	138814
Seq. ID	LIB23-037-Q1-E1-A9
Method	BLASTN
NCBI GI	g2749918
BLAST score	190
E value	1.0e-103
Match length	238
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC F3I6 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	138815
Seq. ID	LIB23-037-Q1-E1-B5
Method	BLASTN
NCBI GI	g1022779
BLAST score	116
E value	7.0e-59
Match length	147
% identity	93
NCBI Description	Arabidopsis thaliana GF14 Kappa isoform mRNA, complete cds
Seq. No.	138816
Seq. ID	LIB23-037-Q1-E1-C12
Method	BLASTN
NCBI GI	g3128141
BLAST score	213
E value	1.0e-116
Match length	382
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQD22, complete sequence [Arabidopsis thaliana]
Seq. No.	138817
Seq. ID	LIB23-037-Q1-E1-D12
Method	BLASTN
NCBI GI	g3449313
BLAST score	259
E value	1.0e-144
Match length	388
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

09604504.050501

K21P3, complete sequence [Arabidopsis thaliana]

Seq. No.	138818
Seq. ID	LIB23-037-Q1-E1-D2
Method	BLASTX
NCBI GI	g4559333
BLAST score	396
E value	1.0e-38
Match length	115
% identity	43
NCBI Description	(AC007087) unknown protein [Arabidopsis thaliana]

Seq. No.	138819
Seq. ID	LIB23-037-Q1-E1-D5
Method	BLASTN
NCBI GI	g2244829
BLAST score	128
E value	4.0e-66
Match length	132
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	138820
Seq. ID	LIB23-037-Q1-E1-E7
Method	BLASTN
NCBI GI	g3600062
BLAST score	346
E value	0.0e+00
Match length	358
% identity	99
NCBI Description	Arabidopsis thaliana BAC T25C13

Seq. No.	138821
Seq. ID	LIB23-037-Q1-E1-F2
Method	BLASTN
NCBI GI	g4191760
BLAST score	171
E value	3.0e-91
Match length	377
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17F8, complete sequence [Arabidopsis thaliana]

Seq. No.	138822
Seq. ID	LIB23-037-Q1-E1-F3
Method	BLASTX
NCBI GI	g4467134
BLAST score	247
E value	1.0e-21
Match length	47
% identity	100
NCBI Description	(AL035540) protein kinase like protein [Arabidopsis thaliana]

Seq. No.	138823
Seq. ID	LIB23-037-Q1-E1-G10

Method	BLASTN
NCBI GI	g3869075
BLAST score	241
E value	1.0e-133
Match length	356
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence [Arabidopsis thaliana]

Seq. No.	138824
Seq. ID	LIB23-037-Q1-E1-G9
Method	BLASTX
NCBI GI	g99742
BLAST score	563
E value	4.0e-58
Match length	126
% identity	88
NCBI Description	2-dehydro-3-deoxyphosphoheptonate aldolase (EC 4.1.2.15) 1 - Arabidopsis thaliana

Seq. No.	138825
Seq. ID	LIB23-037-Q1-E1-H11
Method	BLASTX
NCBI GI	g3482929
BLAST score	369
E value	2.0e-35
Match length	87
% identity	74
NCBI Description	(AC003970) Putative transcription factor [Arabidopsis thaliana]

Seq. No.	138826
Seq. ID	LIB23-037-Q1-E1-H8
Method	BLASTX
NCBI GI	g541816
BLAST score	293
E value	5.0e-27
Match length	57
% identity	95
NCBI Description	protein kinase - common ice plant >gi_457689_emb_CAA82990_ (Z30329) protein kinase [Mesembryanthemum crystallinum]

Seq. No.	138827
Seq. ID	LIB23-038-Q1-E1-C3
Method	BLASTX
NCBI GI	g4038352
BLAST score	335
E value	2.0e-31
Match length	132
% identity	45
NCBI Description	(AF098951) breast cancer resistance protein [Homo sapiens]

Seq. No.	138828
Seq. ID	LIB23-038-Q1-E1-D1
Method	BLASTN
NCBI GI	g3821780
BLAST score	32

E value	1.0e-08
Match length	36
% identity	97
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	138829
Seq. ID	LIB23-038-Q1-E1-D10
Method	BLASTN
NCBI GI	g2351065
BLAST score	318
E value	1.0e-179
Match length	434
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHF15, complete sequence [Arabidopsis thaliana]

Seq. No.	138830
Seq. ID	LIB23-038-Q1-E1-E12
Method	BLASTX
NCBI GI	g120667
BLAST score	493
E value	5.0e-50
Match length	95
% identity	97
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis thaliana >gi_166706 (M64116) cystolic glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No.	138831
Seq. ID	LIB23-038-Q1-E1-E4
Method	BLASTN
NCBI GI	g2564044
BLAST score	388
E value	0.0e+00
Match length	404
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19P17, complete sequence [Arabidopsis thaliana]

Seq. No.	138832
Seq. ID	LIB23-038-Q1-E1-F10
Method	BLASTN
NCBI GI	g4760411
BLAST score	189
E value	1.0e-102
Match length	390
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F25C20 sequence, complete sequence

Seq. No.	138833
Seq. ID	LIB23-038-Q1-E1-G10
Method	BLASTN

NCBI GI	g3299824
BLAST score	189
E value	1.0e-102
Match length	379
% identity	99
NCBI Description	Arabidopsis thaliana BAC F4C21 from chromosome IV, top arm, near 17 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	138834
Seq. ID	LIB23-038-Q1-E1-G3
Method	BLASTX
NCBI GI	g2462746
BLAST score	571
E value	5.0e-59
Match length	116
% identity	96
NCBI Description	(AC002292) Similar to ATP-citrate-lyase [Arabidopsis thaliana]

Seq. No.	138835
Seq. ID	LIB23-038-Q1-E1-G5
Method	BLASTN
NCBI GI	g4220644
BLAST score	374
E value	0.0e+00
Match length	374
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXL8, complete sequence [Arabidopsis thaliana]

Seq. No.	138836
Seq. ID	LIB23-038-Q1-E1-H7
Method	BLASTX
NCBI GI	g2244878
BLAST score	275
E value	3.0e-24
Match length	70
% identity	59
NCBI Description	(Z97338) hypothetical protein [Arabidopsis thaliana]

Seq. No.	138837
Seq. ID	LIB23-039-Q1-E1-C3
Method	BLASTX
NCBI GI	g3046815
BLAST score	258
E value	1.0e-22
Match length	56
% identity	84
NCBI Description	(AL021687) cytochrome P450 [Arabidopsis thaliana]

Seq. No.	138838
Seq. ID	LIB23-039-Q1-E1-E1
Method	BLASTN
NCBI GI	g2392894
BLAST score	289
E value	1.0e-162
Match length	357

% identity	98
NCBI Description	Arabidopsis thaliana brassinosteroid insensitive 1 (BRI1) gene, complete cds

Seq. No.	138839
Seq. ID	LIB23-040-Q1-E1-C3
Method	BLASTN
NCBI GI	g2924731
BLAST score	157
E value	3.0e-83
Match length	224
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSI17, complete sequence [Arabidopsis thaliana]

Seq. No.	138840
Seq. ID	LIB23-040-Q1-E1-E2
Method	BLASTN
NCBI GI	g3859590
BLAST score	92
E value	3.0e-44
Match length	297
% identity	93
NCBI Description	Arabidopsis thaliana BAC T15B16

Seq. No.	138841
Seq. ID	LIB23-040-Q1-E1-E9
Method	BLASTX
NCBI GI	g2388585
BLAST score	321
E value	1.0e-29
Match length	83
% identity	80
NCBI Description	(AC000098) Similar to Caenorhabditis unknown protein T03F1.1 (gb_U88169). [Arabidopsis thaliana]

Seq. No.	138842
Seq. ID	LIB23-040-Q1-E1-G12
Method	BLASTX
NCBI GI	g1168470
BLAST score	503
E value	4.0e-51
Match length	127
% identity	74
NCBI Description	PROTEIN KINASE APK1A >gi_282877_pir__S28615 protein kinase, tyrosine/serine/threonine-specific (EC 2.7.1.-) - Arabidopsis thaliana >gi_217829_dbj_BAA02092_ (D12522) protein tyrosine-serine-threonine kinase [Arabidopsis thaliana]

Seq. No.	138843
Seq. ID	LIB23-040-Q1-E1-H3
Method	BLASTN
NCBI GI	g2564049
BLAST score	274
E value	1.0e-153
Match length	300

% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLE2, complete sequence [Arabidopsis thaliana]

Seq. No.	138844
Seq. ID	LIB23-041-Q1-E1-B11
Method	BLASTN
NCBI GI	g2673901
BLAST score	391
E value	0.0e+00
Match length	391
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T24P15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138845
Seq. ID	LIB23-041-Q1-E1-B9
Method	BLASTX
NCBI GI	g320552
BLAST score	583
E value	2.0e-60
Match length	129
% identity	89
NCBI Description	anthranilate synthase (EC 4.1.3.27) alpha-1 chain - Arabidopsis thaliana

Seq. No.	138846
Seq. ID	LIB23-041-Q1-E1-D12
Method	BLASTX
NCBI GI	g2497702
BLAST score	205
E value	4.0e-16
Match length	117
% identity	44
NCBI Description	OUTER MEMBRANE LIPOPROTEIN BLC PRECURSOR >gi_2121019_pir__I40710 outer membrane lipoprotein - Citrobacter freundii >gi_717136 (U21727) lipocalin precursor [Citrobacter freundii]

Seq. No.	138847
Seq. ID	LIB23-041-Q1-E1-E1
Method	BLASTX
NCBI GI	g2367392
BLAST score	252
E value	8.0e-22
Match length	92
% identity	58
NCBI Description	(U82513) random slug cDNA25 protein [Dictyostelium discoideum]

Seq. No.	138848
Seq. ID	LIB23-041-Q1-E1-F10
Method	BLASTN
NCBI GI	g4585952
BLAST score	406
E value	0.0e+00
Match length	406

% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F26F24, complete sequence

Seq. No.	138849
Seq. ID	LIB23-041-Q1-E1-F9
Method	BLASTX
NCBI GI	g4115931
BLAST score	554
E value	5.0e-57
Match length	137
% identity	79
NCBI Description	(AF118223) contains similarity to Guillardia theta ABC transporter (GB:AF041468) [Arabidopsis thaliana]

Seq. No.	138850
Seq. ID	LIB23-041-Q1-E1-G9
Method	BLASTX
NCBI GI	g3688175
BLAST score	560
E value	9.0e-58
Match length	126
% identity	84
NCBI Description	(AL031804) gamma-VPE (vacuolar processing enzyme) [Arabidopsis thaliana]

Seq. No.	138851
Seq. ID	LIB23-041-Q1-E1-H6
Method	BLASTX
NCBI GI	g2829896
BLAST score	238
E value	4.0e-20
Match length	103
% identity	50
NCBI Description	(AC002311) highly similar to auxin-regulated protein GH3, gp_X60033_18591 [Arabidopsis thaliana]

Seq. No.	138852
Seq. ID	LIB23-041-Q1-E1-H7
Method	BLASTN
NCBI GI	g413731
BLAST score	296
E value	1.0e-166
Match length	321
% identity	98
NCBI Description	Arabidopsis thaliana phytoene synthase mRNA, complete cds

Seq. No.	138853
Seq. ID	LIB23-042-Q1-E1-C9
Method	BLASTN
NCBI GI	g2564048
BLAST score	380
E value	0.0e+00
Match length	420
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKD15, complete sequence [Arabidopsis thaliana]

Seq. No.	138854
Seq. ID	LIB23-042-Q1-E1-D1
Method	BLASTX
NCBI GI	g2914703
BLAST score	243
E value	1.0e-20
Match length	52
% identity	87
NCBI Description	(AC003974) unknown protein [Arabidopsis thaliana]

Seq. No.	138855
Seq. ID	LIB23-042-Q1-E1-D12
Method	BLASTN
NCBI GI	g4519188
BLAST score	257
E value	1.0e-142
Match length	446
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L19, complete sequence

Seq. No.	138856
Seq. ID	LIB23-042-Q1-E1-D2
Method	BLASTX
NCBI GI	g2809252
BLAST score	495
E value	2.0e-50
Match length	98
% identity	99
NCBI Description	(AC002560) F21B7.21 [Arabidopsis thaliana]

Seq. No.	138857
Seq. ID	LIB23-042-Q1-E1-D6
Method	BLASTX
NCBI GI	g3687445
BLAST score	222
E value	3.0e-18
Match length	105
% identity	37
NCBI Description	(AL022398) dJ434O14.5 (novel PUTATIVE protein similar to YIL091C yeast hypoyhetical 84 kD protein from SGA1-KTR7 intergenic region) [Homo sapiens]

Seq. No.	138858
Seq. ID	LIB23-042-Q1-E1-E1
Method	BLASTN
NCBI GI	g3128136
BLAST score	173
E value	1.0e-92
Match length	320
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1F13, complete sequence [Arabidopsis thaliana]

Seq. No.	138859
Seq. ID	LIB23-042-Q1-E1-H4

Method	BLASTX
NCBI GI	g1370152
BLAST score	264
E value	4.0e-23
Match length	62
% identity	79
NCBI Description	(Z73954) RAB11F [Lotus japonicus]

Seq. No.	138860
Seq. ID	LIB23-043-Q1-E1-A5
Method	BLASTX
NCBI GI	g2492784
BLAST score	166
E value	1.0e-11
Match length	54
% identity	57
NCBI Description	2-ISOPROPYLMALATE SYNTHASE (ALPHA-ISOPROPYLMALATE SYNTHASE) (ALPHA-IPM SYNTHETASE) >gi_1770069_emb_CAA99531_ (Z75208) 2-isopropylmalate synthase [Bacillus subtilis] >gi_2635293_emb_CAB14788_ (Z99118) 2-isopropylmalate synthase [Bacillus subtilis]

Seq. No.	138861
Seq. ID	LIB23-043-Q1-E1-B5
Method	BLASTN
NCBI GI	g4220643
BLAST score	219
E value	1.0e-120
Match length	412
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD22, complete sequence [Arabidopsis thaliana]

Seq. No.	138862
Seq. ID	LIB23-043-Q1-E1-C11
Method	BLASTX
NCBI GI	g2281090
BLAST score	574
E value	2.0e-59
Match length	132
% identity	89
NCBI Description	(AC002333) hypothetical protein [Arabidopsis thaliana]

Seq. No.	138863
Seq. ID	LIB23-043-Q1-E1-D7
Method	BLASTN
NCBI GI	g4159704
BLAST score	216
E value	1.0e-118
Match length	356
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MCB17, complete sequence

Seq. No.	138864
Seq. ID	LIB23-043-Q1-E1-E6
Method	BLASTX

NCBI GI	g2194127
BLAST score	662
E value	1.0e-69
Match length	126
% identity	100
NCBI Description	(AC002062) Strong similarity to Arabidopsis receptor-like protein kinase (gb_ATLECGENE) and F20P5.16. [Arabidopsis thaliana]

Seq. No.	138865
Seq. ID	LIB23-043-Q1-E1-F12
Method	BLASTX
NCBI GI	g4262186
BLAST score	419
E value	1.0e-41
Match length	84
% identity	98
NCBI Description	(AC005508) Highly similar to cullin 3 [Arabidopsis thaliana]

Seq. No.	138866
Seq. ID	LIB23-043-Q1-E1-F6
Method	BLASTN
NCBI GI	g2511585
BLAST score	246
E value	1.0e-136
Match length	246
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for proteasome subunit prc2b

Seq. No.	138867
Seq. ID	LIB23-043-Q1-E1-F8
Method	BLASTN
NCBI GI	g2264315
BLAST score	161
E value	2.0e-85
Match length	373
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRN17, complete sequence [Arabidopsis thaliana]

Seq. No.	138868
Seq. ID	LIB23-043-Q1-E1-G3
Method	BLASTN
NCBI GI	g3451055
BLAST score	149
E value	3.0e-78
Match length	343
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F16G20 (ESSAII project)

Seq. No.	138869
Seq. ID	LIB23-043-Q1-E1-G4
Method	BLASTX
NCBI GI	g3582333
BLAST score	279

E value	6.0e-25
Match length	118
% identity	44
NCBI Description	(AC005496) hypothetical protein [Arabidopsis thaliana]

Seq. No.	138870
Seq. ID	LIB23-043-Q1-E1-H11
Method	BLASTX
NCBI GI	g1076348
BLAST score	397
E value	1.0e-38
Match length	92
% identity	82
NCBI Description	myosin MYA1, class V - Arabidopsis thaliana >gi_433663_emb_CAA82234_ (Z28389) myosin [Arabidopsis thaliana]

Seq. No.	138871
Seq. ID	LIB23-044-Q1-E2-B12
Method	BLASTN
NCBI GI	g3985934
BLAST score	406
E value	0.0e+00
Match length	406
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJE7, complete sequence [Arabidopsis thaliana]

Seq. No.	138872
Seq. ID	LIB23-044-Q1-E2-C12
Method	BLASTX
NCBI GI	g2618699
BLAST score	208
E value	2.0e-16
Match length	118
% identity	38
NCBI Description	(AC002510) unknown protein [Arabidopsis thaliana]

Seq. No.	138873
Seq. ID	LIB23-044-Q1-E2-E2
Method	BLASTX
NCBI GI	g3080412
BLAST score	337
E value	8.0e-32
Match length	99
% identity	63
NCBI Description	(AL022604) putative protein [Arabidopsis thaliana]

Seq. No.	138874
Seq. ID	LIB23-044-Q1-E2-F8
Method	BLASTN
NCBI GI	g1419389
BLAST score	80
E value	1.0e-37
Match length	120
% identity	93
NCBI Description	A.thaliana mRNA for thylakoid-bound ascorbate peroxidase

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Seq. No.	138875
Seq. ID	LIB23-044-Q1-E2-G1
Method	BLASTN
NCBI GI	g4220468
BLAST score	79
E value	9.0e-37
Match length	139
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC T8O11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138876
Seq. ID	LIB23-044-Q1-E2-G8
Method	BLASTX
NCBI GI	g3096918
BLAST score	549
E value	2.0e-56
Match length	132
% identity	86
NCBI Description	(AL023094) putative cyclase associated protein CAP [Arabidopsis thaliana] >gi_3169136_dbj_BAA28621_ (AB014759) Atcap1 [Arabidopsis thaliana]

Seq. No.	138877
Seq. ID	LIB23-044-Q1-E2-H12
Method	BLASTN
NCBI GI	g836939
BLAST score	149
E value	1.0e-78
Match length	149
% identity	100
NCBI Description	Arabidopsis thaliana calcium-dependent protein kinase (CDPK6) mRNA, complete cds

Seq. No.	138878
Seq. ID	LIB23-044-Q1-E2-H5
Method	BLASTX
NCBI GI	g2708741
BLAST score	354
E value	4.0e-34
Match length	75
% identity	93
NCBI Description	(AC003952) hypothetical protein [Arabidopsis thaliana]

Seq. No.	138879
Seq. ID	LIB23-044-Q1-E2-H6
Method	BLASTX
NCBI GI	g3152590
BLAST score	627
E value	1.0e-65
Match length	127
% identity	100
NCBI Description	(AC002986) Similar to protein serine/threonine kinase NPK15 gb_D31737 from Nicotiana tabacum. [Arabidopsis thaliana]

Seq. No. 138880

Seq. ID	LIB23-044-Q1-E2-H9
Method	BLASTN
NCBI GI	g4159712
BLAST score	247
E value	1.0e-136
Match length	375
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWI23, complete sequence

Seq. No.	138881
Seq. ID	LIB23-045-Q1-E1-A11
Method	BLASTN
NCBI GI	g3386593
BLAST score	190
E value	1.0e-103
Match length	213
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F4I18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138882
Seq. ID	LIB23-045-Q1-E1-A2
Method	BLASTX
NCBI GI	g4584832
BLAST score	218
E value	6.0e-18
Match length	78
% identity	51
NCBI Description	(AL031764) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	138883
Seq. ID	LIB23-045-Q1-E1-A3
Method	BLASTX
NCBI GI	g1702872
BLAST score	478
E value	2.0e-48
Match length	94
% identity	100
NCBI Description	(Y09667) ferredoxin-dependent glutamate synthase [Arabidopsis thaliana]

Seq. No.	138884
Seq. ID	LIB23-045-Q1-E1-A7
Method	BLASTN
NCBI GI	g4455339
BLAST score	230
E value	1.0e-126
Match length	284
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T12J5 (ESSAII project)

Seq. No.	138885
Seq. ID	LIB23-045-Q1-E1-A9
Method	BLASTX
NCBI GI	g115767

BLAST score	447
E value	8.0e-45
Match length	85
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	138886
Seq. ID	LIB23-045-Q1-E1-B10
Method	BLASTX
NCBI GI	g1172977
BLAST score	404
E value	9.0e-40
Match length	83
% identity	99
NCBI Description	60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]

Seq. No.	138887
Seq. ID	LIB23-045-Q1-E1-B12
Method	BLASTX
NCBI GI	g2507422
BLAST score	173
E value	7.0e-13
Match length	35
% identity	100
NCBI Description	CYSTATHIONINE GAMMA-SYNTHASE PRECURSOR (CGS) (O-SUCCINYLHOMOSERINE (THIOL)-LYASE) >gi_3293261 (AF039206) cystathionine gamma-synthase precursor [Arabidopsis thaliana]

Seq. No.	138888
Seq. ID	LIB23-045-Q1-E1-B2
Method	BLASTX
NCBI GI	g4406816
BLAST score	444
E value	2.0e-44
Match length	84
% identity	100
NCBI Description	(AC006201) 60S ribosomal protein L2 [Arabidopsis thaliana]

Seq. No.	138889
Seq. ID	LIB23-045-Q1-E1-B8
Method	BLASTN
NCBI GI	g4544405
BLAST score	281
E value	1.0e-157
Match length	281
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F28I8 genomic sequence, complete sequence

Seq. No.	138890
Seq. ID	LIB23-045-Q1-E1-C11
Method	BLASTX
NCBI GI	g3269287
BLAST score	367
E value	1.0e-36
Match length	93
% identity	90
NCBI Description	(AL030978) GH3 like protein [Arabidopsis thaliana]

Seq. No.	138891
Seq. ID	LIB23-045-Q1-E1-C12
Method	BLASTX
NCBI GI	g3123745
BLAST score	238
E value	3.0e-20
Match length	92
% identity	52
NCBI Description	(AB013447) aluminum-induced [Brassica napus]

Seq. No.	138892
Seq. ID	LIB23-045-Q1-E1-C2
Method	BLASTN
NCBI GI	g2642427
BLAST score	284
E value	1.0e-159
Match length	284
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T20D16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138893
Seq. ID	LIB23-045-Q1-E1-C3
Method	BLASTX
NCBI GI	g2281635
BLAST score	274
E value	2.0e-24
Match length	80
% identity	71
NCBI Description	(AF003098) AP2 domain containing protein RAP2.5 [Arabidopsis thaliana]

Seq. No.	138894
Seq. ID	LIB23-045-Q1-E1-C6
Method	BLASTX
NCBI GI	g3152606
BLAST score	220
E value	3.0e-18
Match length	54
% identity	70
NCBI Description	(AC004482) putative ring zinc finger protein [Arabidopsis thaliana]

Seq. No.	138895
Seq. ID	LIB23-045-Q1-E1-D10
Method	BLASTX
NCBI GI	g166867

BLAST score 95
E value 3.0e-26
Match length 74
% identity 85
NCBI Description (J05216) ribosomal protein S11 (probable start codon at bp 67) [Arabidopsis thaliana]

Seq. No. 138896
Seq. ID LIB23-045-Q1-E1-D6
Method BLASTX
NCBI GI g232031
BLAST score 280
E value 3.0e-25
Match length 76
% identity 64
NCBI Description ELONGATION FACTOR 1 BETA' >gi_322851_pir__S29224 translation elongation factor eEF-1 beta' chain - rice >gi_218161_dbj_BAA02253_ (D12821) elongation factor 1 beta' [Oryza sativa]

Seq. No. 138897
Seq. ID LIB23-045-Q1-E1-D7
Method BLASTX
NCBI GI g2088654
BLAST score 315
E value 2.0e-29
Match length 69
% identity 90
NCBI Description (AF002109) 60S acidic ribosomal protein P0 isolog [Arabidopsis thaliana]

Seq. No. 138898
Seq. ID LIB23-045-Q1-E1-D8
Method BLASTX
NCBI GI g4314378
BLAST score 361
E value 1.0e-34
Match length 89
% identity 75
NCBI Description (AC006232) putative lipase [Arabidopsis thaliana]

Seq. No. 138899
Seq. ID LIB23-045-Q1-E1-E10
Method BLASTN
NCBI GI g2088638
BLAST score 253
E value 1.0e-140
Match length 253
% identity 100
NCBI Description Arabidopsis thaliana chromosome II BAC T28M21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 138900
Seq. ID LIB23-045-Q1-E1-E3
Method BLASTX
NCBI GI g2129759
BLAST score 464

E value	9.0e-47
Match length	94
% identity	98
NCBI Description	UDPglucose 4-epimerase (EC 5.1.3.2) - Arabidopsis thaliana >gi_1143392_emb_CAA90941_ (Z54214) uridine diphosphate glucose epimerase [Arabidopsis thaliana]

Seq. No.	138901
Seq. ID	LIB23-045-Q1-E1-E6
Method	BLASTX
NCBI GI	g4210334
BLAST score	355
E value	5.0e-34
Match length	88
% identity	82
NCBI Description	(AJ223804) 2-oxoglutarate dehydrogenase, E3 subunit [Arabidopsis thaliana]

Seq. No.	138902
Seq. ID	LIB23-045-Q1-E1-F2
Method	BLASTN
NCBI GI	g3420043
BLAST score	285
E value	1.0e-159
Match length	285
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F23F1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138903
Seq. ID	LIB23-045-Q1-E1-F6
Method	BLASTX
NCBI GI	g3169569
BLAST score	155
E value	4.0e-27
Match length	69
% identity	97
NCBI Description	(AF062589) 3-keto-acyl-CoA thiolase 2 [Arabidopsis thaliana] >gi_3220237 (AF062591) peroxisomal 3-keto-acyl-CoA thiolase 2 precursor [Arabidopsis thaliana]

Seq. No.	138904
Seq. ID	LIB23-045-Q1-E1-F7
Method	BLASTX
NCBI GI	g4587989
BLAST score	241
E value	1.0e-20
Match length	70
% identity	74
NCBI Description	(AF085279) hypothetical Cys-3-His zinc finger protein [Arabidopsis thaliana]

Seq. No.	138905
Seq. ID	LIB23-045-Q1-E1-G10
Method	BLASTX
NCBI GI	g4678924
BLAST score	140

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E value	8.0e-09
Match length	62
% identity	42
NCBI Description	(AL049711) putative protein [Arabidopsis thaliana]

Seq. No.	138906
Seq. ID	LIB23-045-Q1-E1-G2
Method	BLASTX
NCBI GI	g1169598
BLAST score	198
E value	1.0e-15
Match length	48
% identity	75
NCBI Description	OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (DELTA-12 DESATURASE) >gi_438451 (L26296) delta-12 desaturase [Arabidopsis thaliana]

Seq. No.	138907
Seq. ID	LIB23-045-Q1-E1-G3
Method	BLASTX
NCBI GI	g2829869
BLAST score	497
E value	1.0e-50
Match length	93
% identity	100
NCBI Description	(AC002396) pyruvate dehydrogenase E1 alpha subunit [Arabidopsis thaliana]

Seq. No.	138908
Seq. ID	LIB23-045-Q1-E1-G4
Method	BLASTX
NCBI GI	g16245
BLAST score	484
E value	4.0e-49
Match length	93
% identity	100
NCBI Description	(X51514) precursor acetolactate synthase (670 AA) [Arabidopsis thaliana]

Seq. No.	138909
Seq. ID	LIB23-045-Q1-E1-G5
Method	BLASTN
NCBI GI	g3449317
BLAST score	43
E value	4.0e-15
Match length	59
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKM21, complete sequence [Arabidopsis thaliana]

Seq. No.	138910
Seq. ID	LIB23-045-Q1-E1-G8
Method	BLASTX
NCBI GI	g115783
BLAST score	324
E value	2.0e-30
Match length	62

% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	138911
Seq. ID	LIB23-045-Q1-E1-G9
Method	BLASTN
NCBI GI	g1532270
BLAST score	253
E value	1.0e-140
Match length	265
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for delta1-pyrroline-5-carboxylate synthase, complete cds

Seq. No.	138912
Seq. ID	LIB23-045-Q1-E1-H3
Method	BLASTX
NCBI GI	g2894574
BLAST score	407
E value	4.0e-40
Match length	77
% identity	100
NCBI Description	(AL021890) peroxidase prxr1 [Arabidopsis thaliana] >gi_2961341_emb_CAA18099.1_ (AL022140) peroxidase prxr1 [Arabidopsis thaliana]

Seq. No.	138913
Seq. ID	LIB23-045-Q1-E1-H6
Method	BLASTX
NCBI GI	g3176714
BLAST score	304
E value	5.0e-28
Match length	89
% identity	69
NCBI Description	(AC002392) putative tRNA-splicing endonuclease positive effector [Arabidopsis thaliana]

Seq. No.	138914
Seq. ID	LIB23-046-Q1-E1-B3
Method	BLASTN
NCBI GI	g2358139
BLAST score	169
E value	4.0e-90
Match length	387
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 YAC yUP8H12 complete sequence [Arabidopsis thaliana]

Seq. No.	138915
Seq. ID	LIB23-046-Q1-E1-C6
Method	BLASTX
NCBI GI	g4741940
BLAST score	529
E value	4.0e-54

Match length	96
% identity	64
NCBI Description	(AF134120) Lhca2 protein [Arabidopsis thaliana]

Seq. No.	138916
Seq. ID	LIB23-046-Q1-E1-D12
Method	BLASTN
NCBI GI	g4455168
BLAST score	40
E value	1.0e-13
Match length	72
% identity	89
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)

Seq. No.	138917
Seq. ID	LIB23-046-Q1-E1-E2
Method	BLASTN
NCBI GI	g3702315
BLAST score	218
E value	1.0e-119
Match length	406
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T3F17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138918
Seq. ID	LIB23-046-Q1-E1-E7
Method	BLASTN
NCBI GI	g3869069
BLAST score	206
E value	1.0e-112
Match length	396
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence [Arabidopsis thaliana]

Seq. No.	138919
Seq. ID	LIB23-046-Q1-E1-F1
Method	BLASTX
NCBI GI	g322492
BLAST score	677
E value	2.0e-71
Match length	131
% identity	100
NCBI Description	photomorphogenesis repressor COP1 - Arabidopsis thaliana

Seq. No.	138920
Seq. ID	LIB23-046-Q1-E1-F5
Method	BLASTN
NCBI GI	g4220645
BLAST score	256
E value	1.0e-142
Match length	386
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYA6, complete sequence [Arabidopsis thaliana]

Seq. No.	138921
Seq. ID	LIB23-046-Q1-E1-F9
Method	BLASTX
NCBI GI	g2961357
BLAST score	207
E value	2.0e-16
Match length	55
% identity	75
NCBI Description	(AL022140) putative protein [Arabidopsis thaliana]

Seq. No.	138922
Seq. ID	LIB23-046-Q1-E1-G3
Method	BLASTX
NCBI GI	g115783
BLAST score	569
E value	8.0e-59
Match length	108
% identity	99
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	138923
Seq. ID	LIB23-046-Q1-E1-H3
Method	BLASTN
NCBI GI	g2351067
BLAST score	262
E value	1.0e-146
Match length	274
% identity	59
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPO12, complete sequence [Arabidopsis thaliana]

Seq. No.	138924
Seq. ID	LIB23-046-Q1-E1-H4
Method	BLASTX
NCBI GI	g3668093
BLAST score	249
E value	2.0e-21
Match length	83
% identity	63
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	138925
Seq. ID	LIB23-046-Q1-E1-H7
Method	BLASTX
NCBI GI	g2894574
BLAST score	614
E value	4.0e-64
Match length	116
% identity	100
NCBI Description	(AL021890) peroxidase prxr1 [Arabidopsis thaliana] >gi_2961341_emb_CAA18099.1_ (AL022140) peroxidase prxr1 [Arabidopsis thaliana]

Seq. No.	138926
Seq. ID	LIB23-047-Q1-E1-A11
Method	BLASTX
NCBI GI	g2642158
BLAST score	310
E value	1.0e-28
Match length	75
% identity	75
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	138927
Seq. ID	LIB23-047-Q1-E1-A6
Method	BLASTX
NCBI GI	g115783
BLAST score	605
E value	4.0e-63
Match length	114
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	138928
Seq. ID	LIB23-047-Q1-E1-D2
Method	BLASTN
NCBI GI	g3510347
BLAST score	41
E value	9.0e-14
Match length	184
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]

Seq. No.	138929
Seq. ID	LIB23-047-Q1-E1-D7
Method	BLASTX
NCBI GI	g1710581
BLAST score	500
E value	7.0e-51
Match length	100
% identity	98
NCBI Description	60S RIBOSOMAL PROTEIN L9 >gi_2129720_pir__S71255 ribosomal protein L9 - Arabidopsis thaliana >gi_1107489_emb_CAA63024_ (X91958) 60S ribosomal protein L9 [Arabidopsis thaliana]

Seq. No.	138930
Seq. ID	LIB23-047-Q1-E1-F5
Method	BLASTX
NCBI GI	g4455319
BLAST score	171
E value	3.0e-12
Match length	70
% identity	47
NCBI Description	(AL035528) putative disease resistance protein [Arabidopsis thaliana]

Seq. No.	138931
Seq. ID	LIB23-047-Q1-E1-G1
Method	BLASTX
NCBI GI	g4249386
BLAST score	571
E value	3.0e-59
Match length	114
% identity	100
NCBI Description	(AC005966) Strong similarity to gb_AF061286 gamma-adaptin 1 from Arabidopsis thaliana. EST gb_H37393 comes from this gene. [Arabidopsis thaliana]

Seq. No.	138932
Seq. ID	LIB23-047-Q1-E1-G12
Method	BLASTX
NCBI GI	g2880043
BLAST score	473
E value	1.0e-47
Match length	115
% identity	83
NCBI Description	(AC002340) putative 3-hydroxyisobutyryl-coenzyme A hydrolase [Arabidopsis thaliana]

Seq. No.	138933
Seq. ID	LIB23-047-Q1-E1-G6
Method	BLASTN
NCBI GI	g2924651
BLAST score	142
E value	3.0e-74
Match length	243
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana]

Seq. No.	138934
Seq. ID	LIB23-047-Q1-E1-H4
Method	BLASTX
NCBI GI	g4262162
BLAST score	284
E value	1.0e-25
Match length	69
% identity	78
NCBI Description	(AC005275) putative glycosylation enzyme [Arabidopsis thaliana]

Seq. No.	138935
Seq. ID	LIB23-047-Q1-E1-H7
Method	BLASTX
NCBI GI	g3334404
BLAST score	394
E value	2.0e-38
Match length	89
% identity	87
NCBI Description	VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD SUBUNIT) >gi_2266990 (U65638) vacuolar type ATPase subunit A [Arabidopsis thaliana] >gi_3834305 (AC005679) Identical to gb_U65638 Arabidopsis thaliana vacuolar type ATPase

subunit A mRNA. ESTs gb_N96435, gb_N96106, gb_N96189, gb_N96091, gb_AA042286, gb_F14324, gb_W43643, gb_N96027, gb_N96299, gb_R29943, gb_T43460, gb_T43544, gb_T22472

Seq. No.	138936
Seq. ID	LIB23-048-Q1-E1-B1
Method	BLASTN
NCBI GI	g4510360
BLAST score	196
E value	1.0e-106
Match length	348
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F11F19 genomic sequence, complete sequence

Seq. No.	138937
Seq. ID	LIB23-048-Q1-E1-D4
Method	BLASTX
NCBI GI	g3492806
BLAST score	369
E value	2.0e-35
Match length	115
% identity	61
NCBI Description	(AJ225045) adventitious rooting related oxygenase [Malus domestica]

Seq. No.	138938
Seq. ID	LIB23-048-Q1-E1-D7
Method	BLASTX
NCBI GI	g3913418
BLAST score	126
E value	1.0e-54
Match length	109
% identity	97
NCBI Description	S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC) (SAMDC) >gi_1531763_emb_CAA69073_ (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis thaliana]

Seq. No.	138939
Seq. ID	LIB23-048-Q1-E1-E11
Method	BLASTX
NCBI GI	g4512615
BLAST score	531
E value	2.0e-54
Match length	110
% identity	98
NCBI Description	(AC004793) Strong similarity to gb_X59970 3-isopropylmalate dehydrogenase (IMDH) from Brassica napus. EST gb_F14478 comes from this gene. [Arabidopsis thaliana]

Seq. No.	138940
Seq. ID	LIB23-048-Q1-E1-F11
Method	BLASTX
NCBI GI	g1518388
BLAST score	273
E value	3.0e-24
Match length	85

% identity	61
NCBI Description	(X91172) korean-radish isoperoxidase [Raphanus sativus]

Seq. No.	138941
Seq. ID	LIB23-048-Q1-E1-G4
Method	BLASTX
NCBI GI	g4455309
BLAST score	195
E value	5.0e-15
Match length	68
% identity	57
NCBI Description	(AL035528) hypothetical protein [Arabidopsis thaliana]

Seq. No.	138942
Seq. ID	LIB23-048-Q1-E1-H6
Method	BLASTX
NCBI GI	g4587595
BLAST score	294
E value	5.0e-27
Match length	56
% identity	98
NCBI Description	(AC006951) putative proline-rich protein APG [Arabidopsis thaliana]

Seq. No.	138943
Seq. ID	LIB23-049-Q1-E1-A5
Method	BLASTX
NCBI GI	g3249065
BLAST score	369
E value	2.0e-35
Match length	74
% identity	97
NCBI Description	(AC004473) Similar to HAK1 gb_U22945 high affinity potassium transporter from Schwanniomyces occidentalis. [Arabidopsis thaliana]

Seq. No.	138944
Seq. ID	LIB23-049-Q1-E1-A6
Method	BLASTX
NCBI GI	g4588012
BLAST score	484
E value	6.0e-49
Match length	116
% identity	79
NCBI Description	(AF085717) putative callose synthase catalytic subunit [Gossypium hirsutum]

Seq. No.	138945
Seq. ID	LIB23-049-Q1-E1-A8
Method	BLASTX
NCBI GI	g2494896
BLAST score	619
E value	1.0e-64
Match length	114
% identity	56
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 3 DELTA SUBUNIT (EIF-3 DELTA) (EIF3 P36) (TGF-BETA RECEPTOR INTERACTING

PROTEIN 1) (TRIP-1) >gi_2129749_pir__S60256 TGF-beta receptor interacting protein 1 homolog - Arabidopsis thaliana >gi_1036803 (U36765) TGF-beta receptor interacting protein 1 homolog [Arabidopsis thaliana]

Seq. No.	138946
Seq. ID	LIB23-049-Q1-E1-B5
Method	BLASTN
NCBI GI	g3036791
BLAST score	358
E value	0.0e+00
Match length	358
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T19K4 (ESSAII project)

Seq. No.	138947
Seq. ID	LIB23-049-Q1-E1-B7
Method	BLASTX
NCBI GI	g3169176
BLAST score	552
E value	6.0e-57
Match length	120
% identity	91
NCBI Description	(AC004401) putative protein kinase [Arabidopsis thaliana]

Seq. No.	138948
Seq. ID	LIB23-049-Q1-E1-C6
Method	BLASTN
NCBI GI	g3869066
BLAST score	45
E value	4.0e-16
Match length	151
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBM17, complete sequence [Arabidopsis thaliana]

Seq. No.	138949
Seq. ID	LIB23-049-Q1-E1-C8
Method	BLASTN
NCBI GI	g2459406
BLAST score	274
E value	1.0e-153
Match length	278
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F4P9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138950
Seq. ID	LIB23-049-Q1-E1-D10
Method	BLASTX
NCBI GI	g2462757
BLAST score	228
E value	2.0e-19
Match length	63
% identity	81
NCBI Description	(AC002292) Hypothetical protein [Arabidopsis thaliana]

09074050+090740

Seq. No.	138951
Seq. ID	LIB23-049-Q1-E1-D11
Method	BLASTX
NCBI GI	g1911166
BLAST score	579
E value	4.0e-60
Match length	118
% identity	92
NCBI Description	(X94400) soluble-starch-synthase [Solanum tuberosum]

Seq. No.	138952
Seq. ID	LIB23-049-Q1-E1-D4
Method	BLASTX
NCBI GI	g115480
BLAST score	607
E value	2.0e-63
Match length	118
% identity	52
NCBI Description	CALMODULIN-1 >gi_166649 (M38379) calmodulin-1 [Arabidopsis thaliana]

Seq. No.	138953
Seq. ID	LIB23-049-Q1-E1-G11
Method	BLASTN
NCBI GI	g4539290
BLAST score	134
E value	3.0e-69
Match length	344
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F14M19 (ESSA project)

Seq. No.	138954
Seq. ID	LIB23-049-Q1-E1-G2
Method	BLASTN
NCBI GI	g4006885
BLAST score	213
E value	1.0e-116
Match length	327
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	138955
Seq. ID	LIB23-049-Q1-E1-G5
Method	BLASTN
NCBI GI	g4757662
BLAST score	225
E value	1.0e-123
Match length	330
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome I, complete sequence

Seq. No.	138956
Seq. ID	LIB23-049-Q1-E1-G7

Method	BLASTN
NCBI GI	g4220635
BLAST score	205
E value	1.0e-111
Match length	350
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDB19, complete sequence [Arabidopsis thaliana]

Seq. No.	138957
Seq. ID	LIB23-049-Q1-E1-G8
Method	BLASTX
NCBI GI	g1653767
BLAST score	243
E value	6.0e-21
Match length	79
% identity	57
NCBI Description	(D90916) oligopeptidase A [Synechocystis sp.]

Seq. No.	138958
Seq. ID	LIB23-049-Q1-E1-H11
Method	BLASTN
NCBI GI	g3241922
BLAST score	165
E value	4.0e-88
Match length	181
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLM24, complete sequence [Arabidopsis thaliana]

Seq. No.	138959
Seq. ID	LIB23-049-Q1-E1-H9
Method	BLASTX
NCBI GI	g3023848
BLAST score	476
E value	5.0e-48
Match length	100
% identity	50
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA) >gi_2289095 (U77381) WD-40 repeat protein [Arabidopsis thaliana]

Seq. No.	138960
Seq. ID	LIB23-050-Q1-E1-F4
Method	BLASTX
NCBI GI	g3252809
BLAST score	296
E value	4.0e-27
Match length	84
% identity	38
NCBI Description	(AC004705) hypothetical protein [Arabidopsis thaliana]

Seq. No.	138961
Seq. ID	LIB23-050-Q1-E1-H8
Method	BLASTX
NCBI GI	g4512680

BLAST score	254
E value	6.0e-22
Match length	55
% identity	96
NCBI Description	(AC006931) hypothetical protein [Arabidopsis thaliana]

Seq. No.	138962
Seq. ID	LIB23-051-Q1-E1-A9
Method	BLASTX
NCBI GI	g2894574
BLAST score	491
E value	8.0e-50
Match length	93
% identity	100
NCBI Description	(AL021890) peroxidase prxr1 [Arabidopsis thaliana] >gi_2961341_emb_CAA18099.1_ (AL022140) peroxidase prxr1 [Arabidopsis thaliana]

Seq. No.	138963
Seq. ID	LIB23-051-Q1-E1-B7
Method	BLASTN
NCBI GI	g4587582
BLAST score	103
E value	8.0e-51
Match length	147
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T16B14 genomic sequence, complete sequence

Seq. No.	138964
Seq. ID	LIB23-051-Q1-E1-B9
Method	BLASTN
NCBI GI	g3873174
BLAST score	67
E value	3.0e-29
Match length	75
% identity	97
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14N23, complete sequence [Arabidopsis thaliana]

Seq. No.	138965
Seq. ID	LIB23-051-Q1-E1-C4
Method	BLASTN
NCBI GI	g3461810
BLAST score	121
E value	1.0e-61
Match length	232
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T17M13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138966
Seq. ID	LIB23-051-Q1-E1-D10
Method	BLASTX
NCBI GI	g133978
BLAST score	311
E value	1.0e-28

Match length	108
% identity	57
NCBI Description	40S RIBOSOMAL PROTEIN S6 (PHOSPHOPROTEIN NP33) >gi_70932_pir__R3RTS6 ribosomal protein S6 - rat >gi_70933_pir__R3MS6 ribosomal protein S6 - mouse >gi_319910_pir__R3HU6 ribosomal protein S6 - human >gi_36148_emb_CAA47719_ (X67309) ribosomal protein S6 [Homo sapiens] >gi_54010_emb_CAA68430_ (Y00348) ribosomal protein S6 [Mus musculus] >gi_206747 (M29358) ribosomal protein S6 [Rattus norvegicus] >gi_307393 (M77232) ribosomal protein S6 [Homo sapiens] >gi_1177549_emb_CAA90936_ (Z54209) rpS6 [Mus musculus]

Seq. No.	138967
Seq. ID	LIB23-051-Q1-E1-E10
Method	BLASTN
NCBI GI	g2702261
BLAST score	191
E value	1.0e-103
Match length	194
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T21L14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138968
Seq. ID	LIB23-051-Q1-E1-E2
Method	BLASTX
NCBI GI	g1495269
BLAST score	449
E value	1.0e-44
Match length	125
% identity	73
NCBI Description	(X97829) product similar to ccr protein, Citrus paradisi; PIR: S52663 [Arabidopsis thaliana] >gi_1550735_emb_CAA66824_ (X98130) unknown [Arabidopsis thaliana]

Seq. No.	138969
Seq. ID	LIB23-051-Q1-E1-E6
Method	BLASTX
NCBI GI	g2252824
BLAST score	494
E value	5.0e-50
Match length	118
% identity	80
NCBI Description	(AF013293) No definition line found [Arabidopsis thaliana]

Seq. No.	138970
Seq. ID	LIB23-051-Q1-E1-F6
Method	BLASTN
NCBI GI	g4662640
BLAST score	86
E value	1.0e-40
Match length	312
% identity	83
NCBI Description	Arabidopsis thaliana chromosome II BAC F15K19 genomic sequence, complete sequence

Seq. No.	138971
Seq. ID	LIB23-051-Q1-E1-G6
Method	BLASTN
NCBI GI	g3335331
BLAST score	240
E value	1.0e-132
Match length	380
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8F5 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138972
Seq. ID	LIB23-051-Q1-E1-H4
Method	BLASTN
NCBI GI	g4732168
BLAST score	64
E value	1.0e-27
Match length	173
% identity	59
NCBI Description	Arabidopsis thaliana BAC T1J24

Seq. No.	138973
Seq. ID	LIB23-051-Q1-E1-H9
Method	BLASTX
NCBI GI	g2632252
BLAST score	153
E value	2.0e-14
Match length	61
% identity	64
NCBI Description	(Y12464) serine/threonine kinase [Sorghum bicolor]

Seq. No.	138974
Seq. ID	LIB23-052-Q1-E1-B1
Method	BLASTX
NCBI GI	g3241943
BLAST score	443
E value	3.0e-44
Match length	101
% identity	78
NCBI Description	(AC004625) hypothetical protein [Arabidopsis thaliana]

Seq. No.	138975
Seq. ID	LIB23-052-Q1-E1-B2
Method	BLASTN
NCBI GI	g3869072
BLAST score	311
E value	1.0e-175
Match length	335
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJB24, complete sequence [Arabidopsis thaliana]

Seq. No.	138976
Seq. ID	LIB23-052-Q1-E1-C1
Method	BLASTX
NCBI GI	g1169423

BLAST score	237
E value	6.0e-20
Match length	48
% identity	98
NCBI Description	DIHYDROFOLATE REDUCTASE 2 / THYMIDYLATE SYNTHASE 2 (DHFR-TS) >gi_289195 (L08594) dihydrofolate reductase-thymidylate synthase [Arabidopsis thaliana] >gi_3096926_emb_CAA18836.1_ (AL023094) dihydrofolate reductase-thymidylate synthase [Arabidopsis thaliana]

Seq. No.	138977
Seq. ID	LIB23-052-Q1-E1-C9
Method	BLASTN
NCBI GI	g3510342
BLAST score	232
E value	1.0e-128
Match length	240
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MGN6, complete sequence [Arabidopsis thaliana]

Seq. No.	138978
Seq. ID	LIB23-052-Q1-E1-F8
Method	BLASTX
NCBI GI	g3367517
BLAST score	469
E value	4.0e-47
Match length	99
% identity	89
NCBI Description	(AC004392) Similar to F4I1.26 putative beta-glucosidase gi_3128187 from A. thaliana BAC gb_AC004521. ESTs gb_N97083, gb_F19868 and gb_F15482 come from this gene. [Arabidopsis thaliana]

Seq. No.	138979
Seq. ID	LIB23-052-Q1-E1-G5
Method	BLASTX
NCBI GI	g4758918
BLAST score	165
E value	1.0e-11
Match length	83
% identity	40
NCBI Description	phosphatidylinositol glycan, class B >gi_1552169_dbj_BAA07709_ (D42138) PIG-B [Homo sapiens]

Seq. No.	138980
Seq. ID	LIB23-052-Q1-E1-H7
Method	BLASTX
NCBI GI	g4467147
BLAST score	637
E value	7.0e-70
Match length	140
% identity	99
NCBI Description	(AL035540) putative protein [Arabidopsis thaliana]

Seq. No.	138981
Seq. ID	LIB23-053-Q1-E1-B5

Method	BLASTX
NCBI GI	g115783
BLAST score	483
E value	7.0e-49
Match length	91
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	138982
Seq. ID	LIB23-053-Q1-E1-B6
Method	BLASTX
NCBI GI	g3738339
BLAST score	450
E value	5.0e-45
Match length	113
% identity	74
NCBI Description	(AC005170) putative kinase [Arabidopsis thaliana]

Seq. No.	138983
Seq. ID	LIB23-053-Q1-E1-C5
Method	BLASTX
NCBI GI	g399213
BLAST score	599
E value	2.0e-62
Match length	117
% identity	99
NCBI Description	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG CD4B PRECURSOR >gi_100190_pir__B35905 CD4B protein - tomato >gi_170435 (M32604) ATP-dependent protease (CD4B) [Lycopersicon esculentum]

Seq. No.	138984
Seq. ID	LIB23-053-Q1-E1-C9
Method	BLASTX
NCBI GI	g4630748
BLAST score	373
E value	5.0e-36
Match length	90
% identity	83
NCBI Description	(AC007236) putative anion exchange protein 3 [Arabidopsis thaliana]

Seq. No.	138985
Seq. ID	LIB23-053-Q1-E1-D5
Method	BLASTN
NCBI GI	g2266984
BLAST score	159
E value	2.0e-84
Match length	159
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for chloroplast and mitochondrial methionyl-tRNA synthetase

Seq. No. 138986

Seq. ID	LIB23-053-Q1-E1-D6
Method	BLASTX
NCBI GI	g2191168
BLAST score	387
E value	1.0e-37
Match length	93
% identity	86
NCBI Description	(AF007270) contains similarity to myosin heavy chain [Arabidopsis thaliana]

Seq. No.	138987
Seq. ID	LIB23-053-Q1-E1-D7
Method	BLASTX
NCBI GI	g1495251
BLAST score	329
E value	9.0e-31
Match length	66
% identity	95
NCBI Description	(Z70314) heat-shock protein [Arabidopsis thaliana]

Seq. No.	138988
Seq. ID	LIB23-053-Q1-E1-E2
Method	BLASTX
NCBI GI	g115783
BLAST score	479
E value	2.0e-48
Match length	90
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	138989
Seq. ID	LIB23-053-Q1-E1-E5
Method	BLASTN
NCBI GI	g4589438
BLAST score	318
E value	1.0e-179
Match length	359
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQJ2, complete sequence

Seq. No.	138990
Seq. ID	LIB23-053-Q1-E1-H6
Method	BLASTX
NCBI GI	g115767
BLAST score	596
E value	5.0e-62
Match length	113
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana]

>gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	138991
Seq. ID	LIB23-053-Q1-E1-H7
Method	BLASTX
NCBI GI	g3004564
BLAST score	307
E value	1.0e-31
Match length	91
% identity	73
NCBI Description	(AC003673) putative receptor Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No.	138992
Seq. ID	LIB23-054-Q1-E1-A3
Method	BLASTN
NCBI GI	g1877523
BLAST score	221
E value	1.0e-121
Match length	345
% identity	100
NCBI Description	Arabidopsis thaliana BAC T7I23, complete sequence [Arabidopsis thaliana]

Seq. No.	138993
Seq. ID	LIB23-054-Q1-E1-A5
Method	BLASTX
NCBI GI	g4538987
BLAST score	658
E value	3.0e-69
Match length	134
% identity	99
NCBI Description	(AJ133777) gamma-adaptin 2 [Arabidopsis thaliana]

Seq. No.	138994
Seq. ID	LIB23-054-Q1-E1-B8
Method	BLASTX
NCBI GI	g4584110
BLAST score	332
E value	5.0e-31
Match length	124
% identity	52
NCBI Description	(AJ133639) SAH7 protein [Arabidopsis thaliana]

Seq. No.	138995
Seq. ID	LIB23-054-Q1-E1-C11
Method	BLASTN
NCBI GI	g2244950
BLAST score	341
E value	0.0e+00
Match length	341
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	138996

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Seq. ID	LIB23-054-Q1-E1-C7
Method	BLASTN
NCBI GI	g3386593
BLAST score	153
E value	2.0e-80
Match length	324
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F4I18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	138997
Seq. ID	LIB23-054-Q1-E1-D1
Method	BLASTX
NCBI GI	g115767
BLAST score	678
E value	1.0e-71
Match length	130
% identity	99
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	138998
Seq. ID	LIB23-054-Q1-E1-D12
Method	BLASTX
NCBI GI	g3395431
BLAST score	266
E value	2.0e-23
Match length	118
% identity	46
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	138999
Seq. ID	LIB23-054-Q1-E1-D6
Method	BLASTX
NCBI GI	g2827714
BLAST score	179
E value	4.0e-13
Match length	129
% identity	5
NCBI Description	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	139000
Seq. ID	LIB23-054-Q1-E1-D7
Method	BLASTN
NCBI GI	g3337347
BLAST score	271
E value	1.0e-151
Match length	417
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F13P17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139001
Seq. ID	LIB23-054-Q1-E1-D8
Method	BLASTN
NCBI GI	g4490717
BLAST score	166
E value	1.0e-88
Match length	220
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	139002
Seq. ID	LIB23-054-Q1-E1-D9
Method	BLASTX
NCBI GI	g2809255
BLAST score	632
E value	2.0e-66
Match length	111
% identity	99
NCBI Description	(AC002560) F21B7.24 [Arabidopsis thaliana]

Seq. No.	139003
Seq. ID	LIB23-054-Q1-E1-E1
Method	BLASTN
NCBI GI	g2924730
BLAST score	262
E value	1.0e-145
Match length	294
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPI7, complete sequence [Arabidopsis thaliana]

Seq. No.	139004
Seq. ID	LIB23-054-Q1-E1-E2
Method	BLASTN
NCBI GI	g3327922
BLAST score	156
E value	2.0e-82
Match length	342
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T31E10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139005
Seq. ID	LIB23-054-Q1-E1-E4
Method	BLASTX
NCBI GI	g2852447
BLAST score	237
E value	7.0e-20
Match length	75
% identity	65
NCBI Description	(D88206) protein kinase [Arabidopsis thaliana]

Seq. No.	139006
Seq. ID	LIB23-054-Q1-E1-F11
Method	BLASTN

NCBI GI	g3298610
BLAST score	136
E value	2.0e-70
Match length	276
% identity	100
NCBI Description	Arabidopsis thaliana BAC T2H3

Seq. No.	139007
Seq. ID	LIB23-054-Q1-E1-F5
Method	BLASTX
NCBI GI	g2058504
BLAST score	364
E value	9.0e-35
Match length	104
% identity	76
NCBI Description	(U76554) zinc-finger protein-1 [Brassica rapa]

Seq. No.	139008
Seq. ID	LIB23-054-Q1-E1-G1
Method	BLASTX
NCBI GI	g2213884
BLAST score	182
E value	2.0e-13
Match length	76
% identity	53
NCBI Description	(AF004166) 2-isopropylmalate synthase [Lycopersicon pennellii]

Seq. No.	139009
Seq. ID	LIB23-054-Q1-E1-G5
Method	BLASTN
NCBI GI	g3355463
BLAST score	201
E value	1.0e-109
Match length	397
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139010
Seq. ID	LIB23-054-Q1-E1-G6
Method	BLASTX
NCBI GI	g2947063
BLAST score	224
E value	2.0e-18
Match length	99
% identity	44
NCBI Description	(AC002521) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No.	139011
Seq. ID	LIB23-054-Q1-E1-H11
Method	BLASTN
NCBI GI	g3873174
BLAST score	343
E value	0.0e+00
Match length	343

% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14N23, complete sequence [Arabidopsis thaliana]

Seq. No.	139012
Seq. ID	LIB23-055-Q1-E1-A12
Method	BLASTX
NCBI GI	g480450
BLAST score	330
E value	8.0e-31
Match length	80
% identity	86
NCBI Description	ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis thaliana >gi_402552_emb_CAA49506_ (X69880) ketol-acid reductoisomerase [Arabidopsis thaliana]

Seq. No.	139013
Seq. ID	LIB23-055-Q1-E1-A4
Method	BLASTX
NCBI GI	g4559384
BLAST score	206
E value	3.0e-16
Match length	59
% identity	66
NCBI Description	(AC006526) unknown protein [Arabidopsis thaliana]

Seq. No.	139014
Seq. ID	LIB23-055-Q1-E1-B1
Method	BLASTN
NCBI GI	g2864607
BLAST score	313
E value	1.0e-176
Match length	325
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6 (ESSAII project)

Seq. No.	139015
Seq. ID	LIB23-055-Q1-E1-B10
Method	BLASTX
NCBI GI	g4732123
BLAST score	521
E value	7.0e-57
Match length	114
% identity	95
NCBI Description	(AF129087) mitogen-activated protein kinase homologue [Medicago sativa]

Seq. No.	139016
Seq. ID	LIB23-055-Q1-E1-B9
Method	BLASTX
NCBI GI	g1711355
BLAST score	276
E value	1.0e-24
Match length	104
% identity	58
NCBI Description	SHORT-CHAIN TYPE DEHYDROGENASE/REDUCTASE

>gi_421786_pir__S34678 short-chain alcohol dehydrogenase - Norway spruce >gi_395223_emb_CAA52213_ (X74115) short-chain alcohol dehydrogenase [Picea abies]

Seq. No.	139017
Seq. ID	LIB23-055-Q1-E1-C1
Method	BLASTN
NCBI GI	g3492855
BLAST score	149
E value	3.0e-78
Match length	371
% identity	78
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F20N2, complete sequence [Arabidopsis thaliana]

Seq. No.	139018
Seq. ID	LIB23-055-Q1-E1-C8
Method	BLASTX
NCBI GI	g2465923
BLAST score	222
E value	4.0e-18
Match length	112
% identity	45
NCBI Description	(AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	139019
Seq. ID	LIB23-055-Q1-E1-D1
Method	BLASTX
NCBI GI	g4539332
BLAST score	574
E value	2.0e-59
Match length	115
% identity	100
NCBI Description	(AL035539) glycosyltransferase like protein (fragment) [Arabidopsis thaliana]

Seq. No.	139020
Seq. ID	LIB23-055-Q1-E1-D12
Method	BLASTN
NCBI GI	g4468976
BLAST score	385
E value	0.0e+00
Match length	385
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F19F18 (ESSA project)

Seq. No.	139021
Seq. ID	LIB23-055-Q1-E1-D4
Method	BLASTX
NCBI GI	g115783
BLAST score	512
E value	3.0e-52
Match length	97
% identity	99
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	139022
Seq. ID	LIB23-055-Q1-E1-E1
Method	BLASTN
NCBI GI	g2244829
BLAST score	154
E value	3.0e-81
Match length	309
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	139023
Seq. ID	LIB23-055-Q1-E1-E7
Method	BLASTX
NCBI GI	g4455364
BLAST score	337
E value	1.0e-31
Match length	105
% identity	59
NCBI Description	(AL035524) senescence-associated protein-like [Arabidopsis thaliana]

Seq. No.	139024
Seq. ID	LIB23-055-Q1-E1-F5
Method	BLASTN
NCBI GI	g2182287
BLAST score	324
E value	0.0e+00
Match length	413
% identity	96
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T7N9, complete sequence [Arabidopsis thaliana]

Seq. No.	139025
Seq. ID	LIB23-055-Q1-E1-G7
Method	BLASTN
NCBI GI	g2264304
BLAST score	353
E value	0.0e+00
Match length	408
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBG8, complete sequence [Arabidopsis thaliana]

Seq. No.	139026
Seq. ID	LIB23-055-Q1-E1-H3
Method	BLASTX
NCBI GI	g2288988
BLAST score	209
E value	1.0e-16
Match length	112
% identity	38
NCBI Description	(AC002335) hypothetical protein [Arabidopsis thaliana]

Seq. No.	139027
Seq. ID	LIB23-055-Q1-E1-H6
Method	BLASTN
NCBI GI	g2623294
BLAST score	128
E value	1.0e-65
Match length	401
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T20B5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139028
Seq. ID	LIB23-056-Q1-E1-B12
Method	BLASTX
NCBI GI	g3451071
BLAST score	468
E value	5.0e-47
Match length	93
% identity	100
NCBI Description	(AL031326) beta adaptin - like protein [Arabidopsis thaliana]

Seq. No.	139029
Seq. ID	LIB23-056-Q1-E1-B4
Method	BLASTX
NCBI GI	g3152600
BLAST score	232
E value	2.0e-19
Match length	69
% identity	71
NCBI Description	(AC002986) Contains similarity to S. cerevisiae hypothetical protein YOR197w, gb_Z75105. ESTs gb_H37409, gb_AA395290, and gb_T43907 come from this gene. [Arabidopsis thaliana]

Seq. No.	139030
Seq. ID	LIB23-056-Q1-E1-C11
Method	BLASTX
NCBI GI	g2895510
BLAST score	302
E value	1.0e-27
Match length	110
% identity	51
NCBI Description	(AF033204) putative pectin methylesterase [Arabidopsis thaliana]

Seq. No.	139031
Seq. ID	LIB23-056-Q1-E1-C2
Method	BLASTX
NCBI GI	g4734005
BLAST score	547
E value	3.0e-56
Match length	109
% identity	100
NCBI Description	(AC007178) hypothetical protein [Arabidopsis thaliana]

Seq. No.	139032
Seq. ID	LIB23-056-Q1-E1-D2
Method	BLASTX
NCBI GI	g4567245
BLAST score	637
E value	7.0e-67
Match length	121
% identity	36
NCBI Description	(AC007070) unknown protein [Arabidopsis thaliana]

Seq. No.	139033
Seq. ID	LIB23-056-Q1-E1-D3
Method	BLASTN
NCBI GI	g4006885
BLAST score	227
E value	1.0e-125
Match length	227
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	139034
Seq. ID	LIB23-056-Q1-E1-E1
Method	BLASTN
NCBI GI	g3702733
BLAST score	167
E value	3.0e-89
Match length	203
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJP23, complete sequence [Arabidopsis thaliana]

Seq. No.	139035
Seq. ID	LIB23-056-Q1-E1-E2
Method	BLASTX
NCBI GI	g1076287
BLAST score	427
E value	3.0e-42
Match length	107
% identity	78
NCBI Description	amine acid permease - Arabidopsis thaliana >gi_510236_emb_CAA50672_ (X71787) amine acid permease [Arabidopsis thaliana]

Seq. No.	139036
Seq. ID	LIB23-056-Q1-E1-F1
Method	BLASTX
NCBI GI	g4678306
BLAST score	195
E value	5.0e-15
Match length	46
% identity	76
NCBI Description	(AL049655) kinesin-like protein [Arabidopsis thaliana]

Seq. No.	139037
Seq. ID	LIB23-056-Q1-E1-G5
Method	BLASTN

NCBI GI	g3176693
BLAST score	117
E value	4.0e-59
Match length	348
% identity	97
NCBI Description	Arabidopsis thaliana chromosome I BAC T27I1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139038
Seq. ID	LIB23-056-Q1-E1-G6
Method	BLASTX
NCBI GI	g486784
BLAST score	491
E value	9.0e-50
Match length	115
% identity	25
NCBI Description	Golgi-associated particle 102K chain - human

Seq. No.	139039
Seq. ID	LIB23-056-Q1-E1-G9
Method	BLASTX
NCBI GI	g267079
BLAST score	511
E value	4.0e-52
Match length	93
% identity	100
NCBI Description	TUBULIN BETA-6 CHAIN >gi_320187_pir__JQ1590 tubulin beta-6 chain - Arabidopsis thaliana >gi_166904 (M84703) beta-6 tubulin [Arabidopsis thaliana]

Seq. No.	139040
Seq. ID	LIB23-056-Q1-E1-H11
Method	BLASTX
NCBI GI	g1346181
BLAST score	175
E value	9.0e-13
Match length	45
% identity	80
NCBI Description	GLYCINE-RICH RNA-BINDING PROTEIN GRP2A >gi_496237 (L31377) homology with RNA-binding proteins in meristematic tissue [Sinapis alba]

Seq. No.	139041
Seq. ID	LIB23-057-Q1-E1-B11
Method	BLASTX
NCBI GI	g3935183
BLAST score	296
E value	1.0e-31
Match length	86
% identity	80
NCBI Description	(AC004557) F17L21.26 [Arabidopsis thaliana]

Seq. No.	139042
Seq. ID	LIB23-057-Q1-E1-C3
Method	BLASTN
NCBI GI	g4757414
BLAST score	247

E value	1.0e-137
Match length	287
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYF24, complete sequence

Seq. No.	139043
Seq. ID	LIB23-057-Q1-E1-D11
Method	BLASTN
NCBI GI	g4263694
BLAST score	107
E value	3.0e-53
Match length	208
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F22D22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139044
Seq. ID	LIB23-057-Q1-E1-D7
Method	BLASTX
NCBI GI	g2809257
BLAST score	328
E value	1.0e-30
Match length	63
% identity	54
NCBI Description	(AC002560) F21B7.26 [Arabidopsis thaliana]

Seq. No.	139045
Seq. ID	LIB23-057-Q1-E1-D8
Method	BLASTN
NCBI GI	g2264302
BLAST score	75
E value	1.0e-34
Match length	103
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC12, complete sequence [Arabidopsis thaliana]

Seq. No.	139046
Seq. ID	LIB23-057-Q1-E1-H11
Method	BLASTX
NCBI GI	g115783
BLAST score	173
E value	6.0e-13
Match length	46
% identity	83
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	139047
Seq. ID	LIB23-057-Q1-E1-H12
Method	BLASTN
NCBI GI	g4587641
BLAST score	129
E value	2.0e-66

Match length	208
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No.	139048
Seq. ID	LIB23-057-Q1-E1-H6
Method	BLASTX
NCBI GI	g114421
BLAST score	386
E value	1.0e-37
Match length	81
% identity	93
NCBI Description	ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR >gi_82133_pir__A24355 H+-transporting ATP synthase (EC 3.6.1.34) beta-1 chain, mitochondrial - curled-leaved tobacco >gi_19685_emb_CAA26620_ (X02868) ATP synthase beta subunit [Nicotiana plumbaginifolia]

Seq. No.	139049
Seq. ID	LIB23-058-Q1-E1-A6
Method	BLASTN
NCBI GI	g3193311
BLAST score	187
E value	1.0e-101
Match length	279
% identity	100
NCBI Description	Arabidopsis thaliana BAC F6N15

Seq. No.	139050
Seq. ID	LIB23-058-Q1-E1-A8
Method	BLASTN
NCBI GI	g3128135
BLAST score	332
E value	0.0e+00
Match length	371
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E1, complete sequence [Arabidopsis thaliana]

Seq. No.	139051
Seq. ID	LIB23-058-Q1-E1-E5
Method	BLASTN
NCBI GI	g1946354
BLAST score	241
E value	1.0e-133
Match length	285
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T06B20 genomic sequence, complete sequence

Seq. No.	139052
Seq. ID	LIB23-058-Q1-E1-F10
Method	BLASTN
NCBI GI	g2341023
BLAST score	372
E value	0.0e+00

Match length	376
% identity	100
NCBI Description	Sequence of BAC F19P19 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	139053
Seq. ID	LIB23-058-Q1-E1-F5
Method	BLASTN
NCBI GI	g1490552
BLAST score	295
E value	1.0e-165
Match length	295
% identity	100
NCBI Description	Arabidopsis thaliana S-adenosylmethionine decarboxylase (SAMdc) mRNA, complete cds

Seq. No.	139054
Seq. ID	LIB23-058-Q1-E1-G7
Method	BLASTN
NCBI GI	g3241923
BLAST score	101
E value	5.0e-50
Match length	117
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMN10, complete sequence [Arabidopsis thaliana]

Seq. No.	139055
Seq. ID	LIB23-058-Q1-E1-H11
Method	BLASTX
NCBI GI	g4741197
BLAST score	647
E value	5.0e-68
Match length	120
% identity	100
NCBI Description	(AL049746) aldose 1-epimerase-like protein [Arabidopsis thaliana]

Seq. No.	139056
Seq. ID	LIB23-058-Q1-E1-H7
Method	BLASTN
NCBI GI	g4415928
BLAST score	110
E value	4.0e-55
Match length	218
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F13A10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139057
Seq. ID	LIB23-059-Q1-E1-A12
Method	BLASTX
NCBI GI	g2499608
BLAST score	258
E value	1.0e-26
Match length	81
% identity	73

NCBI Description	MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 4 (MAP KINASE 4) (ATMPK4) >gi_2129645_pir__S40470 mitogen-activated protein kinase 4 (EC 2.7.1.-) - Arabidopsis thaliana >gi_457400_dbj_BAA04867_ (D21840) MAP kinase [Arabidopsis thaliana]
Seq. No.	139058
Seq. ID	LIB23-059-Q1-E1-B12
Method	BLASTN
NCBI GI	g2098816
BLAST score	201
E value	1.0e-109
Match length	205
% identity	100
NCBI Description	Arabidopsis thaliana BAC F19G10, complete sequence
Seq. No.	139059
Seq. ID	LIB23-059-Q1-E1-B2
Method	BLASTX
NCBI GI	g132166
BLAST score	250
E value	1.0e-21
Match length	67
% identity	81
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi_81660_pir__S04048 ribulose-bisphosphate carboxylase activase precursor - Arabidopsis thaliana >gi_16471_emb_CAA32429_ (X14212) rubisco activase (AA 1 - 473) [Arabidopsis thaliana]
Seq. No.	139060
Seq. ID	LIB23-059-Q1-E1-B4
Method	BLASTN
NCBI GI	g2924730
BLAST score	78
E value	2.0e-36
Match length	78
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPI7, complete sequence [Arabidopsis thaliana]
Seq. No.	139061
Seq. ID	LIB23-059-Q1-E1-B6
Method	BLASTX
NCBI GI	g3980411
BLAST score	332
E value	2.0e-31
Match length	66
% identity	100
NCBI Description	(AC004561) putative proline-rich protein [Arabidopsis thaliana]
Seq. No.	139062
Seq. ID	LIB23-059-Q1-E1-B7
Method	BLASTN
NCBI GI	g1655481
BLAST score	276

E value	1.0e-154
Match length	276
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for delta subunit of mitochondrial F1-ATPase, complete cds

Seq. No.	139063
Seq. ID	LIB23-059-Q1-E1-C1
Method	BLASTX
NCBI GI	g4512668
BLAST score	167
E value	4.0e-12
Match length	75
% identity	52
NCBI Description	(AC006931) unknown protein [Arabidopsis thaliana]

Seq. No.	139064
Seq. ID	LIB23-059-Q1-E1-C2
Method	BLASTN
NCBI GI	g3449327
BLAST score	161
E value	2.0e-85
Match length	282
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCA23, complete sequence [Arabidopsis thaliana]

Seq. No.	139065
Seq. ID	LIB23-059-Q1-E1-E6
Method	BLASTX
NCBI GI	g401169
BLAST score	267
E value	1.0e-23
Match length	51
% identity	100
NCBI Description	TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)

Seq. No.	139066
Seq. ID	LIB23-059-Q1-E1-E8
Method	BLASTN
NCBI GI	g2828183
BLAST score	117
E value	3.0e-59
Match length	287
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPL12, complete sequence [Arabidopsis thaliana]

Seq. No.	139067
Seq. ID	LIB23-059-Q1-E1-F1
Method	BLASTN
NCBI GI	g2618601
BLAST score	259
E value	1.0e-144
Match length	259
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MHJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	139068
Seq. ID	LIB23-059-Q1-E1-F2
Method	BLASTN
NCBI GI	g4713943
BLAST score	222
E value	1.0e-122
Match length	273
% identity	97
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8K14 sequence, complete sequence

Seq. No.	139069
Seq. ID	LIB23-059-Q1-E1-F4
Method	BLASTX
NCBI GI	g115767
BLAST score	524
E value	8.0e-54
Match length	95
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	139070
Seq. ID	LIB23-059-Q1-E1-F5
Method	BLASTX
NCBI GI	g400976
BLAST score	455
E value	9.0e-46
Match length	91
% identity	100
NCBI Description	RAS-RELATED PROTEIN RHA1 >gi_478671_pir__S23727 GTP-binding protein RHA1 - Arabidopsis thaliana >gi_16484_emb_CAA41863_ (X59152) RHA1 [Arabidopsis thaliana] >gi_397594_emb_CAA80534_ (Z22958) GTP-binding protein [Arabidopsis thaliana]

Seq. No.	139071
Seq. ID	LIB23-059-Q1-E1-F6
Method	BLASTX
NCBI GI	g464707
BLAST score	375
E value	2.0e-36
Match length	76
% identity	100
NCBI Description	40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal protein S18.A - Arabidopsis thaliana >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein

[Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]

Seq. No.	139072
Seq. ID	LIB23-059-Q1-E1-G1
Method	BLASTX
NCBI GI	g2306917
BLAST score	466
E value	5.0e-47
Match length	88
% identity	100
NCBI Description	(AF003728) plasma membrane intrinsic protein [Arabidopsis thaliana]

Seq. No.	139073
Seq. ID	LIB23-059-Q1-E1-G10
Method	BLASTX
NCBI GI	g115783
BLAST score	219
E value	2.0e-18
Match length	52
% identity	83
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	139074
Seq. ID	LIB23-059-Q1-E1-G12
Method	BLASTX
NCBI GI	g1703386
BLAST score	156
E value	6.0e-11
Match length	59
% identity	49
NCBI Description	ACETYLORNITHINE DEACETYLASE (ACETYLORNITHINASE) (AO) (N-ACETYLORNITHINASE) (NAO) >gi_763048 (U23957) N-acetylornithine deacetylase [Dictyostelium discoideum]

Seq. No.	139075
Seq. ID	LIB23-059-Q1-E1-G2
Method	BLASTX
NCBI GI	g4455273
BLAST score	484
E value	4.0e-49
Match length	95
% identity	100
NCBI Description	(AL035527) subtilisin proteinase-like [Arabidopsis thaliana]

Seq. No.	139076
Seq. ID	LIB23-059-Q1-E1-G3
Method	BLASTN
NCBI GI	g3355463
BLAST score	281
E value	1.0e-157
Match length	289
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139077
Seq. ID	LIB23-059-Q1-E1-G8
Method	BLASTN
NCBI GI	g3046856
BLAST score	148
E value	1.0e-77
Match length	277
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXI22, complete sequence [Arabidopsis thaliana]

Seq. No.	139078
Seq. ID	LIB23-059-Q1-E1-H12
Method	BLASTN
NCBI GI	g3241920
BLAST score	119
E value	1.0e-60
Match length	191
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAE1, complete sequence [Arabidopsis thaliana]

Seq. No.	139079
Seq. ID	LIB23-059-Q1-E1-H3
Method	BLASTX
NCBI GI	g4099092
BLAST score	480
E value	1.0e-48
Match length	90
% identity	100
NCBI Description	(U83179) unknown [Arabidopsis thaliana]

Seq. No.	139080
Seq. ID	LIB23-059-Q1-E1-H6
Method	BLASTX
NCBI GI	g2809246
BLAST score	284
E value	1.0e-25
Match length	95
% identity	56
NCBI Description	(AC002560) F24O1.15 [Arabidopsis thaliana]

Seq. No.	139081
Seq. ID	LIB23-059-Q1-E1-H8
Method	BLASTX
NCBI GI	g4417278

BLAST score	239
E value	2.0e-20
Match length	57
% identity	72
NCBI Description	(AC007019) hypothetical protein [Arabidopsis thaliana]

Seq. No.	139082
Seq. ID	LIB23-060-Q1-E1-A10
Method	BLASTN
NCBI GI	g2760173
BLAST score	257
E value	1.0e-143
Match length	273
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH19, complete sequence [Arabidopsis thaliana]

Seq. No.	139083
Seq. ID	LIB23-060-Q1-E1-A11
Method	BLASTX
NCBI GI	g4455210
BLAST score	267
E value	6.0e-24
Match length	73
% identity	78
NCBI Description	(AL035440) putative aspartate-tRNA ligase [Arabidopsis thaliana]

Seq. No.	139084
Seq. ID	LIB23-060-Q1-E1-A2
Method	BLASTN
NCBI GI	g2924733
BLAST score	231
E value	1.0e-127
Match length	313
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]

Seq. No.	139085
Seq. ID	LIB23-060-Q1-E1-B10
Method	BLASTX
NCBI GI	g1707412
BLAST score	245
E value	4.0e-21
Match length	68
% identity	60
NCBI Description	(X95906) Cleavage and Polyadenylation Specifity Factor protein [Bos taurus]

Seq. No.	139086
Seq. ID	LIB23-060-Q1-E1-B11
Method	BLASTX
NCBI GI	g1199804
BLAST score	386
E value	1.0e-37
Match length	73

% identity	100
NCBI Description	(X95639) transmembrane channel protein [Brassica oleracea]

Seq. No.	139087
Seq. ID	LIB23-060-Q1-E1-B9
Method	BLASTN
NCBI GI	g4539448
BLAST score	267
E value	1.0e-149
Match length	267
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T5C23 (ESSA project)

Seq. No.	139088
Seq. ID	LIB23-060-Q1-E1-C10
Method	BLASTX
NCBI GI	g1495251
BLAST score	236
E value	4.0e-20
Match length	47
% identity	94
NCBI Description	(Z70314) heat-shock protein [Arabidopsis thaliana]

Seq. No.	139089
Seq. ID	LIB23-060-Q1-E1-C11
Method	BLASTN
NCBI GI	g2274861
BLAST score	71
E value	5.0e-32
Match length	151
% identity	87
NCBI Description	Arabidopsis thaliana Sbe2.1 gene

Seq. No.	139090
Seq. ID	LIB23-060-Q1-E1-C5
Method	BLASTX
NCBI GI	g1161926
BLAST score	584
E value	1.0e-60
Match length	128
% identity	82
NCBI Description	(U34392) alpha-carboxyltransferase aCT-1 precursor [Glycine max]

Seq. No.	139091
Seq. ID	LIB23-060-Q1-E1-C9
Method	BLASTX
NCBI GI	g1174162
BLAST score	458
E value	4.0e-46
Match length	80
% identity	100
NCBI Description	(U44976) ubiquitin-conjugating enzyme [Arabidopsis thaliana] >gi_3746915 (AF091106) E2 ubiquitin-conjugating-like enzyme [Arabidopsis thaliana]

Seq. No.	139092
Seq. ID	LIB23-060-Q1-E1-D8
Method	BLASTX
NCBI GI	g2244765
BLAST score	168
E value	9.0e-12
Match length	136
% identity	19
NCBI Description	(Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No.	139093
Seq. ID	LIB23-060-Q1-E1-E10
Method	BLASTX
NCBI GI	g3158370
BLAST score	376
E value	2.0e-36
Match length	72
% identity	100
NCBI Description	(AF035382) catalase 3 [Arabidopsis thaliana]

Seq. No.	139094
Seq. ID	LIB23-060-Q1-E1-E11
Method	BLASTX
NCBI GI	g2459443
BLAST score	307
E value	2.0e-28
Match length	60
% identity	100
NCBI Description	(AC002332) putative NAD(P)-dependent cholesterol dehydrogenase [Arabidopsis thaliana]

Seq. No.	139095
Seq. ID	LIB23-060-Q1-E1-F10
Method	BLASTX
NCBI GI	g2146746
BLAST score	302
E value	8.0e-28
Match length	59
% identity	97
NCBI Description	protein kinase (EC 2.7.1.-) - Arabidopsis thaliana >gi_166819 (L05562) protein kinase [Arabidopsis thaliana]

Seq. No.	139096
Seq. ID	LIB23-060-Q1-E1-F3
Method	BLASTN
NCBI GI	g3184270
BLAST score	182
E value	7.0e-98
Match length	405
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T8K22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139097
Seq. ID	LIB23-060-Q1-E1-F9
Method	BLASTN
NCBI GI	g4263753

BLAST score	222
E value	1.0e-122
Match length	249
% identity	96
NCBI Description	Arabidopsis thaliana chromosome V map near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	139098
Seq. ID	LIB23-060-Q1-E1-G11
Method	BLASTX
NCBI GI	g4455351
BLAST score	199
E value	1.0e-15
Match length	68
% identity	54
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	139099
Seq. ID	LIB23-060-Q1-E1-G12
Method	BLASTX
NCBI GI	g4741952
BLAST score	372
E value	5.0e-36
Match length	71
% identity	100
NCBI Description	(AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No.	139100
Seq. ID	LIB23-060-Q1-E1-G2
Method	BLASTN
NCBI GI	g4376087
BLAST score	252
E value	1.0e-139
Match length	382
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	139101
Seq. ID	LIB23-060-Q1-E1-G9
Method	BLASTX
NCBI GI	g120667
BLAST score	349
E value	2.0e-33
Match length	68
% identity	96
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis thaliana >gi_166706 (M64116) cystolic glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No.	139102
Seq. ID	LIB23-060-Q1-E1-H11
Method	BLASTN

NCBI GI	g3894179
BLAST score	268
E value	1.0e-149
Match length	268
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F13H10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139103
Seq. ID	LIB23-060-Q1-E1-H3
Method	BLASTX
NCBI GI	g1173151
BLAST score	379
E value	1.0e-36
Match length	77
% identity	99
NCBI Description	DNA-DIRECTED RNA POLYMERASE BETA CHAIN >gi_629607_pir__S48842 DNA-directed RNA polymerase (EC 2.7.7.6) beta chain - white mustard chloroplast >gi_563343_emb_CAA57814_ (X82417) RNA polymerase subunit beta [Sinapis alba]

Seq. No.	139104
Seq. ID	LIB23-060-Q1-E1-H5
Method	BLASTX
NCBI GI	g2827663
BLAST score	165
E value	2.0e-11
Match length	89
% identity	8
NCBI Description	(AL021637) membrane-associated salt-inducible-like protein [Arabidopsis thaliana]

Seq. No.	139105
Seq. ID	LIB23-060-Q1-E1-H7
Method	BLASTX
NCBI GI	g4835225
BLAST score	442
E value	3.0e-44
Match length	84
% identity	99
NCBI Description	(AL049862) UTP-glucose glucosyltransferase like protein [Arabidopsis thaliana]

Seq. No.	139106
Seq. ID	LIB23-060-Q1-E1-H9
Method	BLASTX
NCBI GI	g3158370
BLAST score	457
E value	5.0e-46
Match length	91
% identity	98
NCBI Description	(AF035382) catalase 3 [Arabidopsis thaliana]

Seq. No.	139107
Seq. ID	LIB23-061-Q1-E1-A10
Method	BLASTN

NCBI GI	g2264312
BLAST score	129
E value	2.0e-66
Match length	200
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK16, complete sequence [Arabidopsis thaliana]

Seq. No.	139108
Seq. ID	LIB23-061-Q1-E1-A9
Method	BLASTN
NCBI GI	g2398848
BLAST score	125
E value	2.0e-64
Match length	125
% identity	100
NCBI Description	Arabidopsis thaliana SIG1 mRNA for plastid RNA polymerase sigma-subunit, complete cds

Seq. No.	139109
Seq. ID	LIB23-061-Q1-E1-B7
Method	BLASTN
NCBI GI	g2708736
BLAST score	251
E value	1.0e-139
Match length	275
% identity	97
NCBI Description	Arabidopsis thaliana BAC T13L16 from chromosome II, near 33 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	139110
Seq. ID	LIB23-061-Q1-E1-E3
Method	BLASTX
NCBI GI	g3894190
BLAST score	244
E value	8.0e-21
Match length	67
% identity	70
NCBI Description	(AC005662) putative RNA polymerase [Arabidopsis thaliana]

Seq. No.	139111
Seq. ID	LIB23-061-Q1-E1-F7
Method	BLASTN
NCBI GI	g4584387
BLAST score	94
E value	5.0e-46
Match length	98
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7 (ESSA project)

Seq. No.	139112
Seq. ID	LIB23-061-Q1-E1-H7
Method	BLASTX
NCBI GI	g4538947
BLAST score	277
E value	8.0e-25

Match length	77
% identity	36
NCBI Description	(AL049483) putative mitochondrial carrier protein [Arabidopsis thaliana]

Seq. No.	139113
Seq. ID	LIB23-061-Q1-E1-H9
Method	BLASTN
NCBI GI	g3293582
BLAST score	38
E value	6.0e-12
Match length	46
% identity	96
NCBI Description	Arabidopsis thaliana BAC T15F16

Seq. No.	139114
Seq. ID	LIB23-062-Q1-E1-A10
Method	BLASTX
NCBI GI	g2623298
BLAST score	525
E value	1.0e-53
Match length	134
% identity	79
NCBI Description	(AC002409) putative 4-alpha-glucanotransferase [Arabidopsis thaliana]

Seq. No.	139115
Seq. ID	LIB23-062-Q1-E1-A11
Method	BLASTX
NCBI GI	g2160188
BLAST score	153
E value	7.0e-58
Match length	118
% identity	98
NCBI Description	(AC000132) Similar to Vicia sucrose transport protein (gb_Z93774). [Arabidopsis thaliana]

Seq. No.	139116
Seq. ID	LIB23-062-Q1-E1-A5
Method	BLASTX
NCBI GI	g4586061
BLAST score	294
E value	4.0e-27
Match length	54
% identity	100
NCBI Description	(AC007020) putative BOP1 protein [Arabidopsis thaliana]

Seq. No.	139117
Seq. ID	LIB23-062-Q1-E1-B6
Method	BLASTX
NCBI GI	g4585976
BLAST score	439
E value	2.0e-43
Match length	140
% identity	63
NCBI Description	(AC005287) Unknown protein [Arabidopsis thaliana]

Seq. No.	139118
Seq. ID	LIB23-062-Q1-E1-C10
Method	BLASTX
NCBI GI	g1279640
BLAST score	319
E value	2.0e-29
Match length	93
% identity	60
NCBI Description	(X92204) NAM [Petunia x hybrida]

Seq. No.	139119
Seq. ID	LIB23-062-Q1-E1-C11
Method	BLASTN
NCBI GI	g2832667
BLAST score	282
E value	1.0e-157
Match length	338
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T10I14 (ESSAII project)

Seq. No.	139120
Seq. ID	LIB23-062-Q1-E1-C7
Method	BLASTN
NCBI GI	g3449318
BLAST score	423
E value	0.0e+00
Match length	423
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLF18, complete sequence [Arabidopsis thaliana]

Seq. No.	139121
Seq. ID	LIB23-062-Q1-E1-D7
Method	BLASTX
NCBI GI	g2271485
BLAST score	741
E value	6.0e-79
Match length	142
% identity	100
NCBI Description	(AF009647) arginine decarboxylase [Arabidopsis thaliana] >gi_3096940_emb_CAA18850.1_ (AL023094) arginine decarboxylase SPE2 [Arabidopsis thaliana]

Seq. No.	139122
Seq. ID	LIB23-062-Q1-E1-E10
Method	BLASTN
NCBI GI	g2656028
BLAST score	194
E value	1.0e-105
Match length	385
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNF13

Seq. No.	139123
Seq. ID	LIB23-062-Q1-E1-F9

Method	BLASTN
NCBI GI	g3033373
BLAST score	233
E value	1.0e-128
Match length	305
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F19I3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139124
Seq. ID	LIB23-063-Q1-E1-A1
Method	BLASTN
NCBI GI	g2924728
BLAST score	74
E value	2.0e-33
Match length	129
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXH1, complete sequence [Arabidopsis thaliana]

Seq. No.	139125
Seq. ID	LIB23-063-Q1-E1-A10
Method	BLASTX
NCBI GI	g1350768
BLAST score	390
E value	8.0e-38
Match length	93
% identity	84
NCBI Description	60S RIBOSOMAL PROTEIN L7A

Seq. No.	139126
Seq. ID	LIB23-063-Q1-E1-A11
Method	BLASTN
NCBI GI	g4580454
BLAST score	47
E value	2.0e-17
Match length	143
% identity	87
NCBI Description	Arabidopsis thaliana chromosome II BAC T2G17 genomic sequence, complete sequence

Seq. No.	139127
Seq. ID	LIB23-063-Q1-E1-A5
Method	BLASTN
NCBI GI	g4519190
BLAST score	323
E value	0.0e+00
Match length	323
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K6A12, complete sequence

Seq. No.	139128
Seq. ID	LIB23-063-Q1-E1-A9
Method	BLASTX
NCBI GI	g3461836
BLAST score	532

E value	2.0e-54
Match length	101
% identity	100
NCBI Description	(AC005315) putative protein kinase [Arabidopsis thaliana] >gi_3927841 (AC005727) putative protein kinase [Arabidopsis thaliana]

Seq. No.	139129
Seq. ID	LIB23-063-Q1-E1-B10
Method	BLASTX
NCBI GI	g1531762
BLAST score	195
E value	6.0e-15
Match length	51
% identity	75
NCBI Description	(Y07765) S-adenosylmethionine decarboxylase [Arabidopsis thaliana]

Seq. No.	139130
Seq. ID	LIB23-063-Q1-E1-B8
Method	BLASTN
NCBI GI	g2264306
BLAST score	164
E value	3.0e-87
Match length	315
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK5, complete sequence [Arabidopsis thaliana]

Seq. No.	139131
Seq. ID	LIB23-063-Q1-E1-D1
Method	BLASTX
NCBI GI	g3335332
BLAST score	417
E value	4.0e-41
Match length	78
% identity	100
NCBI Description	(AC004512) Contains similarity to S-receptor kinase gb_D88193 from Brassica rapa. [Arabidopsis thaliana]

Seq. No.	139132
Seq. ID	LIB23-063-Q1-E1-D9
Method	BLASTX
NCBI GI	g1946369
BLAST score	351
E value	3.0e-33
Match length	99
% identity	67
NCBI Description	(U93215) unknown protein [Arabidopsis thaliana]

Seq. No.	139133
Seq. ID	LIB23-063-Q1-E1-E11
Method	BLASTX
NCBI GI	g3309086
BLAST score	351
E value	3.0e-33
Match length	68

% identity	100
NCBI Description	(AF076253) calcineurin B-like protein 3 [Arabidopsis thaliana]

Seq. No.	139134
Seq. ID	LIB23-063-Q1-E1-G5
Method	BLASTX
NCBI GI	g2961358
BLAST score	676
E value	2.0e-71
Match length	133
% identity	100
NCBI Description	(AL022140) serine/threonine protein kinase like protein [Arabidopsis thaliana]

Seq. No.	139135
Seq. ID	LIB23-063-Q1-E1-H3
Method	BLASTN
NCBI GI	g3128136
BLAST score	152
E value	5.0e-80
Match length	381
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1F13, complete sequence [Arabidopsis thaliana]

Seq. No.	139136
Seq. ID	LIB23-063-Q1-E1-H5
Method	BLASTX
NCBI GI	g3287863
BLAST score	415
E value	9.0e-41
Match length	71
% identity	100
NCBI Description	PUTATIVE TRYPSIN INHIBITOR T01O24.29 PRECURSOR >gi_2288993 (AC002335) trypsin inhibitor isolog [Arabidopsis thaliana]

Seq. No.	139137
Seq. ID	LIB23-063-Q1-E1-H8
Method	BLASTN
NCBI GI	g2618599
BLAST score	373
E value	0.0e+00
Match length	373
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBD2, complete sequence [Arabidopsis thaliana]

Seq. No.	139138
Seq. ID	LIB23-064-Q1-E1-B12
Method	BLASTX
NCBI GI	g1172872
BLAST score	382
E value	5.0e-37
Match length	74
% identity	100
NCBI Description	CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718

	drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_ (D13042) thiol protease [Arabidopsis thaliana] >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]
Seq. No.	139139
Seq. ID	LIB23-064-Q1-E1-H11
Method	BLASTX
NCBI GI	g1800307
BLAST score	201
E value	6.0e-16
Match length	80
% identity	55
NCBI Description	(U83883) p105 coactivator [Rattus norvegicus]
Seq. No.	139140
Seq. ID	LIB23-065-Q1-E1-A2
Method	BLASTN
NCBI GI	g4558586
BLAST score	174
E value	2.0e-93
Match length	178
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T5I8 sequence, complete sequence
Seq. No.	139141
Seq. ID	LIB23-065-Q1-E1-A3
Method	BLASTX
NCBI GI	g266989
BLAST score	393
E value	2.0e-38
Match length	74
% identity	100
NCBI Description	GTP-BINDING PROTEIN SAR1B >gi_322517_pir__S28603 GTP-binding protein - Arabidopsis thaliana >gi_166734 (M95795) GTP-binding protein [Arabidopsis thaliana]
Seq. No.	139142
Seq. ID	LIB23-065-Q1-E1-A6
Method	BLASTN
NCBI GI	g4454022
BLAST score	231
E value	1.0e-127
Match length	239
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16 (ESSAII project)
Seq. No.	139143
Seq. ID	LIB23-065-Q1-E1-A7
Method	BLASTX
NCBI GI	g421836
BLAST score	278
E value	5.0e-25
Match length	57

% identity	100
NCBI Description	G-box-binding factor GF14 - Arabidopsis thaliana >gi_553040 (M96855) GF14 [Arabidopsis thaliana]
Seq. No.	139144
Seq. ID	LIB23-065-Q1-E1-A8
Method	BLASTX
NCBI GI	g2352923
BLAST score	352
E value	1.0e-33
Match length	91
% identity	79
NCBI Description	(AF012863) cytosolic glucose-6-phosphate dehydrogenase 2 [Petroselinum crispum]
Seq. No.	139145
Seq. ID	LIB23-065-Q1-E1-B2
Method	BLASTN
NCBI GI	g3985934
BLAST score	115
E value	5.0e-58
Match length	257
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJE7, complete sequence [Arabidopsis thaliana]
Seq. No.	139146
Seq. ID	LIB23-065-Q1-E1-B3
Method	BLASTN
NCBI GI	g2828183
BLAST score	277
E value	1.0e-154
Match length	277
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPL12, complete sequence [Arabidopsis thaliana]
Seq. No.	139147
Seq. ID	LIB23-065-Q1-E1-B4
Method	BLASTN
NCBI GI	g2245073
BLAST score	278
E value	1.0e-155
Match length	278
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No
Seq. No.	139148
Seq. ID	LIB23-065-Q1-E1-B6
Method	BLASTN
NCBI GI	g2564050
BLAST score	258
E value	1.0e-143
Match length	280
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUA22, complete sequence [Arabidopsis thaliana]

Seq. No.	139149
Seq. ID	LIB23-065-Q1-E1-B8
Method	BLASTX
NCBI GI	g4490329
BLAST score	199
E value	1.0e-15
Match length	85
% identity	53
NCBI Description	(AL035656) extensin-like protein [Arabidopsis thaliana]

Seq. No.	139150
Seq. ID	LIB23-065-Q1-E1-C7
Method	BLASTX
NCBI GI	g266989
BLAST score	385
E value	1.0e-37
Match length	73
% identity	100
NCBI Description	GTP-BINDING PROTEIN SAR1B >gi_322517_pir__S28603 GTP-binding protein - Arabidopsis thaliana >gi_166734 (M95795) GTP-binding protein [Arabidopsis thaliana]

Seq. No.	139151
Seq. ID	LIB23-065-Q1-E1-C8
Method	BLASTX
NCBI GI	g2795809
BLAST score	237
E value	3.0e-20
Match length	50
% identity	82
NCBI Description	(AC003674) putative expansin [Arabidopsis thaliana]

Seq. No.	139152
Seq. ID	LIB23-065-Q1-E1-D12
Method	BLASTX
NCBI GI	g2739389
BLAST score	392
E value	4.0e-38
Match length	125
% identity	21
NCBI Description	(AC002505) Cf-2.2 like protein [Arabidopsis thaliana]

Seq. No.	139153
Seq. ID	LIB23-065-Q1-E1-D3
Method	BLASTX
NCBI GI	g2213882
BLAST score	250
E value	1.0e-21
Match length	92
% identity	49
NCBI Description	(AF004165) 2-isopropylmalate synthase [Lycopersicon pennellii]

Seq. No.	139154
Seq. ID	LIB23-065-Q1-E1-D5

Method	BLASTX
NCBI GI	g4741948
BLAST score	399
E value	3.0e-39
Match length	76
% identity	100
NCBI Description	(AF134124) Lhcb2 protein [Arabidopsis thaliana]

Seq. No.	139155
Seq. ID	LIB23-065-Q1-E1-E1
Method	BLASTX
NCBI GI	g1709535
BLAST score	474
E value	6.0e-48
Match length	93
% identity	100
NCBI Description	DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE B (P5CS B) [CONTAINS: GLUTAMATE 5-KINASE (GAMMA-GLUTAMYL KINASE) (GK); GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMIALDE... >gi_887388_emb_CAA60447_ (X86778) pyrroline-5-carboxylate synthetase B [Arabidopsis thaliana] >gi_1669658_emb_CAA70527_ (Y09355) pyrroline-5-carboxlyate synthetase [Arabidopsis thaliana]

Seq. No.	139156
Seq. ID	LIB23-065-Q1-E1-E6
Method	BLASTX
NCBI GI	g3024526
BLAST score	311
E value	7.0e-29
Match length	62
% identity	100
NCBI Description	RAS-RELATED PROTEIN RAB11 >gi_2118459_pir__S59942 small GTP-binding protein Rab11 - Arabidopsis thaliana >gi_451860 (L18883) small GTP-binding protein [Arabidopsis thaliana]

Seq. No.	139157
Seq. ID	LIB23-065-Q1-E1-E7
Method	BLASTX
NCBI GI	g2213584
BLAST score	412
E value	1.0e-40
Match length	79
% identity	100
NCBI Description	(AC000348) T7N9.4 [Arabidopsis thaliana]

Seq. No.	139158
Seq. ID	LIB23-065-Q1-E1-E8
Method	BLASTX
NCBI GI	g3927836
BLAST score	270
E value	5.0e-24
Match length	74
% identity	66
NCBI Description	(AC005727) unknown protein [Arabidopsis thaliana]

Seq. No.	139159
Seq. ID	LIB23-065-Q1-E1-E9
Method	BLASTX
NCBI GI	g619747
BLAST score	360
E value	2.0e-34
Match length	70
% identity	100
NCBI Description	(U18968) phosphoribosylanthranilate isomerase [Arabidopsis thaliana]

Seq. No.	139160
Seq. ID	LIB23-065-Q1-E1-F10
Method	BLASTN
NCBI GI	g4757678
BLAST score	363
E value	0.0e+00
Match length	363
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC F9H16 genomic sequence, complete sequence

Seq. No.	139161
Seq. ID	LIB23-065-Q1-E1-F2
Method	BLASTN
NCBI GI	g4519193
BLAST score	173
E value	1.0e-92
Match length	281
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC11, complete sequence

Seq. No.	139162
Seq. ID	LIB23-065-Q1-E1-F4
Method	BLASTN
NCBI GI	g2529657
BLAST score	39
E value	1.0e-12
Match length	103
% identity	84
NCBI Description	Arabidopsis thaliana chromosome II BAC T30B22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139163
Seq. ID	LIB23-065-Q1-E1-F5
Method	BLASTX
NCBI GI	g3288821
BLAST score	312
E value	6.0e-29
Match length	74
% identity	80
NCBI Description	(AF063901) alanine:glyoxylate aminotransferase; transaminase [Arabidopsis thaliana] >gi_4733989_gb_AAD28669.1_AC007209_5 (AC007209) alanine-glyoxylate aminotransferase [Arabidopsis thaliana]

Seq. No.	139164
Seq. ID	LIB23-065-Q1-E1-F6
Method	BLASTX
NCBI GI	g3775987
BLAST score	463
E value	1.0e-46
Match length	93
% identity	100
NCBI Description	(AJ010457) RNA helicase [Arabidopsis thaliana]

Seq. No.	139165
Seq. ID	LIB23-065-Q1-E1-F8
Method	BLASTX
NCBI GI	g2829899
BLAST score	240
E value	2.0e-20
Match length	70
% identity	63
NCBI Description	(AC002311) similar to ripening-induced protein, gp_AJ001449_2465015 and major#latex protein, gp_X91961_1107495 [Arabidopsis thaliana]

Seq. No.	139166
Seq. ID	LIB23-065-Q1-E1-G1
Method	BLASTX
NCBI GI	g4680192
BLAST score	304
E value	5.0e-28
Match length	87
% identity	69
NCBI Description	(AF111710) hypothetical protein [Oryza sativa subsp. indica]

Seq. No.	139167
Seq. ID	LIB23-065-Q1-E1-G10
Method	BLASTN
NCBI GI	g4580365
BLAST score	160
E value	9.0e-85
Match length	372
% identity	97
NCBI Description	Arabidopsis thaliana chromosome I BAC F3F20 genomic sequence, complete sequence

Seq. No.	139168
Seq. ID	LIB23-065-Q1-E1-G2
Method	BLASTX
NCBI GI	g1346526
BLAST score	353
E value	9.0e-34
Match length	69
% identity	96
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_1076533_pir__S52218 methionine adenosyltransferase (EC 2.5.1.6) - garden pea >gi_609225_emb_CAA57581_ (X82077) methionine adenosyltransferase [Pisum sativum] >gi_609559

(L36681) S-adenosylmethionine synthase [Pisum sativum]

Seq. No.	139169
Seq. ID	LIB23-065-Q1-E1-G6
Method	BLASTX
NCBI GI	g2462738
BLAST score	186
E value	3.0e-14
Match length	47
% identity	98
NCBI Description	(AC002292) similar to "Mx" GTP binding proteins [Arabidopsis thaliana]

Seq. No.	139170
Seq. ID	LIB23-065-Q1-E1-G7
Method	BLASTN
NCBI GI	g633027
BLAST score	226
E value	1.0e-124
Match length	226
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for protein phosphatase 2C

Seq. No.	139171
Seq. ID	LIB23-065-Q1-E1-G8
Method	BLASTX
NCBI GI	g4753651
BLAST score	429
E value	1.0e-42
Match length	81
% identity	100
NCBI Description	(AL049751) ribosomal protein L13a like protein [Arabidopsis thaliana]

Seq. No.	139172
Seq. ID	LIB23-065-Q1-E1-G9
Method	BLASTX
NCBI GI	g2959767
BLAST score	530
E value	3.0e-54
Match length	121
% identity	85
NCBI Description	(AJ002584) AtMRP4 [Arabidopsis thaliana] >gi_3738292 (AC005309) glutathione-conjugate transporter AtMRP4 [Arabidopsis thaliana]

Seq. No.	139173
Seq. ID	LIB23-065-Q1-E1-H10
Method	BLASTN
NCBI GI	g2828278
BLAST score	34
E value	1.0e-09
Match length	66
% identity	85
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16 (ESSAII project)

Seq. No.	139174
Seq. ID	LIB23-065-Q1-E1-H2
Method	BLASTX
NCBI GI	g2506443
BLAST score	404
E value	9.0e-40
Match length	80
% identity	100
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi_2117520_pir__JQ1285 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde 3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_1402885_emb_CAA66816_ (X98130) glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) [Arabidopsis thaliana]

Seq. No.	139175
Seq. ID	LIB23-065-Q1-E1-H6
Method	BLASTN
NCBI GI	g4454447
BLAST score	40
E value	2.0e-13
Match length	68
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139176
Seq. ID	LIB23-066-Q1-E1-A2
Method	BLASTX
NCBI GI	g2194125
BLAST score	230
E value	4.0e-19
Match length	59
% identity	80
NCBI Description	(AC002062) ESTs gb_R30459,gb_N38441 come from this gene. [Arabidopsis thaliana]

Seq. No.	139177
Seq. ID	LIB23-066-Q1-E1-A6
Method	BLASTX
NCBI GI	g3142300
BLAST score	451
E value	5.0e-45
Match length	125
% identity	69
NCBI Description	(AC002411) Contains similarity to pre-mRNA processing protein PRP39 gb_L29224 from S. cerevisiae. ESTs gb_R64908 and gb_T88158, gb_N38703 and gb_AA651043 come from this gene. [Arabidopsis thaliana]

Seq. No.	139178
Seq. ID	LIB23-066-Q1-E1-B1
Method	BLASTX
NCBI GI	g4585977

BLAST score	410
E value	2.0e-40
Match length	89
% identity	80
NCBI Description	(AC005287) Unknown protein [Arabidopsis thaliana]

Seq. No.	139179
Seq. ID	LIB23-066-Q1-E1-B11
Method	BLASTX
NCBI GI	g115783
BLAST score	328
E value	1.0e-30
Match length	80
% identity	78
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	139180
Seq. ID	LIB23-066-Q1-E1-B3
Method	BLASTX
NCBI GI	g4049354
BLAST score	527
E value	5.0e-54
Match length	101
% identity	99
NCBI Description	(AL034567) glycine hydroxymethyltransferase (EC 2.1.2.1)-like protein [Arabidopsis thaliana]

Seq. No.	139181
Seq. ID	LIB23-066-Q1-E1-C5
Method	BLASTN
NCBI GI	g2623294
BLAST score	397
E value	0.0e+00
Match length	397
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T20B5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139182
Seq. ID	LIB23-066-Q1-E1-C8
Method	BLASTX
NCBI GI	g124224
BLAST score	176
E value	8.0e-13
Match length	41
% identity	80
NCBI Description	INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D) >gi_100345_pir__S21060 translation initiation factor eIF-5A - common tobacco >gi_19887_emb_CAA45105_ (X63543) eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]

Seq. No.	139183
Seq. ID	LIB23-066-Q1-E1-D7
Method	BLASTX

NCBI GI	g4584527
BLAST score	208
E value	1.0e-16
Match length	108
% identity	42
NCBI Description	(AL049607) putative protein [Arabidopsis thaliana]

Seq. No.	139184
Seq. ID	LIB23-066-Q1-E1-E9
Method	BLASTX
NCBI GI	g399091
BLAST score	391
E value	6.0e-38
Match length	101
% identity	78
NCBI Description	PYROPHOSPHATE-ENERGIZED VACUOLAR MEMBRANE PROTON PUMP (PYROPHOSPHATE-ENERGIZED INORGANIC PYROPHOSPHATASE) (H+-PPASE) >gi_282878_pir__A38230 inorganic pyrophosphatase (EC 3.6.1.1), H+-translocating pyrophosphate-energized - Arabidopsis thaliana >gi_166634 (M81892) vacuolar H+-phosphatase [Arabidopsis thaliana]

Seq. No.	139185
Seq. ID	LIB23-066-Q1-E1-H10
Method	BLASTN
NCBI GI	g2828278
BLAST score	230
E value	1.0e-126
Match length	322
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16 (ESSAII project)

Seq. No.	139186
Seq. ID	LIB23-066-Q1-E1-H11
Method	BLASTX
NCBI GI	g2894597
BLAST score	506
E value	2.0e-51
Match length	119
% identity	85
NCBI Description	(AL021889) bHLH protein - like [Arabidopsis thaliana]

Seq. No.	139187
Seq. ID	LIB23-067-Q1-E1-A7
Method	BLASTN
NCBI GI	g897676
BLAST score	118
E value	3.0e-60
Match length	118
% identity	100
NCBI Description	A.thaliana DNA for 40 kDa protein gene

Seq. No.	139188
Seq. ID	LIB23-067-Q1-E1-B1
Method	BLASTN
NCBI GI	g4757414

BLAST score	257
E value	1.0e-142
Match length	278
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYF24, complete sequence

Seq. No.	139189
Seq. ID	LIB23-067-Q1-E1-B3
Method	BLASTX
NCBI GI	g3281865
BLAST score	393
E value	4.0e-38
Match length	138
% identity	39
NCBI Description	(AL031004) putative protein [Arabidopsis thaliana]

Seq. No.	139190
Seq. ID	LIB23-067-Q1-E1-B5
Method	BLASTX
NCBI GI	g4337011
BLAST score	345
E value	5.0e-38
Match length	89
% identity	97
NCBI Description	(AF119572) zinc-binding peroxisomal integral membrane protein [Arabidopsis thaliana]

Seq. No.	139191
Seq. ID	LIB23-067-Q1-E1-C10
Method	BLASTX
NCBI GI	g1706918
BLAST score	251
E value	2.0e-21
Match length	95
% identity	56
NCBI Description	FLAVONOL SULFOTRANSFERASE-LIKE >gi_498647 (U10277) sulfotransferase-like flavonol [Flaveria bidentis]

Seq. No.	139192
Seq. ID	LIB23-067-Q1-E1-C9
Method	BLASTX
NCBI GI	g4106395
BLAST score	329
E value	9.0e-31
Match length	116
% identity	59
NCBI Description	(AF073744) raffinose synthase [Cucumis sativus]

Seq. No.	139193
Seq. ID	LIB23-067-Q1-E1-E3
Method	BLASTN
NCBI GI	g3763944
BLAST score	237
E value	1.0e-131
Match length	306
% identity	99

NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28A23 (ESSAII project)

Seq. No.	139194
Seq. ID	LIB23-067-Q1-E1-E4
Method	BLASTX
NCBI GI	g4467125
BLAST score	195
E value	4.0e-15
Match length	96
% identity	42
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]

Seq. No.	139195
Seq. ID	LIB23-067-Q1-E1-E7
Method	BLASTX
NCBI GI	g3513739
BLAST score	562
E value	5.0e-58
Match length	125
% identity	89
NCBI Description	(AF080118) Similar to uridine diphosphate glucose epimerase; F8M12.10 [Arabidopsis thaliana]

Seq. No.	139196
Seq. ID	LIB23-067-Q1-E1-F4
Method	BLASTX
NCBI GI	g3875004
BLAST score	276
E value	2.0e-24
Match length	85
% identity	35
NCBI Description	(Z81484) similar to multidrug resistance protein (p-glycoprotein) (2 domains); cDNA EST yk303b9.5 comes from this gene; cDNA EST yk303b9.3 comes from this gene [Caenorhabditis elegans] >gi_3879215_emb_CAB07855_ (Z93782) similar to multidrug resistance protein (p-glycoprotein) (2 domains); cDNA EST yk303b9.5 comes from this gene; cDNA EST yk303b9.3 comes from this gene [Caenorhabditis elegans]

Seq. No.	139197
Seq. ID	LIB23-067-Q1-E1-F7
Method	BLASTN
NCBI GI	g3510347
BLAST score	213
E value	1.0e-116
Match length	445
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]

Seq. No.	139198
Seq. ID	LIB23-067-Q1-E1-G6
Method	BLASTN
NCBI GI	g2760172
BLAST score	438
E value	0.0e+00

Match length	445
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUB3, complete sequence [Arabidopsis thaliana]

Seq. No.	139199
Seq. ID	LIB23-067-Q1-E1-H1
Method	BLASTX
NCBI GI	g4388834
BLAST score	230
E value	3.0e-19
Match length	101
% identity	50
NCBI Description	(AC006528) putative disease resistance protein RPP1, 3' partial [Arabidopsis thaliana]

Seq. No.	139200
Seq. ID	LIB23-068-Q1-E1-A3
Method	BLASTN
NCBI GI	g3241926
BLAST score	103
E value	4.0e-51
Match length	151
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSG15, complete sequence [Arabidopsis thaliana]

Seq. No.	139201
Seq. ID	LIB23-068-Q1-E1-B1
Method	BLASTX
NCBI GI	g4510373
BLAST score	235
E value	8.0e-20
Match length	60
% identity	68
NCBI Description	(AC007017) putative harpin-induced protein [Arabidopsis thaliana]

Seq. No.	139202
Seq. ID	LIB23-068-Q1-E1-C6
Method	BLASTX
NCBI GI	g2880051
BLAST score	385
E value	3.0e-37
Match length	109
% identity	72
NCBI Description	(AC002340) putative protein kinase [Arabidopsis thaliana]

Seq. No.	139203
Seq. ID	LIB23-068-Q1-E1-D9
Method	BLASTX
NCBI GI	g2244766
BLAST score	605
E value	4.0e-63
Match length	116
% identity	98
NCBI Description	(Z97335) glucosyltransferase [Arabidopsis thaliana]

Seq. No.	139204
Seq. ID	LIB23-068-Q1-E1-E12
Method	BLASTN
NCBI GI	g2924733
BLAST score	240
E value	1.0e-132
Match length	400
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]

Seq. No.	139205
Seq. ID	LIB23-068-Q1-E1-E8
Method	BLASTN
NCBI GI	g3510343
BLAST score	229
E value	1.0e-126
Match length	404
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJC20, complete sequence [Arabidopsis thaliana]

Seq. No.	139206
Seq. ID	LIB23-068-Q1-E1-F6
Method	BLASTN
NCBI GI	g3702722
BLAST score	298
E value	1.0e-167
Match length	301
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K12B20, complete sequence [Arabidopsis thaliana]

Seq. No.	139207
Seq. ID	LIB23-068-Q1-E1-G2
Method	BLASTX
NCBI GI	g4191777
BLAST score	392
E value	2.0e-38
Match length	80
% identity	90
NCBI Description	(AC005917) putative casein kinase I [Arabidopsis thaliana]

Seq. No.	139208
Seq. ID	LIB23-068-Q1-E1-H12
Method	BLASTN
NCBI GI	g2264304
BLAST score	320
E value	1.0e-180
Match length	414
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBG8, complete sequence [Arabidopsis thaliana]

Seq. No.	139209
Seq. ID	LIB23-069-Q1-E1-A9

Method	BLASTX
NCBI GI	g3158376
BLAST score	586
E value	7.0e-61
Match length	113
% identity	97
NCBI Description	(AF035385) unknown [Arabidopsis thaliana]

Seq. No.	139210
Seq. ID	LIB23-069-Q1-E1-B7
Method	BLASTX
NCBI GI	g3256035
BLAST score	210
E value	1.0e-16
Match length	72
% identity	56
NCBI Description	(Y14274) putative serine/threonine protein kinase [Sorghum bicolor]

Seq. No.	139211
Seq. ID	LIB23-069-Q1-E1-B8
Method	BLASTN
NCBI GI	g4585952
BLAST score	178
E value	2.0e-95
Match length	421
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F26F24, complete sequence

Seq. No.	139212
Seq. ID	LIB23-069-Q1-E1-B9
Method	BLASTX
NCBI GI	g2369714
BLAST score	512
E value	3.0e-52
Match length	111
% identity	91
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	139213
Seq. ID	LIB23-069-Q1-E1-C4
Method	BLASTN
NCBI GI	g4159707
BLAST score	230
E value	1.0e-126
Match length	442
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJK13, complete sequence

Seq. No.	139214
Seq. ID	LIB23-069-Q1-E1-C5
Method	BLASTN
NCBI GI	g3869068
BLAST score	141
E value	2.0e-73

Match length	291
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC16, complete sequence [Arabidopsis thaliana]

Seq. No.	139215
Seq. ID	LIB23-069-Q1-E1-E5
Method	BLASTN
NCBI GI	g457397
BLAST score	264
E value	1.0e-147
Match length	264
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for MAP kinase, complete cds

Seq. No.	139216
Seq. ID	LIB23-069-Q1-E1-F7
Method	BLASTN
NCBI GI	g2160155
BLAST score	142
E value	5.0e-74
Match length	360
% identity	100
NCBI Description	Sequence of BAC F21M12 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	139217
Seq. ID	LIB23-069-Q1-E1-F9
Method	BLASTX
NCBI GI	g3036807
BLAST score	630
E value	6.0e-66
Match length	136
% identity	91
NCBI Description	(AL022373) putative protein [Arabidopsis thaliana]

Seq. No.	139218
Seq. ID	LIB23-069-Q1-E1-G3
Method	BLASTN
NCBI GI	g3980374
BLAST score	336
E value	0.0e+00
Match length	352
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F16P2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139219
Seq. ID	LIB23-069-Q1-E1-G9
Method	BLASTN
NCBI GI	g4115370
BLAST score	354
E value	0.0e+00
Match length	372
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F27D4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139220
Seq. ID	LIB23-070-Q1-E1-B1
Method	BLASTN
NCBI GI	g2827644
BLAST score	158
E value	1.0e-83
Match length	317
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F18F4 (ESSAII project)

Seq. No.	139221
Seq. ID	LIB23-070-Q1-E1-B11
Method	BLASTX
NCBI GI	g4538967
BLAST score	148
E value	2.0e-09
Match length	62
% identity	60
NCBI Description	(AL049488) major intrinsic protein (MIP)-like [Arabidopsis thaliana]

Seq. No.	139222
Seq. ID	LIB23-070-Q1-E1-C5
Method	BLASTN
NCBI GI	g3688169
BLAST score	371
E value	0.0e+00
Match length	371
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F26P21 (ESSAII project)

Seq. No.	139223
Seq. ID	LIB23-070-Q1-E1-C8
Method	BLASTN
NCBI GI	g4510338
BLAST score	358
E value	0.0e+00
Match length	358
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F2H17 genomic sequence, complete sequence

Seq. No.	139224
Seq. ID	LIB23-070-Q1-E1-D4
Method	BLASTX
NCBI GI	g3746059
BLAST score	483
E value	1.0e-48
Match length	130
% identity	65
NCBI Description	(AC005311) putative cysteinyl-tRNA synthetase [Arabidopsis thaliana] >gi_4432812_gb_AAD20662_ (AC006593) putative cysteinyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.	139225
Seq. ID	LIB23-070-Q1-E1-D7
Method	BLASTN
NCBI GI	g1669656
BLAST score	389
E value	0.0e+00
Match length	389
% identity	100
NCBI Description	A.thaliana CER3-like gene

Seq. No.	139226
Seq. ID	LIB23-070-Q1-E1-E5
Method	BLASTX
NCBI GI	g115804
BLAST score	198
E value	1.0e-15
Match length	37
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-25) (LHCP) >gi_72730_pir__CDPJ25 chlorophyll a/b-binding protein 25 precursor - petunia >gi_20483_emb_CAA26211_ (X02358) cab 25 precursor polypeptide (aa -33 to 233) [Petunia sp.]

Seq. No.	139227
Seq. ID	LIB23-070-Q1-E1-F10
Method	BLASTN
NCBI GI	g4159702
BLAST score	249
E value	1.0e-138
Match length	359
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2N11, complete sequence

Seq. No.	139228
Seq. ID	LIB23-070-Q1-E1-F12
Method	BLASTX
NCBI GI	g3249064
BLAST score	576
E value	1.0e-59
Match length	126
% identity	89
NCBI Description	(AC004473) Strong similarity to trehalose-6-phosphate synthase homolog gb_2245136 from A. thaliana chromosome 4 contig gb_Z97344. [Arabidopsis thaliana]

Seq. No.	139229
Seq. ID	LIB23-070-Q1-E1-H9
Method	BLASTN
NCBI GI	g4038029
BLAST score	60
E value	5.0e-25
Match length	218
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC F5O4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139230
Seq. ID	LIB23-071-Q1-E1-A1
Method	BLASTN
NCBI GI	g4567259
BLAST score	202
E value	1.0e-110
Match length	334
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F3K23 genomic sequence, complete sequence

Seq. No.	139231
Seq. ID	LIB23-071-Q1-E1-A3
Method	BLASTN
NCBI GI	g2288979
BLAST score	302
E value	1.0e-169
Match length	306
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T01O24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139232
Seq. ID	LIB23-071-Q1-E1-B2
Method	BLASTX
NCBI GI	g136636
BLAST score	380
E value	1.0e-36
Match length	69
% identity	100
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1) >gi_1076424_pir__S43781 ubiquitin-conjugating enzyme UBC1 - Arabidopsis thaliana >gi_442594_pdb_1AAK_ Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) >gi_2981894_pdb_2AAK_ Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana >gi_166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi_431260 (L19351) ubiquitin conjugating enzyme [Arabidopsis thaliana]

Seq. No.	139233
Seq. ID	LIB23-071-Q1-E1-D2
Method	BLASTN
NCBI GI	g2828186
BLAST score	264
E value	1.0e-147
Match length	264
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18I23, complete sequence [Arabidopsis thaliana]

Seq. No.	139234
Seq. ID	LIB23-071-Q1-E1-F2
Method	BLASTX
NCBI GI	g2146745
BLAST score	376

E value	3.0e-36
Match length	90
% identity	81
NCBI Description	protein kinase (EC 2.7.1.-) - Arabidopsis thaliana >gi_642132_dbj_BAA08215_ (D45354) protein kinase [Arabidopsis thaliana]

Seq. No.	139235
Seq. ID	LIB23-071-Q1-E1-F6
Method	BLASTX
NCBI GI	g4539009
BLAST score	654
E value	8.0e-69
Match length	120
% identity	100
NCBI Description	(AL049481) putative protein [Arabidopsis thaliana]

Seq. No.	139236
Seq. ID	LIB23-071-Q1-E1-H9
Method	BLASTX
NCBI GI	g3850574
BLAST score	252
E value	1.0e-21
Match length	98
% identity	54
NCBI Description	(AC005278) Strong similarity to T08I13.7 gi_2275201 unknown protein from Arabidopsis thaliana BAC gb_AC002337. EST gb_Z17450 comes from this gene. [Arabidopsis thaliana]

Seq. No.	139237
Seq. ID	LIB23-072-Q1-E1-A11
Method	BLASTN
NCBI GI	g1167960
BLAST score	42
E value	3.0e-14
Match length	365
% identity	33
NCBI Description	Arabidopsis thaliana extensin (atExt1) gene, complete cds

Seq. No.	139238
Seq. ID	LIB23-072-Q1-E1-A12
Method	BLASTN
NCBI GI	g4539402
BLAST score	360
E value	0.0e+00
Match length	360
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F7L13 (ESSA project)

Seq. No.	139239
Seq. ID	LIB23-072-Q1-E1-A9
Method	BLASTN
NCBI GI	g4589415
BLAST score	161
E value	3.0e-85
Match length	353

% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K14A3, complete sequence

Seq. No.	139240
Seq. ID	LIB23-072-Q1-E1-B12
Method	BLASTN
NCBI GI	g1931636
BLAST score	274
E value	1.0e-153
Match length	361
% identity	100
NCBI Description	Arabidopsis thaliana BAC T19D16 genomic sequence

Seq. No.	139241
Seq. ID	LIB23-072-Q1-E1-B4
Method	BLASTN
NCBI GI	g166657
BLAST score	209
E value	1.0e-114
Match length	233
% identity	97
NCBI Description	Arabidopsis thaliana Ccr1 mRNA, complete cds

Seq. No.	139242
Seq. ID	LIB23-072-Q1-E1-B7
Method	BLASTN
NCBI GI	g4510338
BLAST score	453
E value	0.0e+00
Match length	453
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F2H17 genomic sequence, complete sequence

Seq. No.	139243
Seq. ID	LIB23-072-Q1-E1-C4
Method	BLASTX
NCBI GI	g3851711
BLAST score	261
E value	1.0e-22
Match length	139
% identity	42
NCBI Description	(AF102265) N-acetylglucosamine-phosphate mutase [Homo sapiens]

Seq. No.	139244
Seq. ID	LIB23-072-Q1-E1-D12
Method	BLASTX
NCBI GI	g3540196
BLAST score	307
E value	3.0e-28
Match length	103
% identity	61
NCBI Description	(AC004260) Putative amp-binding protein [Arabidopsis thaliana]

Seq. No.	139245
Seq. ID	LIB23-072-Q1-E1-D4
Method	BLASTN
NCBI GI	g1209241
BLAST score	400
E value	0.0e+00
Match length	424
% identity	98
NCBI Description	Arabidopsis thaliana metallothionein mRNA sequence

Seq. No.	139246
Seq. ID	LIB23-072-Q1-E1-D6
Method	BLASTN
NCBI GI	g4191771
BLAST score	449
E value	0.0e+00
Match length	449
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F3P11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139247
Seq. ID	LIB23-072-Q1-E1-E7
Method	BLASTX
NCBI GI	g4049353
BLAST score	502
E value	6.0e-51
Match length	142
% identity	60
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	139248
Seq. ID	LIB23-072-Q1-E1-E8
Method	BLASTX
NCBI GI	g2499606
BLAST score	443
E value	5.0e-44
Match length	103
% identity	83
NCBI Description	MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 2 (MAP KINASE 2) (ATMPK2) >gi_533281_dbj_BAA03536_ (D14714) ATMPK2 [Arabidopsis thaliana]

Seq. No.	139249
Seq. ID	LIB23-072-Q1-E1-F8
Method	BLASTX
NCBI GI	g2245066
BLAST score	789
E value	1.0e-84
Match length	146
% identity	100
NCBI Description	(Z97342) Beta-Amylase [Arabidopsis thaliana]

Seq. No.	139250
Seq. ID	LIB23-072-Q1-E1-G4
Method	BLASTN
NCBI GI	g4335744

BLAST score	130
E value	7.0e-67
Match length	253
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T4M8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139251
Seq. ID	LIB23-072-Q1-E1-H12
Method	BLASTN
NCBI GI	g4757410
BLAST score	367
E value	0.0e+00
Match length	388
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MVE11, complete sequence

Seq. No.	139252
Seq. ID	LIB23-072-Q1-E1-H8
Method	BLASTX
NCBI GI	g4006934
BLAST score	265
E value	2.0e-23
Match length	66
% identity	76
NCBI Description	(AJ012571) glutathione transferase [Arabidopsis thaliana]

Seq. No.	139253
Seq. ID	LIB23-073-Q1-E1-A10
Method	BLASTX
NCBI GI	g2129550
BLAST score	391
E value	6.0e-38
Match length	122
% identity	63
NCBI Description	calcium-dependent protein kinase (EC 2.7.1.-) CDPK6 - Arabidopsis thaliana >gi_2129554_pir__S71901 calcium-dependent protein kinase 6 - Arabidopsis thaliana >gi_836940 (U20623) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_836944 (U20625) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_4454034_emb_CAA23031.1_ (AL035394) calcium-dependent protein kinase (CDPK6) [Arabidopsis thaliana]

Seq. No.	139254
Seq. ID	LIB23-073-Q1-E1-B8
Method	BLASTN
NCBI GI	g3241939
BLAST score	299
E value	1.0e-168
Match length	299
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T26J13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 139255

Seq. ID	LIB23-073-Q1-E1-C10
Method	BLASTN
NCBI GI	g4185120
BLAST score	365
E value	0.0e+00
Match length	390
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F5F19 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139256
Seq. ID	LIB23-073-Q1-E1-C6
Method	BLASTX
NCBI GI	g2708752
BLAST score	386
E value	1.0e-37
Match length	94
% identity	82
NCBI Description	(AC003952) putative histidine kinase [Arabidopsis thaliana]

Seq. No.	139257
Seq. ID	LIB23-073-Q1-E1-D10
Method	BLASTX
NCBI GI	g1172599
BLAST score	658
E value	3.0e-69
Match length	127
% identity	99
NCBI Description	PROTEASOME COMPONENT C5 (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C5) (TAS-F22/FAFP98) >gi_600387_emb_CAA47753_ (X67338) proteosome subunit [Arabidopsis thaliana]

Seq. No.	139258
Seq. ID	LIB23-073-Q1-E1-D2
Method	BLASTX
NCBI GI	g421989
BLAST score	243
E value	1.0e-20
Match length	92
% identity	52
NCBI Description	serpin - barley >gi_19071_emb_CAA78822_ (Z15116) protein zx [Hordeum vulgare] >gi_444778_prf__1908213A protein Zx [Hordeum vulgare]

Seq. No.	139259
Seq. ID	LIB23-073-Q1-E1-D8
Method	BLASTX
NCBI GI	g2244859
BLAST score	417
E value	5.0e-41
Match length	109
% identity	79
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	139260
Seq. ID	LIB23-073-Q1-E1-D9

Method	BLASTN
NCBI GI	g4049332
BLAST score	147
E value	3.0e-77
Match length	155
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F8B4 (ESSAII project)

Seq. No.	139261
Seq. ID	LIB23-073-Q1-E1-E11
Method	BLASTX
NCBI GI	g3746071
BLAST score	610
E value	1.0e-63
Match length	120
% identity	100
NCBI Description	(AC005311) putative GTP-binding protein [Arabidopsis thaliana]

Seq. No.	139262
Seq. ID	LIB23-073-Q1-E1-E12
Method	BLASTN
NCBI GI	g2351069
BLAST score	255
E value	1.0e-141
Match length	372
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSH12, complete sequence [Arabidopsis thaliana]

Seq. No.	139263
Seq. ID	LIB23-073-Q1-E1-E4
Method	BLASTN
NCBI GI	g4218109
BLAST score	161
E value	2.0e-85
Match length	304
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F16A16 (ESSAII project)

Seq. No.	139264
Seq. ID	LIB23-073-Q1-E1-E5
Method	BLASTX
NCBI GI	g4587550
BLAST score	287
E value	6.0e-26
Match length	100
% identity	54
NCBI Description	(AC006577) EST gb_R64848 comes from this gene. [Arabidopsis thaliana]

Seq. No.	139265
Seq. ID	LIB23-073-Q1-E1-E7
Method	BLASTX
NCBI GI	g3024526

BLAST score	394
E value	2.0e-38
Match length	78
% identity	100
NCBI Description	RAS-RELATED PROTEIN RAB11 >gi_2118459_pir__S59942 small GTP-binding protein Rab11 - Arabidopsis thaliana >gi_451860 (L18883) small GTP-binding protein [Arabidopsis thaliana]

Seq. No.	139266
Seq. ID	LIB23-073-Q1-E1-E9
Method	BLASTX
NCBI GI	g1922937
BLAST score	669
E value	1.0e-70
Match length	129
% identity	99
NCBI Description	(AC000106) Similar to Glycine SRC2 (gb_AB000130). ESTs gb_H76869,gb_T21700,gb_ATTS5089 come from this gene. [Arabidopsis thaliana]

Seq. No.	139267
Seq. ID	LIB23-073-Q1-E1-F7
Method	BLASTN
NCBI GI	g3128136
BLAST score	192
E value	1.0e-104
Match length	373
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1F13, complete sequence [Arabidopsis thaliana]

Seq. No.	139268
Seq. ID	LIB23-073-Q1-E1-G7
Method	BLASTX
NCBI GI	g3043432
BLAST score	149
E value	6.0e-10
Match length	34
% identity	82
NCBI Description	(AJ005348) Ubiquitin conjugating enzyme [Cicer arietinum]

Seq. No.	139269
Seq. ID	LIB23-073-Q1-E1-H1
Method	BLASTN
NCBI GI	g4454022
BLAST score	340
E value	0.0e+00
Match length	374
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16 (ESSAII project)

Seq. No.	139270
Seq. ID	LIB23-073-Q1-E1-H9
Method	BLASTN
NCBI GI	g4467131
BLAST score	389

E value	0.0e+00
Match length	389
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20M13 (ESSA project)

Seq. No.	139271
Seq. ID	LIB23-074-Q1-E1-A4
Method	BLASTX
NCBI GI	g1402912
BLAST score	147
E value	6.0e-10
Match length	28
% identity	100
NCBI Description	(X98317) peroxidase [Arabidopsis thaliana]

Seq. No.	139272
Seq. ID	LIB23-074-Q1-E1-B6
Method	BLASTX
NCBI GI	g2828267
BLAST score	432
E value	9.0e-43
Match length	108
% identity	81
NCBI Description	(Y14044) geranylgeranyl reductase [Arabidopsis thaliana]

Seq. No.	139273
Seq. ID	LIB23-074-Q1-E1-C8
Method	BLASTX
NCBI GI	g3983125
BLAST score	542
E value	1.0e-55
Match length	130
% identity	82
NCBI Description	(AF097648) phosphate/triose-phosphate translocator precursor [Arabidopsis thaliana]

Seq. No.	139274
Seq. ID	LIB23-074-Q1-E1-D8
Method	BLASTX
NCBI GI	g4220481
BLAST score	162
E value	4.0e-11
Match length	72
% identity	47
NCBI Description	(AC006069) unknown protein [Arabidopsis thaliana]

Seq. No.	139275
Seq. ID	LIB23-074-Q1-E1-E10
Method	BLASTX
NCBI GI	g3123908
BLAST score	200
E value	8.0e-16
Match length	52
% identity	63
NCBI Description	(AF038392) pre-mRNA splicing factor [Homo sapiens]

Seq. No.	139276
Seq. ID	LIB23-074-Q1-E1-E2
Method	BLASTX
NCBI GI	g3879145
BLAST score	179
E value	5.0e-13
Match length	123
% identity	33
NCBI Description	(Z93386) predicted using Genefinder; Similarity to Human placenta (DIFF33) protein (TR:Q13530); cDNA EST yk198a11.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	139277
Seq. ID	LIB23-074-Q1-E1-E5
Method	BLASTN
NCBI GI	g3869075
BLAST score	346
E value	0.0e+00
Match length	385
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence [Arabidopsis thaliana]

Seq. No.	139278
Seq. ID	LIB23-074-Q1-E1-G8
Method	BLASTX
NCBI GI	g3688799
BLAST score	612
E value	7.0e-64
Match length	123
% identity	99
NCBI Description	(AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis thaliana]

Seq. No.	139279
Seq. ID	LIB23-074-Q1-E1-H5
Method	BLASTX
NCBI GI	g115783
BLAST score	590
E value	3.0e-61
Match length	112
% identity	99
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	139280
Seq. ID	LIB23-075-Q1-E1-B9
Method	BLASTX
NCBI GI	g2244765
BLAST score	549
E value	1.0e-56
Match length	110
% identity	54
NCBI Description	(Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No.	139281
Seq. ID	LIB23-075-Q1-E1-C11
Method	BLASTN
NCBI GI	g3176693
BLAST score	74
E value	6.0e-34
Match length	134
% identity	89
NCBI Description	Arabidopsis thaliana chromosome I BAC T27I1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139282
Seq. ID	LIB23-075-Q1-E1-C9
Method	BLASTN
NCBI GI	g304114
BLAST score	51
E value	6.0e-20
Match length	195
% identity	91
NCBI Description	Arabidopsis thaliana thioglucosidase mRNA, complete cds

Seq. No.	139283
Seq. ID	LIB23-075-Q1-E1-G11
Method	BLASTX
NCBI GI	g3242708
BLAST score	292
E value	2.0e-26
Match length	103
% identity	55
NCBI Description	(AC003040) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	139284
Seq. ID	LIB23-075-Q1-E1-H11
Method	BLASTN
NCBI GI	g3128136
BLAST score	78
E value	2.0e-36
Match length	110
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1F13, complete sequence [Arabidopsis thaliana]

Seq. No.	139285
Seq. ID	LIB24-001-Q1-E1-B2
Method	BLASTX
NCBI GI	g4263777
BLAST score	307
E value	3.0e-28
Match length	89
% identity	69
NCBI Description	(AC006068) putative serine carboxypeptidase II [Arabidopsis thaliana] >gi_4510391_gb_AAD21479.1_ (AC007017) putative serine carboxypeptidase II [Arabidopsis thaliana]

Seq. No.	139286
Seq. ID	LIB24-001-Q1-E1-B4

Method	BLASTX
NCBI GI	g2499609
BLAST score	468
E value	6.0e-47
Match length	91
% identity	99
NCBI Description	MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 5 (MAP KINASE 5) (ATMPK5) >gi_629546_pir__S40471 mitogen-activated protein kinase 5 (EC 2.7.1.-) - Arabidopsis thaliana >gi_457402_dbj_BAA04868_ (D21841) MAP kinase [Arabidopsis thaliana]

Seq. No.	139287
Seq. ID	LIB24-001-Q1-E1-B5
Method	BLASTX
NCBI GI	g1351184
BLAST score	311
E value	1.0e-28
Match length	94
% identity	56
NCBI Description	TYROSYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR (TYROSINE--TRNA LIGASE) (TYRRS) >gi_2133198_pir__S59733 tyrosine--tRNA ligase (EC 6.1.1.1), mitochondrial - yeast (Saccharomyces cerevisiae) >gi_825503 (L42333) tyrosyl-tRNA synthetase [Saccharomyces cerevisiae] >gi_1151229 (U43281) Lpg11p [Saccharomyces cerevisiae]

Seq. No.	139288
Seq. ID	LIB24-001-Q1-E1-B9
Method	BLASTN
NCBI GI	g2828184
BLAST score	297
E value	1.0e-166
Match length	390
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSN9, complete sequence [Arabidopsis thaliana]

Seq. No.	139289
Seq. ID	LIB24-001-Q1-E1-D5
Method	BLASTX
NCBI GI	g2341034
BLAST score	550
E value	1.0e-56
Match length	110
% identity	100
NCBI Description	(AC000104) F19P19.13 [Arabidopsis thaliana]

Seq. No.	139290
Seq. ID	LIB24-001-Q1-E1-D6
Method	BLASTN
NCBI GI	g2062153
BLAST score	402
E value	0.0e+00
Match length	402
% identity	100
NCBI Description	Arabidopsis thaliana chromosome III BAC T02O04 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139291
Seq. ID	LIB24-001-Q1-E1-E5
Method	BLASTX
NCBI GI	g3337367
BLAST score	237
E value	7.0e-20
Match length	100
% identity	41
NCBI Description	(AC004481) hypothetical protein [Arabidopsis thaliana]

Seq. No.	139292
Seq. ID	LIB24-001-Q1-E1-F12
Method	BLASTX
NCBI GI	g4455333
BLAST score	269
E value	1.0e-23
Match length	89
% identity	56
NCBI Description	(AL035525) hypothetical protein [Arabidopsis thaliana]

Seq. No.	139293
Seq. ID	LIB24-001-Q1-E1-F8
Method	BLASTN
NCBI GI	g2262155
BLAST score	360
E value	0.0e+00
Match length	363
% identity	100
NCBI Description	DNA sequence of Arabidopsis thaliana BAC F5J6 from chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No.	139294
Seq. ID	LIB24-001-Q1-E1-G6
Method	BLASTX
NCBI GI	g137465
BLAST score	150
E value	7.0e-18
Match length	70
% identity	76
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT B (V-ATPASE B SUBUNIT) (V-ATPASE 57 KD SUBUNIT) >gi_81637_pir__A31886 H+-transporting ATPase (EC 3.6.1.35) 57K chain - Arabidopsis thaliana >gi_166627 (J04185) nucleotide-binding subunit of vacuolar ATPase [Arabidopsis thaliana]

Seq. No.	139295
Seq. ID	LIB24-001-Q1-E1-H12
Method	BLASTN
NCBI GI	g3985958
BLAST score	215
E value	1.0e-117
Match length	317
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZN1, complete sequence [Arabidopsis thaliana]

Seq. No.	139296
Seq. ID	LIB24-002-Q1-E1-A9
Method	BLASTX
NCBI GI	g3913379
BLAST score	518
E value	1.0e-66
Match length	126
% identity	99
NCBI Description	CRYPTOCHROME 2 APOPROTEIN (BLUE LIGHT PHOTORECEPTOR) >gi_1857038 (U43397) cryptochrome 2 apoprotein [Arabidopsis thaliana]

Seq. No.	139297
Seq. ID	LIB24-002-Q1-E1-B9
Method	BLASTX
NCBI GI	g2851508
BLAST score	166
E value	4.0e-12
Match length	33
% identity	94
NCBI Description	60S RIBOSOMAL PROTEIN L21 >gi_2160162 (AC000132) Similar to ribosomal protein L21 (gb_L38826). ESTs gb_AA395597,gb_ATTS5197 come from this gene. [Arabidopsis thaliana] >gi_3482935 (AC003970) Putative ribosomal protein L21 [Arabidopsis thaliana]

Seq. No.	139298
Seq. ID	LIB24-002-Q1-E1-D1
Method	BLASTN
NCBI GI	g2351062
BLAST score	144
E value	3.0e-75
Match length	272
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAH20, complete sequence [Arabidopsis thaliana]

Seq. No.	139299
Seq. ID	LIB24-002-Q1-E1-D3
Method	BLASTX
NCBI GI	g2648032
BLAST score	468
E value	5.0e-47
Match length	113
% identity	81
NCBI Description	(AJ001374) alpha-glucosidase [Solanum tuberosum]

Seq. No.	139300
Seq. ID	LIB24-002-Q1-E1-D8
Method	BLASTN
NCBI GI	g4757388
BLAST score	279
E value	1.0e-155
Match length	411
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

F15L12, complete sequence

Seq. No.	139301
Seq. ID	LIB24-002-Q1-E1-D9
Method	BLASTN
NCBI GI	g4193383
BLAST score	333
E value	0.0e+00
Match length	382
% identity	67
NCBI Description	Arabidopsis thaliana ribosomal protein S27 (ARS27A) gene, complete cds

Seq. No.	139302
Seq. ID	LIB24-002-Q1-E1-E2
Method	BLASTN
NCBI GI	g2337888
BLAST score	265
E value	1.0e-147
Match length	273
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14J16, complete sequence [Arabidopsis thaliana]

Seq. No.	139303
Seq. ID	LIB24-002-Q1-E1-E7
Method	BLASTX
NCBI GI	g4206196
BLAST score	520
E value	4.0e-53
Match length	96
% identity	100
NCBI Description	(AF071527) hypothetical protein [Arabidopsis thaliana]

Seq. No.	139304
Seq. ID	LIB24-002-Q1-E1-H1
Method	BLASTX
NCBI GI	g2136141
BLAST score	316
E value	2.0e-29
Match length	94
% identity	62
NCBI Description	serine C-palmitoyltransferase (EC 2.3.1.50) Lcb2 chain - human (fragment)

Seq. No.	139305
Seq. ID	LIB24-002-Q1-E1-H11
Method	BLASTX
NCBI GI	g4539423
BLAST score	392
E value	4.0e-38
Match length	82
% identity	98
NCBI Description	(AL049171) pyrophosphate-dependent phosphofructo-1-kinase [Arabidopsis thaliana]

Seq. No. 139306

Seq. ID	LIB24-003-Q1-E1-B1
Method	BLASTX
NCBI GI	g3080434
BLAST score	178
E value	4.0e-13
Match length	50
% identity	66
NCBI Description	(AL022605) putative gamma-glutamyltransferase [Arabidopsis thaliana]

Seq. No.	139307
Seq. ID	LIB24-003-Q1-E1-B6
Method	BLASTX
NCBI GI	g2154715
BLAST score	145
E value	2.0e-09
Match length	82
% identity	44
NCBI Description	(Y09418) CDPK-related protein kinase [Arabidopsis thaliana]

Seq. No.	139308
Seq. ID	LIB24-003-Q1-E1-B7
Method	BLASTX
NCBI GI	g2136800
BLAST score	219
E value	9.0e-18
Match length	83
% identity	54
NCBI Description	polyA binding protein II - bovine >gi_1051125_emb_CAA62006_ (X89969) polyA binding protein II [Bos taurus]

Seq. No.	139309
Seq. ID	LIB24-003-Q1-E1-D4
Method	BLASTN
NCBI GI	g4757396
BLAST score	207
E value	1.0e-113
Match length	249
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K8A10, complete sequence

Seq. No.	139310
Seq. ID	LIB24-003-Q1-E1-D5
Method	BLASTX
NCBI GI	g4263796
BLAST score	345
E value	1.0e-32
Match length	93
% identity	71
NCBI Description	(AC006068) hypothetical protein [Arabidopsis thaliana]

Seq. No.	139311
Seq. ID	LIB24-003-Q1-E1-D6
Method	BLASTX
NCBI GI	g132102
BLAST score	237

E value	4.0e-20
Match length	45
% identity	100
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR (RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B2 precursor - Arabidopsis thaliana >gi_16194_emb_CAA32701_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	139312
Seq. ID	LIB24-003-Q1-E1-E8
Method	BLASTX
NCBI GI	g3478700
BLAST score	304
E value	8.0e-28
Match length	75
% identity	81
NCBI Description	(AF034387) AFT protein [Arabidopsis thaliana]

Seq. No.	139313
Seq. ID	LIB24-003-Q1-E1-H9
Method	BLASTX
NCBI GI	g2494898
BLAST score	370
E value	1.0e-35
Match length	112
% identity	35
NCBI Description	PERIODIC TRYPTOPHAN PROTEIN 2 HOMOLOG >gi_1545982 (U53346) PWP2H protein [Homo sapiens] >gi_1737066 (U56085) periodic tryptophan protein 2 [Homo sapiens] >gi_1737072 (U56089) periodic tryptophan protein 2 [Homo sapiens]

Seq. No.	139314
Seq. ID	LIB24-004-Q1-E1-A4
Method	BLASTN
NCBI GI	g4725940
BLAST score	171
E value	2.0e-91
Match length	231
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T1P17 (ESSA project)

Seq. No.	139315
Seq. ID	LIB24-004-Q1-E1-C6
Method	BLASTX
NCBI GI	g480450
BLAST score	391
E value	6.0e-38
Match length	93
% identity	87
NCBI Description	ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis thaliana >gi_402552_emb_CAA49506_ (X69880) ketol-acid reductoisomerase [Arabidopsis thaliana]

Seq. No. 139316

Seq. ID	LIB24-004-Q1-E1-D1
Method	BLASTN
NCBI GI	g3063438
BLAST score	268
E value	1.0e-149
Match length	392
% identity	99
NCBI Description	Complete sequence of Arabidopsis F22013, complete sequence [Arabidopsis thaliana]

Seq. No.	139317
Seq. ID	LIB24-004-Q1-E1-E4
Method	BLASTX
NCBI GI	g2129727
BLAST score	234
E value	9.0e-20
Match length	88
% identity	60
NCBI Description	RNA-binding protein 37 - Arabidopsis thaliana >gi_1174153 (U44134) RNA-binding protein [Arabidopsis thaliana]

Seq. No.	139318
Seq. ID	LIB24-004-Q1-E1-E7
Method	BLASTX
NCBI GI	g2129727
BLAST score	234
E value	1.0e-19
Match length	88
% identity	60
NCBI Description	RNA-binding protein 37 - Arabidopsis thaliana >gi_1174153 (U44134) RNA-binding protein [Arabidopsis thaliana]

Seq. No.	139319
Seq. ID	LIB24-004-Q1-E1-F11
Method	BLASTX
NCBI GI	g2505874
BLAST score	265
E value	3.0e-23
Match length	125
% identity	44
NCBI Description	(Y12776) putative kinase [Arabidopsis thaliana]

Seq. No.	139320
Seq. ID	LIB24-004-Q1-E1-F2
Method	BLASTX
NCBI GI	g4589488
BLAST score	185
E value	3.0e-14
Match length	68
% identity	50
NCBI Description	(AB023145) KIAA0928 protein [Homo sapiens]

Seq. No.	139321
Seq. ID	LIB24-004-Q1-E1-G11
Method	BLASTX
NCBI GI	g2961371
BLAST score	206

E value	2.0e-16
Match length	78
% identity	56
NCBI Description	(AL022141) hypothetical protein (fragment) [Arabidopsis thaliana]

Seq. No.	139322
Seq. ID	LIB24-004-Q1-E1-G7
Method	BLASTX
NCBI GI	g166708
BLAST score	501
E value	8.0e-51
Match length	99
% identity	100
NCBI Description	(M64118) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No.	139323
Seq. ID	LIB24-004-Q1-E1-H5
Method	BLASTX
NCBI GI	g3123264
BLAST score	212
E value	3.0e-17
Match length	45
% identity	96
NCBI Description	60S RIBOSOMAL PROTEIN L27 >gi_2244857_emb_CAB10279_ (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	139324
Seq. ID	LIB24-005-Q1-E1-A12
Method	BLASTN
NCBI GI	g2494106
BLAST score	156
E value	2.0e-82
Match length	355
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139325
Seq. ID	LIB24-005-Q1-E1-A3
Method	BLASTN
NCBI GI	g3869075
BLAST score	139
E value	3.0e-72
Match length	341
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence [Arabidopsis thaliana]

Seq. No.	139326
Seq. ID	LIB24-005-Q1-E1-A6
Method	BLASTX
NCBI GI	g3834310
BLAST score	203
E value	2.0e-16
Match length	38

% identity	100
NCBI Description	(AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD gb_D83004 from Homo sapiens. ESTs gb_T88233, gb_Z24464, gb_N37265, gb_H36151, gb_Z34711, gb_AA040983, and gb_T22122 come from this gene. [Arabidopsis thaliana]

Seq. No.	139327
Seq. ID	LIB24-005-Q1-E1-B7
Method	BLASTX
NCBI GI	g4467152
BLAST score	605
E value	8.0e-66
Match length	128
% identity	97
NCBI Description	(AL035540) putative protein [Arabidopsis thaliana]

Seq. No.	139328
Seq. ID	LIB24-005-Q1-E1-C5
Method	BLASTN
NCBI GI	g2828180
BLAST score	202
E value	1.0e-110
Match length	365
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDK4, complete sequence [Arabidopsis thaliana]

Seq. No.	139329
Seq. ID	LIB24-005-Q1-E1-D1
Method	BLASTX
NCBI GI	g419812
BLAST score	297
E value	6.0e-27
Match length	129
% identity	45
NCBI Description	crm1+ protein - fission yeast (Schizosaccharomyces pombe)

Seq. No.	139330
Seq. ID	LIB24-005-Q1-E1-D5
Method	BLASTN
NCBI GI	g4008005
BLAST score	65
E value	1.0e-28
Match length	125
% identity	88
NCBI Description	Arabidopsis thaliana receptor-like protein kinase (RKL1) gene, complete cds

Seq. No.	139331
Seq. ID	LIB24-005-Q1-E1-F3
Method	BLASTX
NCBI GI	g2392895
BLAST score	543
E value	5.0e-56
Match length	102
% identity	100
NCBI Description	(AF017056) brassinosteroid insensitive 1 [Arabidopsis

thaliana]

Seq. No.	139332
Seq. ID	LIB24-005-Q1-E1-G12
Method	BLASTX
NCBI GI	g4580519
BLAST score	690
E value	5.0e-73
Match length	136
% identity	99
NCBI Description	(AF036303) scarecrow-like 6 [Arabidopsis thaliana]

Seq. No.	139333
Seq. ID	LIB24-005-Q1-E1-H10
Method	BLASTX
NCBI GI	g4581207
BLAST score	127
E value	8.0e-39
Match length	108
% identity	81
NCBI Description	(Y17914) cyclic nucleotide and calmodulin-regulated ion channel [Arabidopsis thaliana]

Seq. No.	139334
Seq. ID	LIB24-005-Q1-E1-H2
Method	BLASTX
NCBI GI	g4758418
BLAST score	163
E value	1.0e-11
Match length	87
% identity	43
NCBI Description	guanylate binding protein 2, interferon-inducible >gi_1169868_sp_P32456_GBP2_HUMAN INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 2 (GUANINE NUCLEOTIDE-BINDING PROTEIN 2) >gi_2135319_pir__S70524 guanine nucleotide-binding protein 2 - human >gi_829177 (M55543) guanylate binding protein isoform II [Homo sapiens]

Seq. No.	139335
Seq. ID	LIB24-006-Q1-E1-A1
Method	BLASTN
NCBI GI	g2618599
BLAST score	66
E value	1.0e-28
Match length	185
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBD2, complete sequence [Arabidopsis thaliana]

Seq. No.	139336
Seq. ID	LIB24-006-Q1-E1-A11
Method	BLASTN
NCBI GI	g2264314
BLAST score	159
E value	4.0e-84
Match length	404
% identity	100

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQK4, complete sequence [Arabidopsis thaliana]
Seq. No.	139337
Seq. ID	LIB24-006-Q1-E1-A2
Method	BLASTX
NCBI GI	g282963
BLAST score	366
E value	5.0e-35
Match length	74
% identity	82
NCBI Description	transforming protein (myb) homolog (clone myb.Ph2) - garden petunia >gi_20561_emb_CAA78387_ (Z13997) protein 2 [Petunia x hybrida]
Seq. No.	139338
Seq. ID	LIB24-006-Q1-E1-A6
Method	BLASTX
NCBI GI	g3075394
BLAST score	705
E value	9.0e-75
Match length	135
% identity	100
NCBI Description	(AC004484) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana] >gi_3559809_emb_CAA09311_ (AJ010713) fiddlehead protein [Arabidopsis thaliana]
Seq. No.	139339
Seq. ID	LIB24-006-Q1-E1-B11
Method	BLASTN
NCBI GI	g3522932
BLAST score	210
E value	1.0e-114
Match length	389
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	139340
Seq. ID	LIB24-006-Q1-E1-B5
Method	BLASTX
NCBI GI	g2956690
BLAST score	413
E value	2.0e-40
Match length	110
% identity	57
NCBI Description	(AJ223306) PSBY [Arabidopsis thaliana] >gi_3414928 (AF079800) PsbY precursor [Arabidopsis thaliana]
Seq. No.	139341
Seq. ID	LIB24-006-Q1-E1-B8
Method	BLASTX
NCBI GI	g3776573
BLAST score	269
E value	1.0e-23
Match length	100
% identity	55

NCBI Description	(AC005388) Similar to nodulins and lipase homolog F14J9.5 gi_3482914 from Arabidopsis thaliana BAC gb_AC003970. Alternate first exon from 72258 to 72509. [Arabidopsis thaliana]
Seq. No.	139342
Seq. ID	LIB24-006-Q1-E1-C7
Method	BLASTX
NCBI GI	g544424
BLAST score	441
E value	8.0e-44
Match length	85
% identity	100
NCBI Description	GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi_419755_pir__S30147 glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana >gi_16301_emb_CAA78711_ (Z14987) glycine rich protein [Arabidopsis thaliana] >gi_166837 (L00648) RNA-binding protein [Arabidopsis thaliana] >gi_4567224_gb_AAD23639.1_AC007119_5 (AC007119) glycine-rich RNA binding protein 7 [Arabidopsis thaliana]
Seq. No.	139343
Seq. ID	LIB24-006-Q1-E1-D11
Method	BLASTN
NCBI GI	g4249393
BLAST score	260
E value	1.0e-144
Match length	384
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T9J23 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	139344
Seq. ID	LIB24-006-Q1-E1-D2
Method	BLASTN
NCBI GI	g4325336
BLAST score	400
E value	0.0e+00
Match length	408
% identity	100
NCBI Description	Arabidopsis thaliana BAC F15P23
Seq. No.	139345
Seq. ID	LIB24-006-Q1-E1-D6
Method	BLASTX
NCBI GI	g4539343
BLAST score	453
E value	3.0e-45
Match length	137
% identity	74
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]
Seq. No.	139346
Seq. ID	LIB24-006-Q1-E1-D7
Method	BLASTX
NCBI GI	g2651316
BLAST score	473

E value	1.0e-47
Match length	95
% identity	100
NCBI Description	(AC002336) unknown protein [Arabidopsis thaliana]

Seq. No.	139347
Seq. ID	LIB24-006-Q1-E1-D8
Method	BLASTX
NCBI GI	g4056502
BLAST score	442
E value	6.0e-44
Match length	91
% identity	100
NCBI Description	(AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]

Seq. No.	139348
Seq. ID	LIB24-006-Q1-E1-E1
Method	BLASTN
NCBI GI	g4680765
BLAST score	141
E value	2.0e-73
Match length	407
% identity	99
NCBI Description	Arabidopsis thaliana BAC F14I23 from chromosome V near 69 cM, complete sequence

Seq. No.	139349
Seq. ID	LIB24-006-Q1-E1-E10
Method	BLASTN
NCBI GI	g4757392
BLAST score	163
E value	7.0e-87
Match length	163
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K14A17, complete sequence

Seq. No.	139350
Seq. ID	LIB24-006-Q1-E1-E12
Method	BLASTN
NCBI GI	g4587641
BLAST score	205
E value	1.0e-111
Match length	424
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No.	139351
Seq. ID	LIB24-006-Q1-E1-E5
Method	BLASTN
NCBI GI	g4220632
BLAST score	327
E value	0.0e+00
Match length	385
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K6M13, complete sequence [Arabidopsis thaliana]

Seq. No.	139352
Seq. ID	LIB24-006-Q1-E1-E8
Method	BLASTX
NCBI GI	g4510345
BLAST score	386
E value	2.0e-37
Match length	72
% identity	100
NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]

Seq. No.	139353
Seq. ID	LIB24-006-Q1-E1-F1
Method	BLASTX
NCBI GI	g2275216
BLAST score	250
E value	2.0e-21
Match length	64
% identity	75
NCBI Description	(AC002337) cytochrome c oxidase Vc subunit isolog [Arabidopsis thaliana]

Seq. No.	139354
Seq. ID	LIB24-006-Q1-E1-F10
Method	BLASTX
NCBI GI	g267077
BLAST score	709
E value	3.0e-75
Match length	131
% identity	100
NCBI Description	TUBULIN BETA-5 CHAIN >gi_320186_pir__JQ1589 tubulin beta-5 chain - Arabidopsis thaliana >gi_166902 (M84702) beta-5 tubulin [Arabidopsis thaliana]

Seq. No.	139355
Seq. ID	LIB24-006-Q1-E1-F7
Method	BLASTN
NCBI GI	g4567237
BLAST score	206
E value	1.0e-112
Match length	354
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T22F11 genomic sequence, complete sequence

Seq. No.	139356
Seq. ID	LIB24-006-Q1-E1-F8
Method	BLASTX
NCBI GI	g1652745
BLAST score	262
E value	8.0e-23
Match length	98
% identity	50
NCBI Description	(D90908) hypothetical protein [Synechocystis sp.]

Seq. No.	139357

Seq. ID	LIB24-006-Q1-E1-G1
Method	BLASTX
NCBI GI	g4531443
BLAST score	395
E value	2.0e-38
Match length	117
% identity	72
NCBI Description	(AC006224) putative 50s ribosomal protein L3 [Arabidopsis thaliana]

Seq. No.	139358
Seq. ID	LIB24-006-Q1-E1-G10
Method	BLASTN
NCBI GI	g2760164
BLAST score	374
E value	0.0e+00
Match length	395
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18P6, complete sequence [Arabidopsis thaliana]

Seq. No.	139359
Seq. ID	LIB24-006-Q1-E1-G2
Method	BLASTN
NCBI GI	g4220643
BLAST score	359
E value	0.0e+00
Match length	359
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD22, complete sequence [Arabidopsis thaliana]

Seq. No.	139360
Seq. ID	LIB24-006-Q1-E1-G5
Method	BLASTN
NCBI GI	g4056476
BLAST score	414
E value	0.0e+00
Match length	414
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F3G5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139361
Seq. ID	LIB24-006-Q1-E1-G7
Method	BLASTN
NCBI GI	g2337888
BLAST score	361
E value	0.0e+00
Match length	419
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14J16, complete sequence [Arabidopsis thaliana]

Seq. No.	139362
Seq. ID	LIB24-006-Q1-E1-H11
Method	BLASTX

NCBI GI	g421826
BLAST score	328
E value	8.0e-31
Match length	65
% identity	100
NCBI Description	chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis thaliana]

Seq. No.	139363
Seq. ID	LIB24-006-Q1-E1-H3
Method	BLASTN
NCBI GI	g3176693
BLAST score	274
E value	1.0e-152
Match length	414
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC T27I1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139364
Seq. ID	LIB24-007-Q1-E1-B3
Method	BLASTN
NCBI GI	g4678371
BLAST score	361
E value	0.0e+00
Match length	382
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T6G15 (ESSA project)

Seq. No.	139365
Seq. ID	LIB24-007-Q1-E1-B5
Method	BLASTN
NCBI GI	g4455262
BLAST score	84
E value	5.0e-40
Match length	88
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22 (ESSAII project)

Seq. No.	139366
Seq. ID	LIB24-007-Q1-E1-C3
Method	BLASTN
NCBI GI	g2760316
BLAST score	117
E value	4.0e-59
Match length	358
% identity	98
NCBI Description	The sequence of BAC F1N21 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	139367
Seq. ID	LIB24-007-Q1-E1-F5
Method	BLASTX
NCBI GI	g99660

BLAST score	369
E value	1.0e-35
Match length	91
% identity	78
NCBI Description	S-locus-specific glycoprotein SLR1 precursor - Arabidopsis thaliana >gi_246209_bbs_84925 (S84921) S-locus related protein SLR1 homolog=AtS1 [Arabidopsis thaliana, Peptide, 439 aa] [Arabidopsis thaliana]

Seq. No.	139368
Seq. ID	LIB24-007-Q1-E1-F8
Method	BLASTX
NCBI GI	g4371280
BLAST score	275
E value	2.0e-24
Match length	103
% identity	57
NCBI Description	(AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No.	139369
Seq. ID	LIB24-007-Q1-E1-G1
Method	BLASTN
NCBI GI	g4454447
BLAST score	100
E value	7.0e-49
Match length	415
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139370
Seq. ID	LIB24-007-Q1-E1-G5
Method	BLASTN
NCBI GI	g3461810
BLAST score	110
E value	5.0e-55
Match length	274
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T17M13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139371
Seq. ID	LIB24-008-Q1-E1-C3
Method	BLASTX
NCBI GI	g3551954
BLAST score	176
E value	6.0e-13
Match length	73
% identity	45
NCBI Description	(AF082030) senescence-associated protein 5 [Hemerocallis hybrid cultivar]

Seq. No.	139372
Seq. ID	LIB24-008-Q1-E1-D10
Method	BLASTN
NCBI GI	g4691223
BLAST score	199

E value	1.0e-108
Match length	207
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15 (ESSA project)

Seq. No.	139373
Seq. ID	LIB24-008-Q1-E1-D11
Method	BLASTN
NCBI GI	g3702315
BLAST score	268
E value	1.0e-149
Match length	363
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T3F17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139374
Seq. ID	LIB24-008-Q1-E1-F1
Method	BLASTX
NCBI GI	g2129578
BLAST score	608
E value	2.0e-63
Match length	119
% identity	98
NCBI Description	dTDP-glucose 4-6-dehydratases homolog - Arabidopsis thaliana >gi_928932_emb_CAA89205_ (Z49239) homolog of dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana] >gi_1585435_prf__2124427B diamide resistance gene [Arabidopsis thaliana]

Seq. No.	139375
Seq. ID	LIB24-008-Q1-E1-F6
Method	BLASTN
NCBI GI	g3548797
BLAST score	370
E value	0.0e+00
Match length	370
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T18E12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139376
Seq. ID	LIB24-008-Q1-E1-F8
Method	BLASTX
NCBI GI	g4218120
BLAST score	376
E value	3.0e-36
Match length	118
% identity	61
NCBI Description	(AL035353) Proline-rich APG-like protein [Arabidopsis thaliana]

Seq. No.	139377
Seq. ID	LIB24-008-Q1-E1-G1
Method	BLASTX
NCBI GI	g1730512

BLAST score	365
E value	5.0e-35
Match length	112
% identity	71
NCBI Description	PHOSPHOGLYCERATE KINASE, CHLOROPLAST >gi_2129669_pir__S71368 phosphoglycerate kinase - Arabidopsis thaliana (fragment) >gi_1022805 (U37701) phosphoglycerate kinase [Arabidopsis thaliana]

Seq. No.	139378
Seq. ID	LIB24-008-Q1-E1-G9
Method	BLASTN
NCBI GI	g4699904
BLAST score	368
E value	0.0e+00
Match length	368
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F1E22, complete sequence

Seq. No.	139379
Seq. ID	LIB24-008-Q1-E1-H10
Method	BLASTN
NCBI GI	g2760164
BLAST score	172
E value	3.0e-92
Match length	172
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18P6, complete sequence [Arabidopsis thaliana]

Seq. No.	139380
Seq. ID	LIB24-008-Q1-E1-H2
Method	BLASTX
NCBI GI	g3193287
BLAST score	75
E value	4.0e-21
Match length	85
% identity	67
NCBI Description	(AF069298) Arabidopsis predicted protein of unknown function T10P11.19 (GB:AC002330) [Arabidopsis thaliana]

Seq. No.	139381
Seq. ID	LIB24-008-Q1-E1-H5
Method	BLASTN
NCBI GI	g4455168
BLAST score	364
E value	0.0e+00
Match length	395
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)

Seq. No.	139382
Seq. ID	LIB24-008-Q1-E1-H9
Method	BLASTN
NCBI GI	g2435510

BLAST score	278
E value	1.0e-155
Match length	401
% identity	100
NCBI Description	Arabidopsis thaliana BAC TM017A05

Seq. No.	139383
Seq. ID	LIB24-009-Q1-E1-A1
Method	BLASTN
NCBI GI	g4468801
BLAST score	160
E value	7.0e-85
Match length	195
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6G17 (ESSA project)

Seq. No.	139384
Seq. ID	LIB24-009-Q1-E1-A10
Method	BLASTN
NCBI GI	g2262097
BLAST score	200
E value	1.0e-109
Match length	200
% identity	100
NCBI Description	Arabidopsis thaliana chromosome IV BAC T19F6 genomic sequence, complete sequence

Seq. No.	139385
Seq. ID	LIB24-009-Q1-E1-A12
Method	BLASTX
NCBI GI	g2829881
BLAST score	160
E value	7.0e-11
Match length	77
% identity	48
NCBI Description	(AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	139386
Seq. ID	LIB24-009-Q1-E1-A8
Method	BLASTN
NCBI GI	g2191126
BLAST score	160
E value	5.0e-85
Match length	188
% identity	96
NCBI Description	Arabidopsis thaliana BAC IG002N01

Seq. No.	139387
Seq. ID	LIB24-009-Q1-E1-D6
Method	BLASTN
NCBI GI	g3821780
BLAST score	35
E value	7.0e-11
Match length	36
% identity	60
NCBI Description	Xenopus laevis cDNA clone 27A6-1

09604769 - 040000

Seq. No.	139388
Seq. ID	LIB24-009-Q1-E1-E11
Method	BLASTX
NCBI GI	g4263722
BLAST score	347
E value	6.0e-33
Match length	78
% identity	78
NCBI Description	(AC006223) putative glucan synthase [Arabidopsis thaliana]

Seq. No.	139389
Seq. ID	LIB24-009-Q1-E1-F4
Method	BLASTX
NCBI GI	g2244946
BLAST score	396
E value	6.0e-39
Match length	80
% identity	96
NCBI Description	(Z97339) unnamed protein product [Arabidopsis thaliana] >gi_2326344_emb_CAA72072_ (Y11187) G14587-6 [Arabidopsis thaliana]

Seq. No.	139390
Seq. ID	LIB24-009-Q1-E1-H1
Method	BLASTX
NCBI GI	g4581116
BLAST score	541
E value	9.0e-56
Match length	102
% identity	100
NCBI Description	(AC005825) putative beta-galactosidase [Arabidopsis thaliana]

Seq. No.	139391
Seq. ID	LIB24-010-Q1-E1-D2
Method	BLASTX
NCBI GI	g2213583
BLAST score	350
E value	3.0e-33
Match length	105
% identity	76
NCBI Description	(AC000348) T7N9.3 [Arabidopsis thaliana]

Seq. No.	139392
Seq. ID	LIB24-010-Q1-E1-F1
Method	BLASTN
NCBI GI	g3426033
BLAST score	305
E value	1.0e-171
Match length	419
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F12C20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139393
Seq. ID	LIB24-010-Q1-E1-F10

Method	BLASTX
NCBI GI	g3402672
BLAST score	288
E value	3.0e-26
Match length	80
% identity	65
NCBI Description	(AC004697) putative white protein [Arabidopsis thaliana]

Seq. No.	139394
Seq. ID	LIB24-010-Q1-E1-F2
Method	BLASTX
NCBI GI	g132677
BLAST score	254
E value	2.0e-22
Match length	55
% identity	93
NCBI Description	50S RIBOSOMAL PROTEIN L15, CHLOROPLAST PRECURSOR (CL15) >gi_71241_pir__R5MUL5 ribosomal protein L15 precursor, chloroplast - Arabidopsis thaliana >gi_16497_emb_CAA77593_ (Z11508) Plastid ribosomal protein CL15 [Arabidopsis thaliana]

Seq. No.	139395
Seq. ID	LIB24-010-Q1-E1-G12
Method	BLASTX
NCBI GI	g3738310
BLAST score	434
E value	4.0e-43
Match length	104
% identity	82
NCBI Description	(AC005309) putative nuclear protein [Arabidopsis thaliana]

Seq. No.	139396
Seq. ID	LIB24-011-Q1-E1-A6
Method	BLASTX
NCBI GI	g1710581
BLAST score	616
E value	3.0e-64
Match length	125
% identity	96
NCBI Description	60S RIBOSOMAL PROTEIN L9 >gi_2129720_pir__S71255 ribosomal protein L9 - Arabidopsis thaliana >gi_1107489_emb_CAA63024_ (X91958) 60S ribosomal protein L9 [Arabidopsis thaliana]

Seq. No.	139397
Seq. ID	LIB24-011-Q1-E1-B2
Method	BLASTN
NCBI GI	g4432811
BLAST score	314
E value	1.0e-176
Match length	318
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F16D14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139398
Seq. ID	LIB24-011-Q1-E1-B7

Method	BLASTN
NCBI GI	g3600045
BLAST score	167
E value	7.0e-89
Match length	338
% identity	100
NCBI Description	Arabidopsis thaliana BAC F2P3

Seq. No.	139399
Seq. ID	LIB24-011-Q1-E1-D1
Method	BLASTX
NCBI GI	g3273743
BLAST score	620
E value	9.0e-65
Match length	118
% identity	100
NCBI Description	(AF057357) lipid transfer protein 2 precursor [Arabidopsis thaliana] >gi_3786019 (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	139400
Seq. ID	LIB24-011-Q1-E1-D10
Method	BLASTN
NCBI GI	g4510323
BLAST score	51
E value	4.0e-20
Match length	87
% identity	90
NCBI Description	Arabidopsis thaliana BAC T7B11 from chromosome IV near 10 cM, complete sequence

Seq. No.	139401
Seq. ID	LIB24-011-Q1-E1-D11
Method	BLASTX
NCBI GI	g1351272
BLAST score	157
E value	4.0e-11
Match length	29
% identity	100
NCBI Description	TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_414550 (U02949) cytosolic triose phosphate isomerase [Arabidopsis thaliana] >gi_742408_prf__2009415A triose phosphate isomerase [Arabidopsis thaliana]

Seq. No.	139402
Seq. ID	LIB24-011-Q1-E1-D4
Method	BLASTN
NCBI GI	g4589419
BLAST score	159
E value	3.0e-84
Match length	381
% identity	74
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2I5, complete sequence

Seq. No.	139403
Seq. ID	LIB24-011-Q1-E1-E1

Method	BLASTN
NCBI GI	g3063438
BLAST score	151
E value	2.0e-79
Match length	381
% identity	99
NCBI Description	Complete sequence of Arabidopsis F22013, complete sequence [Arabidopsis thaliana]

Seq. No.	139404
Seq. ID	LIB24-011-Q1-E1-E7
Method	BLASTN
NCBI GI	g1905875
BLAST score	287
E value	1.0e-160
Match length	291
% identity	100
NCBI Description	Arabidopsis thaliana biotin carboxylase subunit (CAC2) mRNA, complete cds

Seq. No.	139405
Seq. ID	LIB24-011-Q1-E1-F6
Method	BLASTX
NCBI GI	g399091
BLAST score	459
E value	7.0e-46
Match length	109
% identity	85
NCBI Description	PYROPHOSPHATE-ENERGIZED VACUOLAR MEMBRANE PROTON PUMP (PYROPHOSPHATE-ENERGIZED INORGANIC PYROPHOSPHATASE) (H+-PPASE) >gi_282878_pir__A38230 inorganic pyrophosphatase (EC 3.6.1.1), H+-translocating pyrophosphate-energized - Arabidopsis thaliana >gi_166634 (M81892) vacuolar H+-phosphatase [Arabidopsis thaliana]

Seq. No.	139406
Seq. ID	LIB24-011-Q1-E1-F7
Method	BLASTX
NCBI GI	g1706476
BLAST score	196
E value	4.0e-15
Match length	63
% identity	62
NCBI Description	DNAJ-LIKE PROTEIN SLR0093 >gi_1001729_dbj_BAA10566_ (D64004) DnaJ [Synechocystis sp.]

Seq. No.	139407
Seq. ID	LIB24-011-Q1-E1-F8
Method	BLASTX
NCBI GI	g4588012
BLAST score	358
E value	9.0e-41
Match length	89
% identity	97
NCBI Description	(AF085717) putative callose synthase catalytic subunit [Gossypium hirsutum]

Seq. No.	139408
Seq. ID	LIB24-011-Q1-E1-G2
Method	BLASTX
NCBI GI	g1806140
BLAST score	365
E value	6.0e-35
Match length	119
% identity	64
NCBI Description	(X97314) cdc2MsC [Medicago sativa]

Seq. No.	139409
Seq. ID	LIB24-011-Q1-E1-G7
Method	BLASTN
NCBI GI	g3548797
BLAST score	153
E value	2.0e-80
Match length	394
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T18E12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139410
Seq. ID	LIB24-011-Q1-E1-H4
Method	BLASTX
NCBI GI	g544424
BLAST score	204
E value	4.0e-16
Match length	39
% identity	97
NCBI Description	GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi_419755_pir__S30147 glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana >gi_16301_emb_CAA78711_ (Z14987) glycine rich protein [Arabidopsis thaliana] >gi_166837 (L00648) RNA-binding protein [Arabidopsis thaliana] >gi_4567224_gb_AAD23639.1_AC007119_5 (AC007119) glycine-rich RNA binding protein 7 [Arabidopsis thaliana]

Seq. No.	139411
Seq. ID	LIB24-011-Q1-E1-H5
Method	BLASTN
NCBI GI	g4512690
BLAST score	327
E value	0.0e+00
Match length	360
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F11A3 genomic sequence, complete sequence

Seq. No.	139412
Seq. ID	LIB24-012-Q1-E1-A1
Method	BLASTN
NCBI GI	g4490734
BLAST score	299
E value	1.0e-167
Match length	411
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA

project)

Seq. No.	139413
Seq. ID	LIB24-012-Q1-E1-A4
Method	BLASTN
NCBI GI	g3063438
BLAST score	240
E value	1.0e-132
Match length	240
% identity	80
NCBI Description	Complete sequence of Arabidopsis F22013, complete sequence [Arabidopsis thaliana]

Seq. No.	139414
Seq. ID	LIB24-012-Q1-E1-A8
Method	BLASTN
NCBI GI	g2264310
BLAST score	252
E value	1.0e-139
Match length	394
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKP11, complete sequence [Arabidopsis thaliana]

Seq. No.	139415
Seq. ID	LIB24-012-Q1-E1-B1
Method	BLASTN
NCBI GI	g3687221
BLAST score	163
E value	7.0e-87
Match length	189
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F6F22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139416
Seq. ID	LIB24-012-Q1-E1-B10
Method	BLASTX
NCBI GI	g2529665
BLAST score	653
E value	1.0e-68
Match length	133
% identity	95
NCBI Description	(AC002535) putative ribosomal protein L7A [Arabidopsis thaliana]

Seq. No.	139417
Seq. ID	LIB24-012-Q1-E1-C1
Method	BLASTX
NCBI GI	g1931637
BLAST score	721
E value	1.0e-76
Match length	137
% identity	100
NCBI Description	(U95973) receptor-associated kinase isolog [Arabidopsis thaliana]

Seq. No.	139418
Seq. ID	LIB24-012-Q1-E1-D1
Method	BLASTN
NCBI GI	g3341671
BLAST score	415
E value	0.0e+00
Match length	415
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F16B22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139419
Seq. ID	LIB24-012-Q1-E1-D4
Method	BLASTX
NCBI GI	g4580476
BLAST score	291
E value	4.0e-26
Match length	97
% identity	59
NCBI Description	(AC006081) unknown protein [Arabidopsis thaliana]

Seq. No.	139420
Seq. ID	LIB24-012-Q1-E1-E1
Method	BLASTN
NCBI GI	g2660661
BLAST score	128
E value	1.0e-65
Match length	222
% identity	100
NCBI Description	Arabidopsis thaliana chromosome V BAC T19K24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139421
Seq. ID	LIB24-012-Q1-E1-F4
Method	BLASTN
NCBI GI	g2285791
BLAST score	208
E value	1.0e-113
Match length	212
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for cyanase, complete cds

Seq. No.	139422
Seq. ID	LIB24-012-Q1-E1-G7
Method	BLASTN
NCBI GI	g4589440
BLAST score	224
E value	1.0e-123
Match length	354
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSD21, complete sequence

Seq. No.	139423
Seq. ID	LIB24-012-Q1-E1-H2
Method	BLASTN
NCBI GI	g2477521

BLAST score	393
E value	0.0e+00
Match length	393
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC F22K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139424
Seq. ID	LIB24-013-Q1-E1-B11
Method	BLASTX
NCBI GI	g1592545
BLAST score	173
E value	2.0e-12
Match length	111
% identity	38
NCBI Description	(U37486) peroxisomal multifunctional enzyme type II [Rattus norvegicus]

Seq. No.	139425
Seq. ID	LIB24-013-Q1-E1-B3
Method	BLASTN
NCBI GI	g2245073
BLAST score	252
E value	1.0e-139
Match length	369
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	139426
Seq. ID	LIB24-013-Q1-E1-E4
Method	BLASTN
NCBI GI	g2584827
BLAST score	175
E value	9.0e-94
Match length	333
% identity	95
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F12F1 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139427
Seq. ID	LIB24-013-Q1-E1-F8
Method	BLASTN
NCBI GI	g431257
BLAST score	435
E value	0.0e+00
Match length	435
% identity	100
NCBI Description	Arabidopsis thaliana lipoxygenase (Lox2) mRNA, complete cds

Seq. No.	139428
Seq. ID	LIB24-013-Q1-E1-G11
Method	BLASTX
NCBI GI	g2829910
BLAST score	147
E value	7.0e-10
Match length	37

% identity	40
NCBI Description	(AC002291) Unknown protein, contains regulator of chromosome condensation motifs [Arabidopsis thaliana]

Seq. No.	139429
Seq. ID	LIB24-013-Q1-E1-H8
Method	BLASTN
NCBI GI	g3395421
BLAST score	270
E value	1.0e-150
Match length	270
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T19C21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139430
Seq. ID	LIB24-014-Q1-E1-C2
Method	BLASTN
NCBI GI	g2262155
BLAST score	109
E value	1.0e-54
Match length	214
% identity	96
NCBI Description	DNA sequence of Arabidopsis thaliana BAC F5J6 from chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No.	139431
Seq. ID	LIB24-014-Q1-E1-C3
Method	BLASTX
NCBI GI	g544424
BLAST score	204
E value	4.0e-16
Match length	39
% identity	97
NCBI Description	GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi_419755_pir__S30147 glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana >gi_16301_emb_CAA78711_ (Z14987) glycine rich protein [Arabidopsis thaliana] >gi_166837 (L00648) RNA-binding protein [Arabidopsis thaliana] >gi_4567224_gb_AAD23639.1_AC007119_5 (AC007119) glycine-rich RNA binding protein 7 [Arabidopsis thaliana]

Seq. No.	139432
Seq. ID	LIB24-014-Q1-E1-H3
Method	BLASTN
NCBI GI	g2511575
BLAST score	159
E value	1.0e-84
Match length	159
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for proteasome subunit prcfc

Seq. No.	139433
Seq. ID	LIB24-015-Q1-E1-A11
Method	BLASTX
NCBI GI	g3914212
BLAST score	264

E value	4.0e-23
Match length	127
% identity	46
NCBI Description	5-OXOPROLINASE (5-OXO-L-PROLINASE) (PYROGLUTAMASE) (5-OPASE) >gi_1732065 (U70825) 5-oxo-L-prolinase [Rattus norvegicus]

Seq. No.	139434
Seq. ID	LIB24-015-Q1-E1-A2
Method	BLASTN
NCBI GI	g2494106
BLAST score	142
E value	4.0e-74
Match length	142
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139435
Seq. ID	LIB24-015-Q1-E1-A8
Method	BLASTX
NCBI GI	g3643611
BLAST score	535
E value	7.0e-55
Match length	124
% identity	73
NCBI Description	(AC005395) putative casein kinase [Arabidopsis thaliana]

Seq. No.	139436
Seq. ID	LIB24-015-Q1-E1-B4
Method	BLASTX
NCBI GI	g131398
BLAST score	343
E value	2.0e-32
Match length	70
% identity	100
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No.	139437
Seq. ID	LIB24-015-Q1-E1-D11
Method	BLASTX
NCBI GI	g3688195
BLAST score	395
E value	7.0e-39
Match length	78
% identity	95
NCBI Description	(AJ010092) MAP3K beta 3 protein kinase [Arabidopsis thaliana]

Seq. No.	139438
Seq. ID	LIB24-015-Q1-E1-E5
Method	BLASTX
NCBI GI	g3004555
BLAST score	613
E value	5.0e-64
Match length	122
% identity	20
NCBI Description	(AC003673) similar to salt inducible protein [Arabidopsis thaliana]

Seq. No.	139439
Seq. ID	LIB24-015-Q1-E1-F3
Method	BLASTN
NCBI GI	g3236234
BLAST score	263
E value	1.0e-146
Match length	376
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F13M22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139440
Seq. ID	LIB24-015-Q1-E1-H10
Method	BLASTX
NCBI GI	g4539419
BLAST score	415
E value	8.0e-41
Match length	105
% identity	80
NCBI Description	(AL049171) putative ribosomal protein [Arabidopsis thaliana]

Seq. No.	139441
Seq. ID	LIB24-015-Q1-E1-H9
Method	BLASTX
NCBI GI	g2961085
BLAST score	388
E value	9.0e-38
Match length	103
% identity	83
NCBI Description	(AF037228) transcription factor [Arabidopsis thaliana]

Seq. No.	139442
Seq. ID	LIB24-016-Q1-E1-A9
Method	BLASTN
NCBI GI	g3335331
BLAST score	163
E value	1.0e-86
Match length	299
% identity	90
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8F5 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139443
Seq. ID	LIB24-016-Q1-E1-D12
Method	BLASTN

NCBI GI	g4263694
BLAST score	166
E value	1.0e-88
Match length	166
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F22D22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139444
Seq. ID	LIB24-016-Q1-E1-D3
Method	BLASTN
NCBI GI	g2696018
BLAST score	132
E value	3.0e-68
Match length	238
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC9, complete sequence [Arabidopsis thaliana]

Seq. No.	139445
Seq. ID	LIB24-016-Q1-E1-D9
Method	BLASTX
NCBI GI	g141435
BLAST score	190
E value	2.0e-14
Match length	83
% identity	42
NCBI Description	DIHYDRONEOPTERIN ALDOLASE (DHNA) >gi_98360_pir__E37854 folate biosynthesis protein 1 (sul 3' region) - Bacillus subtilis >gi_143411 (M34053) ORF1 [Bacillus subtilis] >gi_467467_dbj_BAA05313_ (D26185) unknown [Bacillus subtilis] >gi_2632345_emb_CAB11854_ (Z99104) dihydroneopterin aldolase [Bacillus subtilis]

Seq. No.	139446
Seq. ID	LIB24-016-Q1-E1-E1
Method	BLASTN
NCBI GI	g4757678
BLAST score	136
E value	2.0e-70
Match length	136
% identity	86
NCBI Description	Arabidopsis thaliana chromosome I BAC F9H16 genomic sequence, complete sequence

Seq. No.	139447
Seq. ID	LIB24-016-Q1-E1-E2
Method	BLASTX
NCBI GI	g1076389
BLAST score	478
E value	3.0e-48
Match length	96
% identity	100
NCBI Description	protein phosphatase 2A pDF1 - Arabidopsis thaliana >gi_683502_emb_CAA57528_ (X82002) protein phosphatase 2A 65 kDa regulatory subunit [Arabidopsis thaliana]

Seq. No.	139448
Seq. ID	LIB24-016-Q1-E1-F8
Method	BLASTX
NCBI GI	g4432846
BLAST score	200
E value	1.0e-15
Match length	115
% identity	41
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	139449
Seq. ID	LIB24-016-Q1-E1-G2
Method	BLASTX
NCBI GI	g2498977
BLAST score	204
E value	5.0e-16
Match length	114
% identity	39
NCBI Description	SURFEIT LOCUS PROTEIN 5 >gi_1150512_emb_CAA59453_ (X85169) SURF-5 protein [Mus musculus]

Seq. No.	139450
Seq. ID	LIB24-016-Q1-E1-G7
Method	BLASTN
NCBI GI	g2760169
BLAST score	230
E value	1.0e-126
Match length	242
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFB13, complete sequence [Arabidopsis thaliana]

Seq. No.	139451
Seq. ID	LIB24-016-Q1-E1-G9
Method	BLASTX
NCBI GI	g3334404
BLAST score	175
E value	7.0e-13
Match length	77
% identity	96
NCBI Description	VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD SUBUNIT) >gi_2266990 (U65638) vacuolar type ATPase subunit A [Arabidopsis thaliana] >gi_3834305 (AC005679) Identical to gb_U65638 Arabidopsis thaliana vacuolar type ATPase subunit A mRNA. ESTs gb_N96435, gb_N96106, gb_N96189, gb_N96091, gb_AA042286, gb_F14324, gb_W43643, gb_N96027, gb_N96299, gb_R29943, gb_T43460, gb_T43544, gb_T22472

Seq. No.	139452
Seq. ID	LIB24-017-Q1-E1-A9
Method	BLASTN
NCBI GI	g3080406
BLAST score	370
E value	0.0e+00
Match length	370
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F23E12

(ESSA project)

Seq. No.	139453
Seq. ID	LIB24-017-Q1-E1-B12
Method	BLASTN
NCBI GI	g2281081
BLAST score	195
E value	1.0e-105
Match length	195
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F18O19 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139454
Seq. ID	LIB24-017-Q1-E1-B7
Method	BLASTX
NCBI GI	g2651313
BLAST score	571
E value	4.0e-59
Match length	126
% identity	64
NCBI Description	(AC002336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	139455
Seq. ID	LIB24-017-Q1-E1-B9
Method	BLASTX
NCBI GI	g3426051
BLAST score	626
E value	1.0e-65
Match length	125
% identity	100
NCBI Description	(AC005168) hypothetical protein [Arabidopsis thaliana]

Seq. No.	139456
Seq. ID	LIB24-017-Q1-E1-C3
Method	BLASTN
NCBI GI	g3687221
BLAST score	71
E value	3.0e-32
Match length	101
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F6F22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139457
Seq. ID	LIB24-017-Q1-E1-C8
Method	BLASTN
NCBI GI	g3047074
BLAST score	160
E value	7.0e-85
Match length	301
% identity	100
NCBI Description	Arabidopsis thaliana BAC F21E10

Seq. No.	139458
Seq. ID	LIB24-018-Q1-E1-B4
Method	BLASTN

NCBI GI	g4217996
BLAST score	166
E value	2.0e-88
Match length	203
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F24H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139459
Seq. ID	LIB24-018-Q1-E1-C12
Method	BLASTX
NCBI GI	g2499708
BLAST score	217
E value	8.0e-18
Match length	95
% identity	48
NCBI Description	PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE) (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D) >gi_1020409_dbj_BAA11135_ (D73410) phospholipase D [Zea mays]

Seq. No.	139460
Seq. ID	LIB24-018-Q1-E1-E4
Method	BLASTX
NCBI GI	g4325369
BLAST score	451
E value	4.0e-45
Match length	112
% identity	83
NCBI Description	(AF128396) T3H13.3 gene product [Arabidopsis thaliana]

Seq. No.	139461
Seq. ID	LIB24-018-Q1-E1-G6
Method	BLASTX
NCBI GI	g99681
BLAST score	510
E value	6.0e-52
Match length	130
% identity	83
NCBI Description	cold-regulated protein cor47 - Arabidopsis thaliana (fragment) >gi_388259_emb_CAA42483_ (X59814) Cold and ABA regulated gene [Arabidopsis thaliana]

Seq. No.	139462
Seq. ID	LIB24-019-Q1-E1-A5
Method	BLASTX
NCBI GI	g2576361
BLAST score	262
E value	8.0e-23
Match length	118
% identity	38
NCBI Description	(U39782) lysine and histidine specific transporter [Arabidopsis thaliana]

Seq. No.	139463
Seq. ID	LIB24-019-Q1-E1-B2
Method	BLASTX

NCBI GI	g68510
BLAST score	212
E value	2.0e-17
Match length	63
% identity	62
NCBI Description	translation releasing factor eRF - rabbit

Seq. No.	139464
Seq. ID	LIB24-019-Q1-E1-B3
Method	BLASTN
NCBI GI	g4204848
BLAST score	174
E value	4.0e-93
Match length	174
% identity	100
NCBI Description	Arabidopsis thaliana protein kinase (RPK1) mRNA, complete cds

Seq. No.	139465
Seq. ID	LIB24-019-Q1-E1-H9
Method	BLASTX
NCBI GI	g730465
BLAST score	155
E value	2.0e-10
Match length	105
% identity	32
NCBI Description	DNA REPAIR AND RECOMBINATION PROTEIN RAD26 >gi_626090_pir__JC2227 probable helicase RAD26 - yeast (Saccharomyces cerevisiae) >gi_506419 (L26910) gtA1085 [Saccharomyces cerevisiae] >gi_1015683_emb_CAA89562_ (Z49535) ORF YJR035w [Saccharomyces cerevisiae]

Seq. No.	139466
Seq. ID	LIB24-020-Q1-E1-A6
Method	BLASTN
NCBI GI	g2351063
BLAST score	212
E value	1.0e-116
Match length	410
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCL19, complete sequence [Arabidopsis thaliana]

Seq. No.	139467
Seq. ID	LIB24-020-Q1-E1-B9
Method	BLASTN
NCBI GI	g3292807
BLAST score	185
E value	1.0e-100
Match length	230
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F7H19 (ESSAII project)

Seq. No.	139468
Seq. ID	LIB24-020-Q1-E1-D4
Method	BLASTX

NCBI GI	g549848
BLAST score	284
E value	2.0e-25
Match length	131
% identity	44
NCBI Description	(M86958) putative [Caenorhabditis elegans]

Seq. No.	139469
Seq. ID	LIB24-020-Q1-E1-D8
Method	BLASTX
NCBI GI	g544285
BLAST score	206
E value	3.0e-16
Match length	44
% identity	86
NCBI Description	FIBRILLARIN >gi_422056_pir__S33690 fibrillarin - fission yeast (Schizosaccharomyces pombe) >gi_296704_emb_CAA49550_ (X69930) fibrillarin [Schizosaccharomyces pombe] >gi_3687500_emb_CAA21168_ (AL031788) fibrillarin [Schizosaccharomyces pombe]

Seq. No.	139470
Seq. ID	LIB24-020-Q1-E1-E1
Method	BLASTX
NCBI GI	g4454036
BLAST score	226
E value	1.0e-18
Match length	56
% identity	70
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	139471
Seq. ID	LIB24-020-Q1-E1-E3
Method	BLASTN
NCBI GI	g4585896
BLAST score	287
E value	1.0e-160
Match length	347
% identity	75
NCBI Description	Arabidopsis thaliana chromosome II BAC F13I13 genomic sequence, complete sequence

Seq. No.	139472
Seq. ID	LIB24-020-Q1-E1-E5
Method	BLASTX
NCBI GI	g3935148
BLAST score	223
E value	3.0e-18
Match length	111
% identity	42
NCBI Description	(AC005106) T25N20.12 [Arabidopsis thaliana]

Seq. No.	139473
Seq. ID	LIB24-020-Q1-E1-F8
Method	BLASTX
NCBI GI	g2245009

BLAST score	523
E value	2.0e-53
Match length	122
% identity	86
NCBI Description	(Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No.	139474
Seq. ID	LIB24-021-Q1-E1-A3
Method	BLASTX
NCBI GI	g4406814
BLAST score	384
E value	4.0e-37
Match length	77
% identity	100
NCBI Description	(AC006201) putative peptidyl-prolyl isomerase [Arabidopsis thaliana]

Seq. No.	139475
Seq. ID	LIB24-021-Q1-E1-A8
Method	BLASTX
NCBI GI	g2583123
BLAST score	166
E value	1.0e-11
Match length	38
% identity	74
NCBI Description	(AC002387) putative nucleotide sugar epimerase [Arabidopsis thaliana]

Seq. No.	139476
Seq. ID	LIB24-021-Q1-E1-B1
Method	BLASTX
NCBI GI	g1805654
BLAST score	611
E value	9.0e-64
Match length	131
% identity	90
NCBI Description	(X99972) calmodulin-stimulated calcium-ATPase [Brassica oleracea]

Seq. No.	139477
Seq. ID	LIB24-021-Q1-E1-B4
Method	BLASTX
NCBI GI	g4263722
BLAST score	582
E value	2.0e-60
Match length	129
% identity	87
NCBI Description	(AC006223) putative glucan synthase [Arabidopsis thaliana]

Seq. No.	139478
Seq. ID	LIB24-021-Q1-E1-B8
Method	BLASTX
NCBI GI	g4490714
BLAST score	208
E value	5.0e-17
Match length	51
% identity	80

NCBI Description	(AL035680) kinesin-related protein katB [Arabidopsis thaliana]

Seq. No.	139479
Seq. ID	LIB24-021-Q1-E1-B9
Method	BLASTX
NCBI GI	g4325375
BLAST score	685
E value	2.0e-72
Match length	134
% identity	100
NCBI Description	(AF128396) similar to arginases (Pfam: PF00491, Score=353.2, E=1.4e-119, N=1) [Arabidopsis thaliana]

Seq. No.	139480
Seq. ID	LIB24-021-Q1-E1-C12
Method	BLASTN
NCBI GI	g4220633
BLAST score	326
E value	0.0e+00
Match length	398
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K7J8, complete sequence [Arabidopsis thaliana]

Seq. No.	139481
Seq. ID	LIB24-021-Q1-E1-C5
Method	BLASTN
NCBI GI	g3241916
BLAST score	139
E value	3.0e-72
Match length	400
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15N18, complete sequence [Arabidopsis thaliana]

Seq. No.	139482
Seq. ID	LIB24-021-Q1-E1-C7
Method	BLASTX
NCBI GI	g4263704
BLAST score	460
E value	4.0e-46
Match length	124
% identity	77
NCBI Description	(AC006223) putative sugar starvation-induced protein [Arabidopsis thaliana]

Seq. No.	139483
Seq. ID	LIB24-021-Q1-E1-D6
Method	BLASTX
NCBI GI	g99752
BLAST score	654
E value	9.0e-69
Match length	134
% identity	99
NCBI Description	protochlorophyllide reductase (EC 1.3.1.33) precursor - Arabidopsis thaliana

Seq. No.	139484
Seq. ID	LIB24-021-Q1-E1-E1
Method	BLASTN
NCBI GI	g4725940
BLAST score	398
E value	0.0e+00
Match length	398
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T1P17 (ESSA project)

Seq. No.	139485
Seq. ID	LIB24-021-Q1-E1-E6
Method	BLASTX
NCBI GI	g4049353
BLAST score	458
E value	8.0e-46
Match length	133
% identity	68
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	139486
Seq. ID	LIB24-021-Q1-E1-F8
Method	BLASTN
NCBI GI	g2696018
BLAST score	126
E value	2.0e-64
Match length	126
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC9, complete sequence [Arabidopsis thaliana]

Seq. No.	139487
Seq. ID	LIB24-021-Q1-E1-G6
Method	BLASTX
NCBI GI	g1710394
BLAST score	664
E value	6.0e-70
Match length	132
% identity	99
NCBI Description	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN (RIBONUCLEOTIDE REDUCTASE) (R2 SUBUNIT) >gi_840719_emb_CAA54549_ (X77336) ribonucleotide reductase R2 [Arabidopsis thaliana]

Seq. No.	139488
Seq. ID	LIB24-022-Q1-E1-B4
Method	BLASTN
NCBI GI	g3193282
BLAST score	202
E value	1.0e-110
Match length	383
% identity	100
NCBI Description	Arabidopsis thaliana BAC T14P8

Seq. No.	139489

Seq. ID	LIB24-022-Q1-E1-D10
Method	BLASTN
NCBI GI	g4519193
BLAST score	244
E value	1.0e-135
Match length	388
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC11, complete sequence

Seq. No.	139490
Seq. ID	LIB24-022-Q1-E1-D12
Method	BLASTN
NCBI GI	g2914688
BLAST score	32
E value	9.0e-09
Match length	32
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F24L7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139491
Seq. ID	LIB24-022-Q1-E1-E3
Method	BLASTN
NCBI GI	g4567237
BLAST score	210
E value	1.0e-115
Match length	210
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T22F11 genomic sequence, complete sequence

Seq. No.	139492
Seq. ID	LIB24-022-Q1-E1-E8
Method	BLASTX
NCBI GI	g2245131
BLAST score	303
E value	1.0e-27
Match length	98
% identity	69
NCBI Description	(Z97344) hypothetical protein [Arabidopsis thaliana]

Seq. No.	139493
Seq. ID	LIB24-022-Q1-E1-F7
Method	BLASTN
NCBI GI	g3386593
BLAST score	58
E value	7.0e-24
Match length	94
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC F4I18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139494
Seq. ID	LIB24-022-Q1-E1-G7
Method	BLASTX
NCBI GI	g2459417

BLAST score 446
E value 2.0e-44
Match length 85
% identity 100
NCBI Description (AC002332) putative pre-mRNA splicing factor PRP19 [Arabidopsis thaliana]

Seq. No. 139495
Seq. ID LIB24-022-Q1-E1-H11
Method BLASTX
NCBI GI g4220514
BLAST score 260
E value 1.0e-22
Match length 81
% identity 63
NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 139496
Seq. ID LIB24-022-Q1-E1-H5
Method BLASTX
NCBI GI g3915847
BLAST score 403
E value 2.0e-39
Match length 88
% identity 90
NCBI Description 40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative 40S ribosomal protein S2 [Arabidopsis thaliana]

Seq. No. 139497
Seq. ID LIB24-023-Q1-E1-A11
Method BLASTX
NCBI GI g115783
BLAST score 508
E value 1.0e-51
Match length 98
% identity 98
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No. 139498
Seq. ID LIB24-023-Q1-E1-A9
Method BLASTN
NCBI GI g3449322
BLAST score 307
E value 1.0e-172
Match length 315
% identity 99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC17, complete sequence [Arabidopsis thaliana]

Seq. No. 139499
Seq. ID LIB24-023-Q1-E1-B2
Method BLASTX
NCBI GI g2244760
BLAST score 286

E value	3.0e-26
Match length	71
% identity	75
NCBI Description	(Z97335) selenium-binding protein [Arabidopsis thaliana]

Seq. No.	139500
Seq. ID	LIB24-023-Q1-E1-C9
Method	BLASTX
NCBI GI	g3367516
BLAST score	485
E value	5.0e-49
Match length	93
% identity	100
NCBI Description	(AC004392) Similar to beta-glucosidase BGQ60 precursor gb_L41869 from Hordeum vulgare. [Arabidopsis thaliana]

Seq. No.	139501
Seq. ID	LIB24-023-Q1-E1-D8
Method	BLASTN
NCBI GI	g3869069
BLAST score	123
E value	8.0e-63
Match length	223
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence [Arabidopsis thaliana]

Seq. No.	139502
Seq. ID	LIB24-023-Q1-E1-E9
Method	BLASTN
NCBI GI	g2827513
BLAST score	342
E value	0.0e+00
Match length	366
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4; BAC clone F8F16 (ESSAII project)

Seq. No.	139503
Seq. ID	LIB24-023-Q1-E1-G3
Method	BLASTN
NCBI GI	g2947056
BLAST score	141
E value	1.0e-73
Match length	197
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC T20F6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139504
Seq. ID	LIB24-023-Q1-E1-H7
Method	BLASTN
NCBI GI	g4490734
BLAST score	46
E value	3.0e-17
Match length	99
% identity	93

NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	139505
Seq. ID	LIB24-024-Q1-E1-D2
Method	BLASTN
NCBI GI	g4454447
BLAST score	202
E value	1.0e-110
Match length	210
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139506
Seq. ID	LIB24-024-Q1-E1-E2
Method	BLASTN
NCBI GI	g3985934
BLAST score	82
E value	1.0e-38
Match length	146
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJE7, complete sequence [Arabidopsis thaliana]

Seq. No.	139507
Seq. ID	LIB24-024-Q1-E1-F3
Method	BLASTN
NCBI GI	g3927822
BLAST score	31
E value	3.0e-08
Match length	148
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F8N16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139508
Seq. ID	LIB24-025-Q1-E1-C8
Method	BLASTX
NCBI GI	g1239959
BLAST score	205
E value	4.0e-16
Match length	41
% identity	100
NCBI Description	(X95469) MADS-box gene [Antirrhinum majus]

Seq. No.	139509
Seq. ID	LIB24-025-Q1-E1-D1
Method	BLASTN
NCBI GI	g2924653
BLAST score	71
E value	3.0e-32
Match length	95
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDA7, complete sequence [Arabidopsis thaliana]

Seq. No.	139510
Seq. ID	LIB24-025-Q1-E1-D10
Method	BLASTN
NCBI GI	g4584339
BLAST score	253
E value	1.0e-140
Match length	253
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T23A1 genomic sequence, complete sequence

Seq. No.	139511
Seq. ID	LIB24-025-Q1-E1-E10
Method	BLASTX
NCBI GI	g585536
BLAST score	250
E value	5.0e-22
Match length	62
% identity	74
NCBI Description	MYROSINASE PRECURSOR (SINIGRINASE) (THIOGLUCOSIDASE) >gi_1362006_pir__S56653 thioglucosidase (EC 3.2.3.1) - Arabidopsis thaliana >gi_304115 (L11454) thioglucosidase [Arabidopsis thaliana] >gi_871990_emb_CAA55786_ (X79194) thioglucosidase [Arabidopsis thaliana]

Seq. No.	139512
Seq. ID	LIB24-025-Q1-E1-E3
Method	BLASTX
NCBI GI	g2924512
BLAST score	585
E value	8.0e-61
Match length	115
% identity	98
NCBI Description	(AL022023) beta-galactosidase-like protein [Arabidopsis thaliana]

Seq. No.	139513
Seq. ID	LIB24-025-Q1-E1-E4
Method	BLASTN
NCBI GI	g4567300
BLAST score	286
E value	1.0e-160
Match length	315
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II P1 MHK10 genomic sequence, complete sequence

Seq. No.	139514
Seq. ID	LIB24-025-Q1-E1-F6
Method	BLASTN
NCBI GI	g3738275
BLAST score	175
E value	5.0e-94
Match length	191
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F17A22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139515
Seq. ID	LIB24-025-Q1-E1-G3
Method	BLASTN
NCBI GI	g4220645
BLAST score	188
E value	1.0e-102
Match length	204
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYA6, complete sequence [Arabidopsis thaliana]

Seq. No.	139516
Seq. ID	LIB24-025-Q1-E1-G5
Method	BLASTN
NCBI GI	g3702728
BLAST score	173
E value	2.0e-92
Match length	360
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M13, complete sequence [Arabidopsis thaliana]

Seq. No.	139517
Seq. ID	LIB24-026-Q1-E1-C4
Method	BLASTX
NCBI GI	g1353352
BLAST score	224
E value	6.0e-19
Match length	62
% identity	68
NCBI Description	(U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No.	139518
Seq. ID	LIB24-026-Q1-E1-C8
Method	BLASTX
NCBI GI	g2507281
BLAST score	556
E value	2.0e-57
Match length	101
% identity	100
NCBI Description	GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi_1668706_emb_CAA66048_ (X97380) atran2 [Arabidopsis thaliana]

Seq. No.	139519
Seq. ID	LIB24-026-Q1-E1-D4
Method	BLASTX
NCBI GI	g629511
BLAST score	331
E value	5.0e-31
Match length	111
% identity	72
NCBI Description	cold-regulated protein cor15b precursor - Arabidopsis thaliana >gi_4559338_gb_AAD23000.1_AC007087_19 (AC007087) cold-regulated protein cor15b precursor [Arabidopsis thaliana]

Seq. No.	139520
Seq. ID	LIB24-026-Q1-E1-E1
Method	BLASTN
NCBI GI	g3738313
BLAST score	385
E value	0.0e+00
Match length	385
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T29E15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139521
Seq. ID	LIB24-027-Q1-E1-A11
Method	BLASTN
NCBI GI	g4165340
BLAST score	102
E value	1.0e-50
Match length	155
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC F11M15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139522
Seq. ID	LIB24-027-Q1-E1-A6
Method	BLASTN
NCBI GI	g3702315
BLAST score	98
E value	5.0e-48
Match length	186
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC T3F17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139523
Seq. ID	LIB24-027-Q1-E1-A8
Method	BLASTN
NCBI GI	g4733953
BLAST score	21
E value	9.0e-02
Match length	410
% identity	93
NCBI Description	Arabidopsis thaliana chromosome I BAC F13O11 genomic sequence, complete sequence

Seq. No.	139524
Seq. ID	LIB24-027-Q1-E1-B1
Method	BLASTX
NCBI GI	g2739010
BLAST score	281
E value	4.0e-25
Match length	109
% identity	54
NCBI Description	(AF022464) CYP77A3p [Glycine max]

Seq. No.	139525
Seq. ID	LIB24-027-Q1-E1-B2

Method	BLASTX
NCBI GI	g1749412
BLAST score	481
E value	2.0e-48
Match length	135
% identity	64
NCBI Description	(D89102) similar to Saccharomyces cerevisiae ADP,ATP carrier protein (ADP/ATP translocase), SWISS-PROT Accession Number P18239 [Schizosaccharomyces pombe]

Seq. No.	139526
Seq. ID	LIB24-027-Q1-E1-D10
Method	BLASTX
NCBI GI	g2280528
BLAST score	178
E value	6.0e-13
Match length	33
% identity	100
NCBI Description	(AB005888) ATMYB3 [Arabidopsis thaliana]

Seq. No.	139527
Seq. ID	LIB24-027-Q1-E1-D8
Method	BLASTX
NCBI GI	g115783
BLAST score	549
E value	2.0e-56
Match length	107
% identity	97
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	139528
Seq. ID	LIB24-027-Q1-E1-E11
Method	BLASTN
NCBI GI	g4589430
BLAST score	89
E value	1.0e-42
Match length	156
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLD14, complete sequence

Seq. No.	139529
Seq. ID	LIB24-027-Q1-E1-F10
Method	BLASTX
NCBI GI	g2262163
BLAST score	207
E value	2.0e-16
Match length	38
% identity	100
NCBI Description	(AC002329) hypothetical protein similar to F5J6.10 [Arabidopsis thaliana]

Seq. No.	139530
Seq. ID	LIB24-027-Q1-E1-G12

Method	BLASTN
NCBI GI	g1488526
BLAST score	193
E value	1.0e-104
Match length	205
% identity	99
NCBI Description	B.juncea ribosomal intergenic spacer

Seq. No.	139531
Seq. ID	LIB24-027-Q1-E1-G5
Method	BLASTX
NCBI GI	g3461813
BLAST score	240
E value	8.0e-21
Match length	63
% identity	78
NCBI Description	(AC004138) putative sucrose/H+ symporter [Arabidopsis thaliana]

Seq. No.	139532
Seq. ID	LIB24-027-Q1-E1-G8
Method	BLASTX
NCBI GI	g2493289
BLAST score	169
E value	6.0e-12
Match length	112
% identity	39
NCBI Description	RIBONUCLEASE

Seq. No.	139533
Seq. ID	LIB24-027-Q1-E1-H2
Method	BLASTN
NCBI GI	g4490701
BLAST score	224
E value	1.0e-123
Match length	392
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T24A18 (ESSA project)

Seq. No.	139534
Seq. ID	LIB24-027-Q1-E1-H5
Method	BLASTN
NCBI GI	g3449334
BLAST score	268
E value	1.0e-149
Match length	300
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH9, complete sequence [Arabidopsis thaliana]

Seq. No.	139535
Seq. ID	LIB24-027-Q1-E1-H6
Method	BLASTX
NCBI GI	g3885341
BLAST score	197
E value	3.0e-15

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Match length	72
% identity	53
NCBI Description	(AC005623) unknown protein [Arabidopsis thaliana]

Seq. No.	139536
Seq. ID	LIB24-028-Q1-E1-B10
Method	BLASTX
NCBI GI	g4262149
BLAST score	418
E value	3.0e-41
Match length	72
% identity	100
NCBI Description	(AC005275) putative xyloglucan endotransglycosylase [Arabidopsis thaliana]

Seq. No.	139537
Seq. ID	LIB24-028-Q1-E1-C12
Method	BLASTX
NCBI GI	g1184953
BLAST score	317
E value	3.0e-29
Match length	60
% identity	100
NCBI Description	(U46574) protein farnesyl transferase beta subunit [Arabidopsis thaliana]

Seq. No.	139538
Seq. ID	LIB24-028-Q1-E1-C9
Method	BLASTN
NCBI GI	g4519188
BLAST score	125
E value	6.0e-64
Match length	313
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L19, complete sequence

Seq. No.	139539
Seq. ID	LIB24-028-Q1-E1-E11
Method	BLASTX
NCBI GI	g4510398
BLAST score	300
E value	3.0e-27
Match length	95
% identity	67
NCBI Description	(AC006587) hypothetical protein [Arabidopsis thaliana]

Seq. No.	139540
Seq. ID	LIB24-028-Q1-E1-E3
Method	BLASTX
NCBI GI	g2341034
BLAST score	325
E value	2.0e-30
Match length	62
% identity	100
NCBI Description	(AC000104) F19P19.13 [Arabidopsis thaliana]

Seq. No.	139541
Seq. ID	LIB24-028-Q1-E1-G1
Method	BLASTX
NCBI GI	g3805846
BLAST score	280
E value	4.0e-25
Match length	94
% identity	98
NCBI Description	(AL031986) DNA-directed RNA polymerase (EC 2.7.7.6) II largest chain [Arabidopsis thaliana]

Seq. No.	139542
Seq. ID	LIB24-028-Q1-E1-G3
Method	BLASTX
NCBI GI	g4006827
BLAST score	329
E value	1.0e-30
Match length	124
% identity	54
NCBI Description	(AC005970) subtilisin-like protease [Arabidopsis thaliana]

Seq. No.	139543
Seq. ID	LIB24-028-Q1-E1-H2
Method	BLASTN
NCBI GI	g4468801
BLAST score	330
E value	0.0e+00
Match length	330
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6G17 (ESSA project)

Seq. No.	139544
Seq. ID	LIB24-028-Q1-E1-H4
Method	BLASTN
NCBI GI	g3128141
BLAST score	130
E value	6.0e-67
Match length	316
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQD22, complete sequence [Arabidopsis thaliana]

Seq. No.	139545
Seq. ID	LIB24-029-Q1-E1-A1
Method	BLASTN
NCBI GI	g3212846
BLAST score	111
E value	6.0e-56
Match length	135
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139546
Seq. ID	LIB24-029-Q1-E1-A10
Method	BLASTX

NCBI GI	g4056433
BLAST score	306
E value	5.0e-28
Match length	115
% identity	57
NCBI Description	(AC005990) Similar to anter-specific proline-rich protein (CEX) gb_X60376 from Brassica napus. [Arabidopsis thaliana]

Seq. No.	139547
Seq. ID	LIB24-029-Q1-E1-B5
Method	BLASTX
NCBI GI	g2129608
BLAST score	382
E value	1.0e-44
Match length	98
% identity	100
NCBI Description	GTP-binding protein, 68K - Arabidopsis thaliana >gi_807577 (L38614) GTP-binding protein [Arabidopsis thaliana]

Seq. No.	139548
Seq. ID	LIB24-029-Q1-E1-C2
Method	BLASTN
NCBI GI	g4567300
BLAST score	366
E value	0.0e+00
Match length	395
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II P1 MHK10 genomic sequence, complete sequence

Seq. No.	139549
Seq. ID	LIB24-029-Q1-E1-D11
Method	BLASTX
NCBI GI	g4678226
BLAST score	511
E value	5.0e-52
Match length	119
% identity	88
NCBI Description	(AC007135) putative 40S ribosomal protein S14 [Arabidopsis thaliana]

Seq. No.	139550
Seq. ID	LIB24-029-Q1-E1-F9
Method	BLASTN
NCBI GI	g3341671
BLAST score	142
E value	3.0e-74
Match length	211
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC F16B22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139551
Seq. ID	LIB24-029-Q1-E1-G1
Method	BLASTN
NCBI GI	g4589445
BLAST score	43

E value	6.0e-15
Match length	159
% identity	82
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWL2, complete sequence

Seq. No.	139552
Seq. ID	LIB24-030-Q1-E1-A10
Method	BLASTX
NCBI GI	g2275201
BLAST score	352
E value	6.0e-34
Match length	72
% identity	93
NCBI Description	(AC002337) unknown protein [Arabidopsis thaliana]

Seq. No.	139553
Seq. ID	LIB24-030-Q1-E1-B2
Method	BLASTX
NCBI GI	g2961357
BLAST score	612
E value	7.0e-64
Match length	132
% identity	84
NCBI Description	(AL022140) putative protein [Arabidopsis thaliana]

Seq. No.	139554
Seq. ID	LIB24-030-Q1-E1-B5
Method	BLASTN
NCBI GI	g3135250
BLAST score	248
E value	1.0e-137
Match length	277
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC F27F23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139555
Seq. ID	LIB24-030-Q1-E1-B9
Method	BLASTN
NCBI GI	g2245073
BLAST score	350
E value	0.0e+00
Match length	350
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	139556
Seq. ID	LIB24-030-Q1-E1-D9
Method	BLASTN
NCBI GI	g4757392
BLAST score	96
E value	7.0e-47
Match length	179
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:

K14A17, complete sequence

Seq. No.	139557
Seq. ID	LIB24-030-Q1-E1-E11
Method	BLASTN
NCBI GI	g4580744
BLAST score	165
E value	7.0e-88
Match length	250
% identity	97
NCBI Description	Sequence of BAC F15I1 from Arabidopsis thaliana chromosome 1, complete sequence

Seq. No.	139558
Seq. ID	LIB24-030-Q1-E1-E7
Method	BLASTN
NCBI GI	g2494106
BLAST score	109
E value	1.0e-54
Match length	230
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139559
Seq. ID	LIB24-030-Q1-E1-E9
Method	BLASTX
NCBI GI	g3176726
BLAST score	205
E value	1.0e-16
Match length	50
% identity	78
NCBI Description	(AC002392) putative serine proteinase [Arabidopsis thaliana]

Seq. No.	139560
Seq. ID	LIB24-030-Q1-E1-F10
Method	BLASTX
NCBI GI	g349470
BLAST score	454
E value	1.0e-45
Match length	85
% identity	94
NCBI Description	(L23114) binding protein [Homo sapiens]

Seq. No.	139561
Seq. ID	LIB24-030-Q1-E1-F2
Method	BLASTN
NCBI GI	g2264306
BLAST score	375
E value	0.0e+00
Match length	375
% identity	42
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK5, complete sequence [Arabidopsis thaliana]

Seq. No. 139562

Seq. ID	LIB24-030-Q1-E1-F3
Method	BLASTX
NCBI GI	g131381
BLAST score	194
E value	2.0e-15
Match length	46
% identity	91
NCBI Description	OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN) >gi_99745_pir__S11852 photosystem II oxygen-evolving complex protein 1 precursor - Arabidopsis thaliana >gi_22571_emb_CAA36675_ (X52428) 33 kDa oxygen-evolving protein [Arabidopsis thaliana]

Seq. No.	139563
Seq. ID	LIB24-030-Q1-E1-H12
Method	BLASTX
NCBI GI	g4754062
BLAST score	360
E value	2.0e-34
Match length	75
% identity	91
NCBI Description	(AF072881) SOCS box-containing WD protein SWiP-2 [Mus musculus]

Seq. No.	139564
Seq. ID	LIB24-030-Q1-E1-H3
Method	BLASTN
NCBI GI	g2749918
BLAST score	134
E value	1.0e-69
Match length	166
% identity	94
NCBI Description	Arabidopsis thaliana chromosome I BAC F3I6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139565
Seq. ID	LIB24-031-Q1-E1-C7
Method	BLASTN
NCBI GI	g4063737
BLAST score	184
E value	3.0e-99
Match length	208
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F24D13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139566
Seq. ID	LIB24-031-Q1-E1-D7
Method	BLASTN
NCBI GI	g3241922
BLAST score	166
E value	2.0e-88
Match length	256
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLM24, complete sequence [Arabidopsis thaliana]

Seq. No.	139567
Seq. ID	LIB24-031-Q1-E1-D9
Method	BLASTX
NCBI GI	g4585998
BLAST score	592
E value	2.0e-61
Match length	137
% identity	86
NCBI Description	(AC005287) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	139568
Seq. ID	LIB24-031-Q1-E1-E8
Method	BLASTX
NCBI GI	g3377814
BLAST score	520
E value	3.0e-53
Match length	103
% identity	95
NCBI Description	(AF076275) similar to protein kinases (Pfam: pkinase.hmm, score: 228.02) [Arabidopsis thaliana]

Seq. No.	139569
Seq. ID	LIB24-031-Q1-E1-F2
Method	BLASTN
NCBI GI	g3869075
BLAST score	61
E value	3.0e-26
Match length	85
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence [Arabidopsis thaliana]

Seq. No.	139570
Seq. ID	LIB24-031-Q1-E1-F5
Method	BLASTX
NCBI GI	g2443878
BLAST score	228
E value	4.0e-19
Match length	58
% identity	74
NCBI Description	(AC002294) Unknown protein [Arabidopsis thaliana]

Seq. No.	139571
Seq. ID	LIB24-031-Q1-E1-G11
Method	BLASTX
NCBI GI	g2244865
BLAST score	524
E value	8.0e-54
Match length	93
% identity	99
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	139572
Seq. ID	LIB24-031-Q1-E1-H4
Method	BLASTN
NCBI GI	g4455168

BLAST score	283
E value	1.0e-158
Match length	324
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)

Seq. No.	139573
Seq. ID	LIB24-032-Q1-E1-A2
Method	BLASTX
NCBI GI	g2459418
BLAST score	244
E value	6.0e-21
Match length	56
% identity	86
NCBI Description	(AC002332) hypothetical protein [Arabidopsis thaliana]

Seq. No.	139574
Seq. ID	LIB24-032-Q1-E1-B10
Method	BLASTN
NCBI GI	g3985931
BLAST score	150
E value	6.0e-79
Match length	286
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21H1, complete sequence [Arabidopsis thaliana]

Seq. No.	139575
Seq. ID	LIB24-032-Q1-E1-B6
Method	BLASTX
NCBI GI	g3169173
BLAST score	290
E value	2.0e-26
Match length	63
% identity	89
NCBI Description	(AC004401) putative serine carboxypeptidase I [Arabidopsis thaliana] >gi_3445215 (AC004786) putative serine carboxypeptidase I [Arabidopsis thaliana]

Seq. No.	139576
Seq. ID	LIB24-032-Q1-E1-E12
Method	BLASTN
NCBI GI	g4587641
BLAST score	109
E value	9.0e-55
Match length	137
% identity	95
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No.	139577
Seq. ID	LIB24-032-Q1-E1-E9
Method	BLASTN
NCBI GI	g4589418
BLAST score	208
E value	1.0e-113

09460746.060700

Match length	228
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21G20, complete sequence

Seq. No.	139578
Seq. ID	LIB24-032-Q1-E1-F10
Method	BLASTX
NCBI GI	g267073
BLAST score	630
E value	6.0e-66
Match length	115
% identity	100
NCBI Description	TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin beta chain - Arabidopsis thaliana >gi_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701) beta-3 tubulin [Arabidopsis thaliana]

Seq. No.	139579
Seq. ID	LIB24-032-Q1-E1-H1
Method	BLASTN
NCBI GI	g3046854
BLAST score	48
E value	6.0e-18
Match length	174
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRG7, complete sequence [Arabidopsis thaliana]

Seq. No.	139580
Seq. ID	LIB24-033-Q1-E1-A4
Method	BLASTN
NCBI GI	g4753195
BLAST score	123
E value	5.0e-63
Match length	192
% identity	99
NCBI Description	Arabidopsis thaliana BAC F15A18 from chromosome V near 68.5 cM, complete sequence

Seq. No.	139581
Seq. ID	LIB24-033-Q1-E1-A7
Method	BLASTN
NCBI GI	g3128139
BLAST score	244
E value	1.0e-135
Match length	381
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIK19, complete sequence [Arabidopsis thaliana]

Seq. No.	139582
Seq. ID	LIB24-033-Q1-E1-B8
Method	BLASTN
NCBI GI	g3859590
BLAST score	213
E value	1.0e-116

Match length	381
% identity	100
NCBI Description	Arabidopsis thaliana BAC T15B16

Seq. No.	139583
Seq. ID	LIB24-033-Q1-E1-B9
Method	BLASTN
NCBI GI	g3510344
BLAST score	53
E value	7.0e-21
Match length	130
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJG14, complete sequence [Arabidopsis thaliana]

Seq. No.	139584
Seq. ID	LIB24-033-Q1-E1-C11
Method	BLASTN
NCBI GI	g2642152
BLAST score	225
E value	1.0e-123
Match length	388
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T5I7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139585
Seq. ID	LIB24-033-Q1-E1-C3
Method	BLASTN
NCBI GI	g2827698
BLAST score	206
E value	1.0e-112
Match length	365
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 5, BAC clone F6H11 (ESSAII project)

Seq. No.	139586
Seq. ID	LIB24-033-Q1-E1-C9
Method	BLASTX
NCBI GI	g3915023
BLAST score	474
E value	1.0e-47
Match length	105
% identity	87
NCBI Description	SUCROSE-PHOSPHATE SYNTHASE 1 (UDP-GLUCOSE-FRUCTOSE-PHOSPHATE GLUCOSYLTRANSFERASE 1) >gi_2588888_dbj_BAA23213_ (AB005023) sucrose-phosphate synthase [Citrus unshiu]

Seq. No.	139587
Seq. ID	LIB24-033-Q1-E1-D12
Method	BLASTX
NCBI GI	g3549670
BLAST score	522
E value	2.0e-53
Match length	101

% identity	98
NCBI Description	(AL031394) putative protein [Arabidopsis thaliana]
Seq. No.	139588
Seq. ID	LIB24-033-Q1-E1-E12
Method	BLASTX
NCBI GI	g4538923
BLAST score	202
E value	2.0e-16
Match length	55
% identity	73
NCBI Description	(AL049483) predicted protein destination factor [Arabidopsis thaliana]
Seq. No.	139589
Seq. ID	LIB24-033-Q1-E1-E6
Method	BLASTN
NCBI GI	g4220635
BLAST score	230
E value	1.0e-126
Match length	394
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDB19, complete sequence [Arabidopsis thaliana]
Seq. No.	139590
Seq. ID	LIB24-033-Q1-E1-F1
Method	BLASTN
NCBI GI	g2244829
BLAST score	364
E value	0.0e+00
Match length	364
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No
Seq. No.	139591
Seq. ID	LIB24-033-Q1-E1-F12
Method	BLASTX
NCBI GI	g3953471
BLAST score	406
E value	9.0e-40
Match length	124
% identity	56
NCBI Description	(AC002328) F22O2.16 [Arabidopsis thaliana]
Seq. No.	139592
Seq. ID	LIB24-034-Q1-E1-C3
Method	BLASTX
NCBI GI	g4755189
BLAST score	230
E value	1.0e-19
Match length	59
% identity	71
NCBI Description	(AC007018) putative cytochrome P450 [Arabidopsis thaliana]
Seq. No.	139593

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Seq. ID	LIB24-034-Q1-E1-C8
Method	BLASTN
NCBI GI	g3242700
BLAST score	240
E value	1.0e-132
Match length	284
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F26B6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139594
Seq. ID	LIB24-034-Q1-E1-G12
Method	BLASTN
NCBI GI	g4159708
BLAST score	202
E value	1.0e-110
Match length	226
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MKP6, complete sequence

Seq. No.	139595
Seq. ID	LIB24-035-Q1-E1-C2
Method	BLASTX
NCBI GI	g2408068
BLAST score	323
E value	6.0e-30
Match length	124
% identity	48
NCBI Description	(Z99165) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	139596
Seq. ID	LIB24-035-Q1-E1-E5
Method	BLASTX
NCBI GI	g4646198
BLAST score	101
E value	2.0e-36
Match length	105
% identity	78
NCBI Description	(AC007230) T23K8.6 [Arabidopsis thaliana]

Seq. No.	139597
Seq. ID	LIB24-035-Q1-E1-F8
Method	BLASTN
NCBI GI	g3335331
BLAST score	290
E value	1.0e-162
Match length	368
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8F5 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139598
Seq. ID	LIB24-035-Q1-E1-G12
Method	BLASTX
NCBI GI	g2190187
BLAST score	196

E value	3.0e-15
Match length	91
% identity	16
NCBI Description	(D64087) nuclear matrix constituent protein 1 (NMCP1) [Daucus carota]

Seq. No.	139599
Seq. ID	LIB24-036-Q1-E1-A4
Method	BLASTX
NCBI GI	g2317901
BLAST score	477
E value	4.0e-48
Match length	108
% identity	80
NCBI Description	(U89959) Similar to vesicle transport protein, PIR Accession Number A55931 [Arabidopsis thaliana]

Seq. No.	139600
Seq. ID	LIB24-036-Q1-E1-A8
Method	BLASTN
NCBI GI	g1322277
BLAST score	220
E value	1.0e-121
Match length	220
% identity	100
NCBI Description	Arabidopsis thaliana cyclophilin (ROC4) gene, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	139601
Seq. ID	LIB24-036-Q1-E1-B2
Method	BLASTN
NCBI GI	g4691223
BLAST score	96
E value	4.0e-47
Match length	112
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15 (ESSA project)

Seq. No.	139602
Seq. ID	LIB24-036-Q1-E1-D2
Method	BLASTN
NCBI GI	g4519183
BLAST score	181
E value	2.0e-97
Match length	221
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15C23, complete sequence

Seq. No.	139603
Seq. ID	LIB24-036-Q1-E1-D3
Method	BLASTX
NCBI GI	g3461814
BLAST score	484
E value	4.0e-49
Match length	95

% identity	97
NCBI Description	(AC004138) hypothetical protein [Arabidopsis thaliana]
Seq. No.	139604
Seq. ID	LIB24-036-Q1-E1-E8
Method	BLASTN
NCBI GI	g2275194
BLAST score	178
E value	2.0e-95
Match length	182
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T08I13 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	139605
Seq. ID	LIB24-036-Q1-E1-F7
Method	BLASTX
NCBI GI	g4056434
BLAST score	262
E value	5.0e-23
Match length	52
% identity	100
NCBI Description	(AC005990) Similar to OBP32pep protein gb_U37698 from Arabidopsis thaliana. [Arabidopsis thaliana]
Seq. No.	139606
Seq. ID	LIB24-036-Q1-E1-G3
Method	BLASTN
NCBI GI	g3831448
BLAST score	110
E value	2.0e-55
Match length	131
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T32F6 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	139607
Seq. ID	LIB24-036-Q1-E1-G6
Method	BLASTX
NCBI GI	g1171429
BLAST score	56
E value	2.0e-12
Match length	70
% identity	61
NCBI Description	(U44028) CKC [Arabidopsis thaliana]
Seq. No.	139608
Seq. ID	LIB24-037-Q1-E1-A12
Method	BLASTX
NCBI GI	g4586248
BLAST score	363
E value	1.0e-34
Match length	68
% identity	100
NCBI Description	(AL049640) growth factor like protein [Arabidopsis thaliana]

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Seq. No.	139609
Seq. ID	LIB24-037-Q1-E2-A4
Method	BLASTX
NCBI GI	g4539404
BLAST score	195
E value	4.0e-15
Match length	106
% identity	43
NCBI Description	(AL049524) putative protein [Arabidopsis thaliana]

Seq. No.	139610
Seq. ID	LIB24-037-Q1-E2-B1
Method	BLASTN
NCBI GI	g2494106
BLAST score	132
E value	3.0e-68
Match length	219
% identity	96
NCBI Description	Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139611
Seq. ID	LIB24-037-Q1-E2-D12
Method	BLASTX
NCBI GI	g1174592
BLAST score	408
E value	3.0e-40
Match length	74
% identity	100
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum sativum]

Seq. No.	139612
Seq. ID	LIB24-037-Q1-E2-E3
Method	BLASTX
NCBI GI	g4583656
BLAST score	170
E value	3.0e-12
Match length	85
% identity	47
NCBI Description	(AJ010592) ubiquitin-conjugating enzyme [Guillardia theta]

Seq. No.	139613
Seq. ID	LIB24-038-Q1-E1-F12
Method	BLASTN
NCBI GI	g2828278
BLAST score	173
E value	1.0e-92
Match length	311
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16 (ESSAII project)

Seq. No.	139614
Seq. ID	LIB24-038-Q1-E1-F9
Method	BLASTN

NCBI GI	g3309085
BLAST score	83
E value	6.0e-39
Match length	91
% identity	98
NCBI Description	Arabidopsis thaliana calcineurin B-like protein 3 (CBL3) mRNA, complete cds

Seq. No.	139615
Seq. ID	LIB24-038-Q1-E1-G6
Method	BLASTX
NCBI GI	g2245070
BLAST score	201
E value	1.0e-15
Match length	92
% identity	43
NCBI Description	(Z97342) hypothetical protein [Arabidopsis thaliana]

Seq. No.	139616
Seq. ID	LIB24-038-Q1-E1-G7
Method	BLASTX
NCBI GI	g3924596
BLAST score	532
E value	1.0e-54
Match length	108
% identity	93
NCBI Description	(AF069442) putative phospho-ser/thr phosphatase [Arabidopsis thaliana]

Seq. No.	139617
Seq. ID	LIB24-038-Q1-E1-H7
Method	BLASTN
NCBI GI	g4567259
BLAST score	105
E value	3.0e-52
Match length	205
% identity	43
NCBI Description	Arabidopsis thaliana chromosome II BAC F3K23 genomic sequence, complete sequence

Seq. No.	139618
Seq. ID	LIB24-038-Q1-E1-H9
Method	BLASTX
NCBI GI	g3885334
BLAST score	352
E value	2.0e-33
Match length	108
% identity	62
NCBI Description	(AC005623) putative argonaute protein [Arabidopsis thaliana]

Seq. No.	139619
Seq. ID	LIB24-039-Q1-E1-F10
Method	BLASTN
NCBI GI	g4079614
BLAST score	170
E value	1.0e-90

Match length	364
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC F21M11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139620
Seq. ID	LIB24-039-Q1-E1-G4
Method	BLASTX
NCBI GI	g115783
BLAST score	444
E value	3.0e-44
Match length	83
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	139621
Seq. ID	LIB24-039-Q1-E1-H12
Method	BLASTX
NCBI GI	g2347209
BLAST score	404
E value	9.0e-40
Match length	80
% identity	96
NCBI Description	(AC002338) EGF receptor like protein isolog [Arabidopsis thaliana]

Seq. No.	139622
Seq. ID	LIB24-040-Q1-E1-B12
Method	BLASTX
NCBI GI	g2317910
BLAST score	292
E value	2.0e-26
Match length	54
% identity	98
NCBI Description	(U89959) CER1 protein [Arabidopsis thaliana]

Seq. No.	139623
Seq. ID	LIB24-040-Q1-E1-F11
Method	BLASTN
NCBI GI	g4309683
BLAST score	251
E value	1.0e-139
Match length	312
% identity	96
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T31J12 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139624
Seq. ID	LIB24-040-Q1-E1-G11
Method	BLASTN
NCBI GI	g3128137
BLAST score	328
E value	0.0e+00
Match length	344

% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9I9, complete sequence [Arabidopsis thaliana]
Seq. No.	139625
Seq. ID	LIB24-041-Q1-E1-A6
Method	BLASTN
NCBI GI	g2342673
BLAST score	414
E value	0.0e+00
Match length	414
% identity	100
NCBI Description	Sequence of BAC F7G19 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]
Seq. No.	139626
Seq. ID	LIB24-041-Q1-E1-C1
Method	BLASTN
NCBI GI	g4454587
BLAST score	75
E value	3.0e-34
Match length	235
% identity	98
NCBI Description	Arabidopsis thaliana BAC F21A20 from chromosome V near 61 cM, complete sequence [Arabidopsis thaliana]
Seq. No.	139627
Seq. ID	LIB24-041-Q1-E1-D3
Method	BLASTX
NCBI GI	g2459421
BLAST score	518
E value	8.0e-53
Match length	111
% identity	88
NCBI Description	(AC002332) putative calcium-binding EF-hand protein [Arabidopsis thaliana]
Seq. No.	139628
Seq. ID	LIB24-041-Q1-E1-D7
Method	BLASTX
NCBI GI	g3025189
BLAST score	245
E value	6.0e-21
Match length	94
% identity	50
NCBI Description	HYPOTHETICAL 67.1 KD PROTEIN SLL1770 >gi_1652753_dbj_BAA17672_ (D90908) ABC1-like [Synechocystis sp.]
Seq. No.	139629
Seq. ID	LIB24-041-Q1-E1-E12
Method	BLASTX
NCBI GI	g3212877
BLAST score	541
E value	2.0e-55
Match length	123
% identity	89

NCBI Description	(AC004005) Lea-like protein [Arabidopsis thaliana]
Seq. No.	139630
Seq. ID	LIB24-041-Q1-E1-G7
Method	BLASTN
NCBI GI	g4519183
BLAST score	375
E value	0.0e+00
Match length	402
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15C23, complete sequence
Seq. No.	139631
Seq. ID	LIB24-042-Q1-E1-B12
Method	BLASTN
NCBI GI	g4217996
BLAST score	144
E value	1.0e-75
Match length	152
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F24H14 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	139632
Seq. ID	LIB24-042-Q1-E1-D1
Method	BLASTN
NCBI GI	g4757396
BLAST score	61
E value	1.0e-25
Match length	216
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K8A10, complete sequence
Seq. No.	139633
Seq. ID	LIB24-042-Q1-E1-E1
Method	BLASTN
NCBI GI	g4757662
BLAST score	215
E value	1.0e-117
Match length	413
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome I, complete sequence
Seq. No.	139634
Seq. ID	LIB24-042-Q1-E1-E12
Method	BLASTX
NCBI GI	g1706318
BLAST score	514
E value	2.0e-52
Match length	119
% identity	80
NCBI Description	GLUTAMATE DECARBOXYLASE (GAD) (ERT D1) >gi_1362098_pir__S56177 probable glutamate decarboxylase - tomato >gi_995555_emb_CAA56812_ (X80840) homology to

pyroxidal-5'-phosphate-dependant glutamate decarboxylases; putative start codon [Lycopersicon esculentum]

Seq. No.	139635
Seq. ID	LIB24-042-Q1-E1-E4
Method	BLASTN
NCBI GI	g4063737
BLAST score	198
E value	1.0e-107
Match length	198
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F24D13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139636
Seq. ID	LIB24-042-Q1-E1-E5
Method	BLASTN
NCBI GI	g2191126
BLAST score	179
E value	5.0e-96
Match length	400
% identity	100
NCBI Description	Arabidopsis thaliana BAC IG002N01

Seq. No.	139637
Seq. ID	LIB24-042-Q1-E1-F2
Method	BLASTN
NCBI GI	g4757392
BLAST score	216
E value	1.0e-118
Match length	412
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K14A17, complete sequence

Seq. No.	139638
Seq. ID	LIB24-042-Q1-E1-F4
Method	BLASTX
NCBI GI	g4760345
BLAST score	156
E value	2.0e-10
Match length	90
% identity	38
NCBI Description	(AL049769) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	139639
Seq. ID	LIB24-042-Q1-E1-F5
Method	BLASTX
NCBI GI	g3426035
BLAST score	478
E value	4.0e-48
Match length	128
% identity	77
NCBI Description	(AC005168) putative ripening-associated protein [Arabidopsis thaliana]

Seq. No.	139640

Seq. ID	LIB24-042-Q1-E1-F8
Method	BLASTX
NCBI GI	g1702986
BLAST score	508
E value	1.0e-51
Match length	103
% identity	100
NCBI Description	14-3-3-LIKE PROTEIN GF14 CHI >gi_1255987 (U09377) GF14chi isoform [Arabidopsis thaliana] >gi_1256534 (L09112) GF14 chi chain [Arabidopsis thaliana]

Seq. No.	139641
Seq. ID	LIB24-042-Q1-E1-G2
Method	BLASTX
NCBI GI	g1362007
BLAST score	729
E value	1.0e-77
Match length	136
% identity	99
NCBI Description	thioglucosidase (EC 3.2.3.1) - Arabidopsis thaliana >gi_871992_emb_CAA55787_ (X79195) thioglucosidase [Arabidopsis thaliana]

Seq. No.	139642
Seq. ID	LIB24-042-Q1-E1-H12
Method	BLASTX
NCBI GI	g2982583
BLAST score	652
E value	1.0e-68
Match length	126
% identity	100
NCBI Description	(AJ003135) polygalacturonase [Arabidopsis thaliana] >gi_3152948_emb_CAA06610_ (AJ005584) polygalacturonase [Arabidopsis thaliana]

Seq. No.	139643
Seq. ID	LIB24-042-Q1-E1-H8
Method	BLASTX
NCBI GI	g416758
BLAST score	335
E value	7.0e-32
Match length	73
% identity	79
NCBI Description	SERINE CARBOXYPEPTIDASE PRECURSOR >gi_166674 (M81130) carboxypeptidase Y-like protein [Arabidopsis thaliana] >gi_445120_prf__1908426A carboxypeptidase Y [Arabidopsis thaliana]

Seq. No.	139644
Seq. ID	LIB24-043-Q1-E1-A6
Method	BLASTN
NCBI GI	g2529657
BLAST score	93
E value	2.0e-45
Match length	114
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T30B22 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139645
Seq. ID	LIB24-043-Q1-E1-B9
Method	BLASTN
NCBI GI	g3046852
BLAST score	195
E value	1.0e-106
Match length	199
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQJ16, complete sequence [Arabidopsis thaliana]

Seq. No.	139646
Seq. ID	LIB24-043-Q1-E1-F8
Method	BLASTN
NCBI GI	g3420042
BLAST score	110
E value	4.0e-55
Match length	231
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T13E15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139647
Seq. ID	LIB24-043-Q1-E1-G4
Method	BLASTN
NCBI GI	g3449329
BLAST score	201
E value	1.0e-109
Match length	365
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDH9, complete sequence [Arabidopsis thaliana]

Seq. No.	139648
Seq. ID	LIB24-043-Q1-E1-G5
Method	BLASTX
NCBI GI	g4234768
BLAST score	495
E value	4.0e-50
Match length	92
% identity	100
NCBI Description	(AF069468) sterol-C5-desaturase [Arabidopsis thaliana]

Seq. No.	139649
Seq. ID	LIB24-044-Q1-E1-A2
Method	BLASTX
NCBI GI	g4454037
BLAST score	655
E value	6.0e-69
Match length	123
% identity	98
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	139650

Seq. ID	LIB24-044-Q1-E1-A9
Method	BLASTX
NCBI GI	g418133
BLAST score	265
E value	3.0e-23
Match length	51
% identity	100
NCBI Description	ANTHRANILATE SYNTHASE COMPONENT I-1 PRECURSOR >gi_166604 (M92353) anthranilate synthase alpha subunit [Arabidopsis thaliana]

Seq. No.	139651
Seq. ID	LIB24-044-Q1-E1-B8
Method	BLASTX
NCBI GI	g3403234
BLAST score	328
E value	1.0e-30
Match length	111
% identity	53
NCBI Description	(AF071543) ribulose-1,5-bisphosphate carboxylase/oxygenase N-methyltransferase [Spinacia oleracea] >gi_3403238 (AF071545) ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase II [Spinacia oleracea]

Seq. No.	139652
Seq. ID	LIB24-044-Q1-E1-D4
Method	BLASTX
NCBI GI	g2501603
BLAST score	158
E value	1.0e-10
Match length	44
% identity	66
NCBI Description	HYPOTHETICAL 77.0 KD PROTEIN IN HES1-SEC63 INTERGENIC REGION >gi_2132095_pir__S67136 hypothetical protein YOR243c - yeast (Saccharomyces cerevisiae) >gi_1420554_emb_CAA99464_ (Z75151) ORF YOR243c [Saccharomyces cerevisiae]

Seq. No.	139653
Seq. ID	LIB24-044-Q1-E1-E1
Method	BLASTN
NCBI GI	g1181530
BLAST score	85
E value	5.0e-40
Match length	85
% identity	100
NCBI Description	Arabidopsis thaliana thionin (Thi2.1) mRNA, complete cds

Seq. No.	139654
Seq. ID	LIB24-044-Q1-E1-F11
Method	BLASTN
NCBI GI	g3212846
BLAST score	324
E value	0.0e+00
Match length	328
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F6E13 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139655
Seq. ID	LIB24-044-Q1-E1-G12
Method	BLASTN
NCBI GI	g2564050
BLAST score	221
E value	1.0e-121
Match length	225
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUA22, complete sequence [Arabidopsis thaliana]

Seq. No.	139656
Seq. ID	LIB24-044-Q1-E1-G8
Method	BLASTN
NCBI GI	g4757406
BLAST score	80
E value	3.0e-37
Match length	214
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPF21, complete sequence

Seq. No.	139657
Seq. ID	LIB24-044-Q1-E1-H3
Method	BLASTX
NCBI GI	g3608140
BLAST score	255
E value	5.0e-22
Match length	84
% identity	61
NCBI Description	(AC005314) unknown protein [Arabidopsis thaliana]

Seq. No.	139658
Seq. ID	LIB24-045-Q1-E1-A4
Method	BLASTX
NCBI GI	g2244752
BLAST score	208
E value	5.0e-17
Match length	55
% identity	75
NCBI Description	(Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No.	139659
Seq. ID	LIB24-045-Q1-E1-B10
Method	BLASTX
NCBI GI	g2673917
BLAST score	339
E value	2.0e-32
Match length	68
% identity	97
NCBI Description	(AC002561) putative ATP-dependent RNA helicase [Arabidopsis thaliana]

Seq. No.	139660
Seq. ID	LIB24-045-Q1-E1-D6

09604705.060704

Method	BLASTX
NCBI GI	g2914700
BLAST score	298
E value	1.0e-27
Match length	60
% identity	95
NCBI Description	(AC003974) tRNA-processing protein SEN3-like [Arabidopsis thaliana]

Seq. No.	139661
Seq. ID	LIB24-045-Q1-E1-E4
Method	BLASTN
NCBI GI	g3608126
BLAST score	362
E value	0.0e+00
Match length	383
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T32F12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139662
Seq. ID	LIB24-045-Q1-E1-F2
Method	BLASTX
NCBI GI	g3292820
BLAST score	144
E value	4.0e-09
Match length	35
% identity	86
NCBI Description	(AL031018) putative MADS Box / AGL protein [Arabidopsis thaliana]

Seq. No.	139663
Seq. ID	LIB24-045-Q1-E1-F4
Method	BLASTX
NCBI GI	g4580953
BLAST score	316
E value	3.0e-29
Match length	126
% identity	52
NCBI Description	(AF117734) glycerol kinase-like protein 2 [Mus musculus]

Seq. No.	139664
Seq. ID	LIB24-045-Q1-E1-F5
Method	BLASTX
NCBI GI	g3152585
BLAST score	241
E value	2.0e-20
Match length	64
% identity	72
NCBI Description	(AC002986) Contains similarity to auxin-induced protein TM018A10.6 from A. thaliana BAC gb_AF013294. [Arabidopsis thaliana]

Seq. No.	139665
Seq. ID	LIB24-045-Q1-E1-G8
Method	BLASTX
NCBI GI	g4586117

BLAST score	267
E value	5.0e-24
Match length	67
% identity	75
NCBI Description	(AL049638) putative protein [Arabidopsis thaliana]

Seq. No.	139666
Seq. ID	LIB24-045-Q1-E1-H10
Method	BLASTX
NCBI GI	g4106340
BLAST score	234
E value	4.0e-20
Match length	46
% identity	100
NCBI Description	(AF062396) protein phosphatase 2A regulatory subunit isoform B' delta [Arabidopsis thaliana]

Seq. No.	139667
Seq. ID	LIB24-045-Q1-E1-H6
Method	BLASTX
NCBI GI	g1076294
BLAST score	346
E value	1.0e-32
Match length	91
% identity	71
NCBI Description	ATAF2 protein - Arabidopsis thaliana

Seq. No.	139668
Seq. ID	LIB24-046-Q1-E1-B5
Method	BLASTX
NCBI GI	g1350783
BLAST score	200
E value	1.0e-15
Match length	125
% identity	5
NCBI Description	RECEPTOR-LIKE PROTEIN KINASE 5 PRECURSOR >gi_282883_pir__S27756 receptor-like protein kinase precursor - Arabidopsis thaliana >gi_166850 (M84660) receptor-like protein kinase [Arabidopsis thaliana] >gi_2842492_emb_CAA16889_ (AL021749) receptor-like protein kinase 5 precursor (RLK5) [Arabidopsis thaliana]

Seq. No.	139669
Seq. ID	LIB24-046-Q1-E1-B7
Method	BLASTN
NCBI GI	g3641835
BLAST score	336
E value	0.0e+00
Match length	381
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T4L20 (ESSAII project)

Seq. No.	139670
Seq. ID	LIB24-046-Q1-E1-C11
Method	BLASTN
NCBI GI	g2150022

BLAST score	95
E value	2.0e-46
Match length	155
% identity	95
NCBI Description	Arabidopsis thaliana receptor-like kinase LECRK1 (LECRK1) gene, complete cds

Seq. No.	139671
Seq. ID	LIB24-046-Q1-E1-C8
Method	BLASTN
NCBI GI	g2477521
BLAST score	109
E value	7.0e-55
Match length	109
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC F22K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139672
Seq. ID	LIB24-046-Q1-E1-E7
Method	BLASTX
NCBI GI	g4544445
BLAST score	157
E value	2.0e-10
Match length	81
% identity	48
NCBI Description	(AC006592) putative pyrophosphate--fructose 6-phosphate 1-phosphotransferase [Arabidopsis thaliana]

Seq. No.	139673
Seq. ID	LIB24-046-Q1-E1-F2
Method	BLASTN
NCBI GI	g4027862
BLAST score	250
E value	1.0e-138
Match length	262
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T7A14 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139674
Seq. ID	LIB24-046-Q1-E1-F3
Method	BLASTX
NCBI GI	g3668173
BLAST score	576
E value	1.0e-59
Match length	121
% identity	93
NCBI Description	(AB006777) vegetative storage protein [Arabidopsis thaliana]

Seq. No.	139675
Seq. ID	LIB24-046-Q1-E1-G5
Method	BLASTX
NCBI GI	g3738338
BLAST score	243
E value	1.0e-20

Match length	84
% identity	62
NCBI Description	(AC005170) putative polygalacturonase [Arabidopsis thaliana]

Seq. No.	139676
Seq. ID	LIB24-046-Q1-E1-H3
Method	BLASTN
NCBI GI	g2651294
BLAST score	81
E value	2.0e-38
Match length	85
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T2P4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139677
Seq. ID	LIB24-046-Q1-E1-H7
Method	BLASTX
NCBI GI	g2335099
BLAST score	210
E value	6.0e-17
Match length	72
% identity	57
NCBI Description	(AC002339) unknown protein [Arabidopsis thaliana]

Seq. No.	139678
Seq. ID	LIB24-047-Q1-E1-A11
Method	BLASTX
NCBI GI	g2511590
BLAST score	608
E value	2.0e-63
Match length	119
% identity	100
NCBI Description	(Y13692) multicatalytic endopeptidase complex, proteasome component, beta subunit [Arabidopsis thaliana] >gi_3421111 (AF043534) 20S proteasome beta subunit PBD1 [Arabidopsis thaliana]

Seq. No.	139679
Seq. ID	LIB24-047-Q1-E1-A6
Method	BLASTN
NCBI GI	g4589410
BLAST score	385
E value	0.0e+00
Match length	385
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F2O15, complete sequence

Seq. No.	139680
Seq. ID	LIB24-047-Q1-E1-B5
Method	BLASTX
NCBI GI	g2245080
BLAST score	249
E value	3.0e-21
Match length	121

% identity	49
NCBI Description	(Z97343) myosin heavy chain homolog [Arabidopsis thaliana]

Seq. No.	139681
Seq. ID	LIB24-047-Q1-E1-B8
Method	BLASTX
NCBI GI	g166765
BLAST score	525
E value	1.0e-53
Match length	104
% identity	96
NCBI Description	(M23106) heat shock protein HSP70-1 [Arabidopsis thaliana]

Seq. No.	139682
Seq. ID	LIB24-047-Q1-E1-C4
Method	BLASTX
NCBI GI	g2244987
BLAST score	659
E value	2.0e-69
Match length	134
% identity	92
NCBI Description	(Z97340) similarity to protein kinase - slime mold (Dictyostelium) [Arabidopsis thaliana]

Seq. No.	139683
Seq. ID	LIB24-047-Q1-E1-D6
Method	BLASTX
NCBI GI	g2499607
BLAST score	718
E value	3.0e-76
Match length	138
% identity	99
NCBI Description	MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 3 (MAP KINASE 3) (ATMPK3) >gi_629544_pir__S40469 mitogen-activated protein kinase 3 (EC 2.7.1.-) - Arabidopsis thaliana >gi_457398_dbj_BAA04866_ (D21839) MAP kinase [Arabidopsis thaliana]

Seq. No.	139684
Seq. ID	LIB24-047-Q1-E1-E2
Method	BLASTX
NCBI GI	g3025299
BLAST score	363
E value	1.0e-34
Match length	73
% identity	96
NCBI Description	HYPOTHETICAL 62.3 KD PROTEIN T29M21.25 >gi_2088660 (AF002109) ABC1 isolog [Arabidopsis thaliana]

Seq. No.	139685
Seq. ID	LIB24-047-Q1-E1-E5
Method	BLASTN
NCBI GI	g4220643
BLAST score	88
E value	4.0e-42
Match length	195
% identity	94

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD22, complete sequence [Arabidopsis thaliana]
Seq. No.	139686
Seq. ID	LIB24-047-Q1-E1-E7
Method	BLASTX
NCBI GI	g399392
BLAST score	370
E value	2.0e-35
Match length	119
% identity	65
NCBI Description	DIHYDROLIPOAMIDE DEHYDROGENASE PRECURSOR (GLYCINE CLEAVAGE SYSTEM L PROTEIN) >gi_100037_pir__S22384 dihydrolipoamide dehydrogenase (EC 1.8.1.4) - garden pea >gi_20806_emb_CAA45066_ (X63464) dihydrolipoamide dehydrogenase [Pisum sativum]
Seq. No.	139687
Seq. ID	LIB24-047-Q1-E1-F5
Method	BLASTN
NCBI GI	g3063690
BLAST score	148
E value	1.0e-77
Match length	373
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11 (ESSAII project)
Seq. No.	139688
Seq. ID	LIB24-047-Q1-E1-F9
Method	BLASTX
NCBI GI	g729478
BLAST score	624
E value	3.0e-65
Match length	130
% identity	86
NCBI Description	FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR) >gi_442481_dbj_BAA04616_ (D17790) ferredoxin-NADP+ reductase [Oryza sativa]
Seq. No.	139689
Seq. ID	LIB24-047-Q1-E1-G10
Method	BLASTX
NCBI GI	g4587552
BLAST score	685
E value	2.0e-72
Match length	139
% identity	100
NCBI Description	(AC006577) Strong similarity to gb_S77096 aldehyde dehydrogenase homolog from Brassica napus and is a member of PF_00171 Aldehyde dehydrogenase family. ESTs gb_T46213, gb_T42164, gb_T43682, gb_N96380, gb_T42973, gb
Seq. No.	139690
Seq. ID	LIB24-047-Q1-E1-G4
Method	BLASTN
NCBI GI	g3399678

BLAST score	382
E value	0.0e+00
Match length	398
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F13M7 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139691
Seq. ID	LIB24-048-Q1-E1-G10
Method	BLASTX
NCBI GI	g4185142
BLAST score	572
E value	3.0e-59
Match length	111
% identity	99
NCBI Description	(AC005724) putative DNA repair and recombination protein of the SNF2 family [Arabidopsis thaliana]

Seq. No.	139692
Seq. ID	LIB24-048-Q1-E1-G2
Method	BLASTN
NCBI GI	g3702724
BLAST score	149
E value	1.0e-78
Match length	149
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K17N15, complete sequence [Arabidopsis thaliana]

Seq. No.	139693
Seq. ID	LIB24-048-Q1-E1-H3
Method	BLASTN
NCBI GI	g2914688
BLAST score	92
E value	3.0e-44
Match length	306
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F24L7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139694
Seq. ID	LIB24-048-Q1-E2-A4
Method	BLASTN
NCBI GI	g4584841
BLAST score	413
E value	0.0e+00
Match length	413
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T23E23, complete sequence

Seq. No.	139695
Seq. ID	LIB24-048-Q1-E2-D3
Method	BLASTN
NCBI GI	g3510337
BLAST score	237
E value	1.0e-131

Match length	305
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E20, complete sequence [Arabidopsis thaliana]

Seq. No.	139696
Seq. ID	LIB24-048-Q1-E2-D7
Method	BLASTX
NCBI GI	g99688
BLAST score	372
E value	1.0e-35
Match length	73
% identity	100
NCBI Description	translation elongation factor eEF-1 alpha chain (gene A4) - Arabidopsis thaliana >gi_295789_emb_CAA34456_ (X16432) elongation factor 1-alpha [Arabidopsis thaliana]

Seq. No.	139697
Seq. ID	LIB24-048-Q1-E2-E8
Method	BLASTX
NCBI GI	g4325324
BLAST score	774
E value	8.0e-83
Match length	145
% identity	100
NCBI Description	(AF125574) lysyl-tRNA synthetase; LysRS [Arabidopsis thaliana]

Seq. No.	139698
Seq. ID	LIB24-048-Q1-E2-G7
Method	BLASTN
NCBI GI	g2244991
BLAST score	426
E value	0.0e+00
Match length	426
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	139699
Seq. ID	LIB24-049-Q1-E2-C11
Method	BLASTN
NCBI GI	g4204173
BLAST score	158
E value	2.0e-83
Match length	411
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T2K10 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139700
Seq. ID	LIB24-049-Q1-E2-E10
Method	BLASTN
NCBI GI	g2815404
BLAST score	290
E value	1.0e-162
Match length	298

% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMG4, complete sequence [Arabidopsis thaliana]

Seq. No.	139701
Seq. ID	LIB24-049-Q1-E2-E11
Method	BLASTX
NCBI GI	g2997767
BLAST score	724
E value	6.0e-77
Match length	139
% identity	34
NCBI Description	(AF054906) myrosinase-binding protein homolog [Arabidopsis thaliana]

Seq. No.	139702
Seq. ID	LIB24-049-Q1-E2-F9
Method	BLASTX
NCBI GI	g1912286
BLAST score	559
E value	1.0e-57
Match length	106
% identity	100
NCBI Description	(U39568) type 2A serine/threonine protein phosphatase [Arabidopsis thaliana] >gi_2194141 (AC002062) Match to Arabidopsis protein phosphatase PP2A (gb_U39568). EST gb_T41959 comes from this gene. [Arabidopsis thaliana]

Seq. No.	139703
Seq. ID	LIB24-049-Q1-E2-H5
Method	BLASTX
NCBI GI	g4467147
BLAST score	220
E value	4.0e-18
Match length	103
% identity	52
NCBI Description	(AL035540) putative protein [Arabidopsis thaliana]

Seq. No.	139704
Seq. ID	LIB24-050-Q1-E1-B11
Method	BLASTN
NCBI GI	g1946354
BLAST score	281
E value	1.0e-157
Match length	281
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T06B20 genomic sequence, complete sequence

Seq. No.	139705
Seq. ID	LIB24-050-Q1-E1-H2
Method	BLASTN
NCBI GI	g2924505
BLAST score	119
E value	2.0e-60
Match length	221
% identity	97

NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone M4E13 (ESSAII project)

Seq. No.	139706
Seq. ID	LIB24-050-Q1-E1-H5
Method	BLASTX
NCBI GI	g3702339
BLAST score	445
E value	2.0e-44
Match length	104
% identity	85
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	139707
Seq. ID	LIB24-051-Q1-E1-B3
Method	BLASTN
NCBI GI	g3746057
BLAST score	301
E value	1.0e-169
Match length	301
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T16B12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139708
Seq. ID	LIB24-051-Q1-E1-B9
Method	BLASTX
NCBI GI	g2462749
BLAST score	164
E value	2.0e-14
Match length	54
% identity	76
NCBI Description	(AC002292) Putative Serine/Threonine protein kinase [Arabidopsis thaliana]

Seq. No.	139709
Seq. ID	LIB24-051-Q1-E1-F9
Method	BLASTN
NCBI GI	g4159708
BLAST score	203
E value	1.0e-110
Match length	280
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MKP6, complete sequence

Seq. No.	139710
Seq. ID	LIB24-051-Q1-E1-G1
Method	BLASTX
NCBI GI	g1076511
BLAST score	352
E value	1.0e-33
Match length	86
% identity	73
NCBI Description	H+-transporting ATPase (EC 3.6.1.35) - kidney bean >gi_758250_emb_CAA59799_ (X85804) H(+)-transporting ATPase [Phaseolus vulgaris]

Seq. No.	139711
Seq. ID	LIB24-051-Q1-E1-G12
Method	BLASTX
NCBI GI	g2315451
BLAST score	158
E value	9.0e-11
Match length	88
% identity	32
NCBI Description	(AF016448) No definition line found [Caenorhabditis elegans]

Seq. No.	139712
Seq. ID	LIB24-051-Q1-E1-G2
Method	BLASTN
NCBI GI	g4220632
BLAST score	105
E value	2.0e-52
Match length	146
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K6M13, complete sequence [Arabidopsis thaliana]

Seq. No.	139713
Seq. ID	LIB24-052-Q1-E1-B5
Method	BLASTN
NCBI GI	g3927822
BLAST score	79
E value	4.0e-37
Match length	83
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F8N16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139714
Seq. ID	LIB24-052-Q1-E1-B7
Method	BLASTX
NCBI GI	g832876
BLAST score	437
E value	2.0e-43
Match length	98
% identity	86
NCBI Description	(L41345) ascorbate free radical reductase [Solanum lycopersicum] >gi_1097368_prf__2113407A ascorbate free radical reductase [Lycopersicon esculentum]

Seq. No.	139715
Seq. ID	LIB24-052-Q1-E1-F10
Method	BLASTX
NCBI GI	g2832674
BLAST score	248
E value	9.0e-22
Match length	58
% identity	86
NCBI Description	(AL021712) fibrillin precursor-like protein [Arabidopsis thaliana]

Seq. No.	139716
Seq. ID	LIB24-052-Q1-E1-H10
Method	BLASTX
NCBI GI	g2129738
BLAST score	448
E value	6.0e-45
Match length	88
% identity	97
NCBI Description	shaggy-like kinase dzeta - Arabidopsis thaliana >gi_1225913_emb_CAA64408_ (X94938) shaggy-like kinase dzeta [Arabidopsis thaliana] >gi_1669653_emb_CAA70483_ (Y09300) serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	139717
Seq. ID	LIB24-052-Q1-E1-H3
Method	BLASTN
NCBI GI	g4371278
BLAST score	223
E value	1.0e-122
Match length	227
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T2N18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139718
Seq. ID	LIB24-052-Q1-E1-H8
Method	BLASTX
NCBI GI	g2129755
BLAST score	382
E value	3.0e-37
Match length	87
% identity	90
NCBI Description	tryptophan synthase (EC 4.2.1.20) alpha chain - Arabidopsis thaliana >gi_619753 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana] >gi_1585768_prf__2201482A Trp synthase:SUBUNIT=alpha [Arabidopsis thaliana]

Seq. No.	139719
Seq. ID	LIB24-052-Q1-E2-C12
Method	BLASTN
NCBI GI	g2880038
BLAST score	159
E value	2.0e-84
Match length	171
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T11J7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139720
Seq. ID	LIB24-052-Q1-E2-H10
Method	BLASTX
NCBI GI	g2129738
BLAST score	371
E value	4.0e-36
Match length	75
% identity	96
NCBI Description	shaggy-like kinase dzeta - Arabidopsis thaliana

	>gi_1225913_emb_CAA64408_ (X94938) shaggy-like kinase dzeta [Arabidopsis thaliana] >gi_1669653_emb_CAA70483_ (Y09300) serine/threonine kinase [Arabidopsis thaliana]
Seq. No.	139721
Seq. ID	LIB24-053-Q1-E1-B11
Method	BLASTX
NCBI GI	g3287270
BLAST score	655
E value	6.0e-69
Match length	134
% identity	88
NCBI Description	(Y09533) involved in starch metabalism [Solanum tuberosum]
Seq. No.	139722
Seq. ID	LIB24-053-Q1-E1-C3
Method	BLASTN
NCBI GI	g2696018
BLAST score	52
E value	1.0e-20
Match length	56
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC9, complete sequence [Arabidopsis thaliana]
Seq. No.	139723
Seq. ID	LIB24-053-Q1-E2-C5
Method	BLASTX
NCBI GI	g4587553
BLAST score	300
E value	3.0e-27
Match length	60
% identity	100
NCBI Description	(AC006577) F15I1.20 [Arabidopsis thaliana]
Seq. No.	139724
Seq. ID	LIB24-053-Q1-E2-C6
Method	BLASTX
NCBI GI	g2129575
BLAST score	534
E value	1.0e-54
Match length	109
% identity	93
NCBI Description	DNA repair protein homolog XPBara - Arabidopsis thaliana
Seq. No.	139725
Seq. ID	LIB24-053-Q1-E2-D3
Method	BLASTN
NCBI GI	g4741184
BLAST score	160
E value	4.0e-85
Match length	160
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone T23J7 (ESSA project)
Seq. No.	139726

Seq. ID	LIB24-054-Q1-E1-C1
Method	BLASTX
NCBI GI	g3668173
BLAST score	565
E value	2.0e-58
Match length	120
% identity	93
NCBI Description	(AB006777) vegetative storage protein [Arabidopsis thaliana]

Seq. No.	139727
Seq. ID	LIB24-054-Q1-E1-F7
Method	BLASTN
NCBI GI	g3510336
BLAST score	154
E value	1.0e-81
Match length	166
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18J17, complete sequence [Arabidopsis thaliana]

Seq. No.	139728
Seq. ID	LIB24-054-Q1-E1-G7
Method	BLASTX
NCBI GI	g3738302
BLAST score	498
E value	1.0e-50
Match length	103
% identity	94
NCBI Description	(AC005309) tubby-like protein [Arabidopsis thaliana] >gi_4249398 (AC006072) putative tubby protein [Arabidopsis thaliana]

Seq. No.	139729
Seq. ID	LIB24-056-Q1-E2-E2
Method	BLASTX
NCBI GI	g4185511
BLAST score	445
E value	2.0e-44
Match length	88
% identity	98
NCBI Description	(AF102822) actin depolymerizing factor 4 [Arabidopsis thaliana]

Seq. No.	139730
Seq. ID	LIB24-056-Q1-E2-E6
Method	BLASTN
NCBI GI	g2656025
BLAST score	38
E value	4.0e-12
Match length	204
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCD7

Seq. No.	139731
Seq. ID	LIB24-056-Q1-E2-E7

Method	BLASTX
NCBI GI	g2459445
BLAST score	181
E value	2.0e-13
Match length	85
% identity	21
NCBI Description	(AC002332) putative ribonucleoprotein [Arabidopsis thaliana]

Seq. No.	139732
Seq. ID	LIB24-056-Q1-E2-E8
Method	BLASTN
NCBI GI	g4589430
BLAST score	201
E value	1.0e-109
Match length	217
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLD14, complete sequence

Seq. No.	139733
Seq. ID	LIB24-056-Q1-E2-F7
Method	BLASTX
NCBI GI	g585536
BLAST score	340
E value	3.0e-32
Match length	82
% identity	79
NCBI Description	MYROSINASE PRECURSOR (SINIGRINASE) (THIOGLUCOSIDASE) >gi_1362006_pir__S56653 thioglucosidase (EC 3.2.3.1) - Arabidopsis thaliana >gi_304115 (L11454) thioglucosidase [Arabidopsis thaliana] >gi_871990_emb_CAA55786_ (X79194) thioglucosidase [Arabidopsis thaliana]

Seq. No.	139734
Seq. ID	LIB24-058-Q1-E1-A11
Method	BLASTN
NCBI GI	g2914688
BLAST score	164
E value	4.0e-87
Match length	292
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F24L7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139735
Seq. ID	LIB24-058-Q1-E1-A3
Method	BLASTN
NCBI GI	g3158375
BLAST score	79
E value	6.0e-37
Match length	127
% identity	91
NCBI Description	Arabidopsis thaliana SEN5 mRNA, partial cds

Seq. No.	139736
Seq. ID	LIB24-058-Q1-E1-C6

Method	BLASTX
NCBI GI	g401213
BLAST score	418
E value	2.0e-41
Match length	93
% identity	88
NCBI Description	ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE PRECURSOR >gi_166792 (M96073) phosphoribosylanthranilate transferase [Arabidopsis thaliana] >gi_445600_prf__1909347A phosphoribosylanthranilate transferase [Arabidopsis thaliana]

Seq. No.	139737
Seq. ID	LIB24-058-Q1-E1-D10
Method	BLASTN
NCBI GI	g2252848
BLAST score	38
E value	6.0e-12
Match length	46
% identity	96
NCBI Description	Arabidopsis thaliana BAC TM018A10

Seq. No.	139738
Seq. ID	LIB24-058-Q1-E1-D5
Method	BLASTN
NCBI GI	g1297301
BLAST score	82
E value	2.0e-38
Match length	233
% identity	96
NCBI Description	Arabidopsis thaliana phospholipase D mRNA, complete cds

Seq. No.	139739
Seq. ID	LIB24-058-Q1-E1-D9
Method	BLASTN
NCBI GI	g4589446
BLAST score	99
E value	1.0e-48
Match length	175
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: T12B11, complete sequence

Seq. No.	139740
Seq. ID	LIB24-058-Q1-E1-G10
Method	BLASTX
NCBI GI	g3461835
BLAST score	176
E value	9.0e-13
Match length	130
% identity	34
NCBI Description	(AC005315) putative protein kinase [Arabidopsis thaliana] >gi_3927840 (AC005727) putative protein kinase [Arabidopsis thaliana]

Seq. No.	139741
Seq. ID	LIB24-059-Q1-E1-A8

Method	BLASTN
NCBI GI	g2351073
BLAST score	115
E value	6.0e-58
Match length	319
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	139742
Seq. ID	LIB24-059-Q1-E1-D11
Method	BLASTN
NCBI GI	g2880038
BLAST score	133
E value	9.0e-69
Match length	301
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T11J7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139743
Seq. ID	LIB24-059-Q1-E1-E12
Method	BLASTX
NCBI GI	g3785977
BLAST score	342
E value	3.0e-32
Match length	122
% identity	49
NCBI Description	(AC005560) putative growth regulator protein [Arabidopsis thaliana]

Seq. No.	139744
Seq. ID	LIB24-059-Q1-E1-F10
Method	BLASTN
NCBI GI	g4191771
BLAST score	173
E value	2.0e-92
Match length	345
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F3P11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139745
Seq. ID	LIB24-060-Q1-E1-B7
Method	BLASTX
NCBI GI	g2598227
BLAST score	701
E value	3.0e-74
Match length	141
% identity	98
NCBI Description	(AJ222585) AT-hook protein 1 [Arabidopsis thaliana]

Seq. No.	139746
Seq. ID	LIB24-060-Q1-E1-C5
Method	BLASTX
NCBI GI	g4455159
BLAST score	430

E value	2.0e-42
Match length	114
% identity	67
NCBI Description	(AL021687) putative protein [Arabidopsis thaliana]

Seq. No.	139747
Seq. ID	LIB24-060-Q1-E1-D2
Method	BLASTX
NCBI GI	g3402697
BLAST score	597
E value	3.0e-62
Match length	111
% identity	32
NCBI Description	(AC004261) putative phosphatidylinositol-4-phosphate 5-kinase [Arabidopsis thaliana]

Seq. No.	139748
Seq. ID	LIB24-060-Q1-E1-D8
Method	BLASTN
NCBI GI	g2760168
BLAST score	117
E value	5.0e-59
Match length	345
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MEE6, complete sequence [Arabidopsis thaliana]

Seq. No.	139749
Seq. ID	LIB24-060-Q1-E1-E7
Method	BLASTX
NCBI GI	g3776567
BLAST score	614
E value	4.0e-64
Match length	141
% identity	87
NCBI Description	(AC005388) Strong similarity to F21B7.33 gi_2809264 from A. thaliana BAC gb_AC002560. EST gb_N65119 comes from this gene. [Arabidopsis thaliana]

Seq. No.	139750
Seq. ID	LIB24-060-Q1-E1-G10
Method	BLASTN
NCBI GI	g2351070
BLAST score	176
E value	2.0e-94
Match length	230
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTH12, complete sequence [Arabidopsis thaliana]

Seq. No.	139751
Seq. ID	LIB24-060-Q1-E1-G5
Method	BLASTX
NCBI GI	g1617036
BLAST score	427
E value	2.0e-42
Match length	106

% identity	79
NCBI Description	(Y08624) Ted2 [Vigna unguiculata]

Seq. No.	139752
Seq. ID	LIB24-060-Q1-E1-G7
Method	BLASTX
NCBI GI	g2529668
BLAST score	215
E value	1.0e-17
Match length	89
% identity	47
NCBI Description	(AC002535) putative photolyase/blue-light receptor [Arabidopsis thaliana] >gi_3319288 (AF053366) photolyase/blue light photoreceptor PHR2 [Arabidopsis thaliana]

Seq. No.	139753
Seq. ID	LIB24-060-Q1-E1-G8
Method	BLASTN
NCBI GI	g1946354
BLAST score	164
E value	2.0e-87
Match length	176
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T06B20 genomic sequence, complete sequence

Seq. No.	139754
Seq. ID	LIB24-061-Q1-E1-A11
Method	BLASTX
NCBI GI	g3228517
BLAST score	188
E value	1.0e-14
Match length	44
% identity	84
NCBI Description	(AF007788) ETTIN [Arabidopsis thaliana]

Seq. No.	139755
Seq. ID	LIB24-061-Q1-E1-A6
Method	BLASTN
NCBI GI	g4521999
BLAST score	293
E value	1.0e-164
Match length	297
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F2G1 genomic sequence, complete sequence

Seq. No.	139756
Seq. ID	LIB24-061-Q1-E1-A9
Method	BLASTN
NCBI GI	g3046854
BLAST score	108
E value	5.0e-54
Match length	108
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

D0504705 - D0504900

MRG7, complete sequence [Arabidopsis thaliana]

Seq. No.	139757
Seq. ID	LIB24-061-Q1-E1-B7
Method	BLASTN
NCBI GI	g3449329
BLAST score	393
E value	0.0e+00
Match length	393
% identity	50
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDH9, complete sequence [Arabidopsis thaliana]

Seq. No.	139758
Seq. ID	LIB24-061-Q1-E1-B8
Method	BLASTX
NCBI GI	g4432846
BLAST score	298
E value	2.0e-27
Match length	78
% identity	76
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	139759
Seq. ID	LIB24-061-Q1-E1-C11
Method	BLASTX
NCBI GI	g585012
BLAST score	425
E value	6.0e-42
Match length	84
% identity	100
NCBI Description	PHYTOENE DEHYDROGENASE PRECURSOR (PHYTOENE DESATURASE) >gi_289205 (L16237) phytoene desaturase [Arabidopsis thaliana] >gi_2244777_emb_CAB10200_ (Z97335) unnamed protein product [Arabidopsis thaliana]

Seq. No.	139760
Seq. ID	LIB24-061-Q1-E1-C12
Method	BLASTX
NCBI GI	g4567263
BLAST score	534
E value	1.0e-54
Match length	103
% identity	100
NCBI Description	(AC006841) putative cell division inhibitor [Arabidopsis thaliana]

Seq. No.	139761
Seq. ID	LIB24-061-Q1-E1-D10
Method	BLASTN
NCBI GI	g4512656
BLAST score	159
E value	4.0e-84
Match length	345
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

09604074.0960404

Seq. No.	139762
Seq. ID	LIB24-061-Q1-E1-D9
Method	BLASTX
NCBI GI	g2342690
BLAST score	235
E value	1.0e-19
Match length	88
% identity	35
NCBI Description	(AC000106) Similar to Homo copine I (gb_U83246). [Arabidopsis thaliana]

Seq. No.	139763
Seq. ID	LIB24-061-Q1-E1-F3
Method	BLASTX
NCBI GI	g3056584
BLAST score	240
E value	3.0e-20
Match length	90
% identity	48
NCBI Description	(AC004255) T1F9.5 [Arabidopsis thaliana]

Seq. No.	139764
Seq. ID	LIB24-062-Q1-E1-A11
Method	BLASTN
NCBI GI	g2623294
BLAST score	150
E value	9.0e-79
Match length	404
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T20B5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139765
Seq. ID	LIB24-062-Q1-E1-A12
Method	BLASTN
NCBI GI	g2623294
BLAST score	32
E value	7.0e-09
Match length	56
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC T20B5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139766
Seq. ID	LIB24-062-Q1-E1-A4
Method	BLASTX
NCBI GI	g3688193
BLAST score	196
E value	4.0e-15
Match length	126
% identity	40
NCBI Description	(AJ010091) MAP3K alpha 1 protein kinase [Brassica napus]

Seq. No.	139767
Seq. ID	LIB24-062-Q1-E1-C6
Method	BLASTN

NCBI GI	g2924732
BLAST score	120
E value	3.0e-61
Match length	144
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUA2, complete sequence [Arabidopsis thaliana]

Seq. No.	139768
Seq. ID	LIB24-062-Q1-E1-D9
Method	BLASTN
NCBI GI	g4263753
BLAST score	326
E value	0.0e+00
Match length	350
% identity	98
NCBI Description	Arabidopsis thaliana chromosome V map near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	139769
Seq. ID	LIB24-062-Q1-E1-E6
Method	BLASTN
NCBI GI	g4572664
BLAST score	58
E value	7.0e-24
Match length	183
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC F25P17 genomic sequence, complete sequence

Seq. No.	139770
Seq. ID	LIB24-062-Q1-E1-G7
Method	BLASTX
NCBI GI	g2052383
BLAST score	280
E value	4.0e-25
Match length	91
% identity	58
NCBI Description	(U66345) calreticulin [Arabidopsis thaliana]

Seq. No.	139771
Seq. ID	LIB24-062-Q1-E1-G8
Method	BLASTX
NCBI GI	g544424
BLAST score	191
E value	2.0e-14
Match length	36
% identity	97
NCBI Description	GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi_419755_pir__S30147 glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana >gi_16301_emb_CAA78711_ (Z14987) glycine rich protein [Arabidopsis thaliana] >gi_166837 (L00648) RNA-binding protein [Arabidopsis thaliana] >gi_4567224_gb_AAD23639.1_AC007119_5 (AC007119) glycine-rich RNA binding protein 7 [Arabidopsis thaliana]

Seq. No. 139772

Seq. ID	LIB24-063-Q1-E1-C12
Method	BLASTX
NCBI GI	g625977
BLAST score	605
E value	5.0e-63
Match length	117
% identity	100
NCBI Description	p40 protein homolog - Arabidopsis thaliana >gi_402904 (U01955) laminin receptor-like protein [Arabidopsis thaliana]

Seq. No.	139773
Seq. ID	LIB24-063-Q1-E1-C9
Method	BLASTN
NCBI GI	g3449333
BLAST score	134
E value	3.0e-69
Match length	396
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXF12, complete sequence [Arabidopsis thaliana]

Seq. No.	139774
Seq. ID	LIB24-063-Q1-E1-E1
Method	BLASTN
NCBI GI	g3128137
BLAST score	159
E value	4.0e-84
Match length	410
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9I9, complete sequence [Arabidopsis thaliana]

Seq. No.	139775
Seq. ID	LIB24-063-Q1-E1-F12
Method	BLASTN
NCBI GI	g2564051
BLAST score	154
E value	2.0e-81
Match length	253
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD9, complete sequence [Arabidopsis thaliana]

Seq. No.	139776
Seq. ID	LIB24-063-Q1-E1-F2
Method	BLASTX
NCBI GI	g4646203
BLAST score	190
E value	2.0e-14
Match length	65
% identity	52
NCBI Description	(AC007230) Belongs to PF_00026 Eukaryotic aspartyl protease family. [Arabidopsis thaliana]

Seq. No.	139777
Seq. ID	LIB24-063-Q1-E1-F8

Method	BLASTX
NCBI GI	g4732123
BLAST score	667
E value	2.0e-70
Match length	128
% identity	95
NCBI Description	(AF129087) mitogen-activated protein kinase homologue [Medicago sativa]

Seq. No.	139778
Seq. ID	LIB24-063-Q1-E1-H11
Method	BLASTN
NCBI GI	g2264304
BLAST score	115
E value	3.0e-58
Match length	155
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBG8, complete sequence [Arabidopsis thaliana]

Seq. No.	139779
Seq. ID	LIB24-063-Q1-E1-H7
Method	BLASTX
NCBI GI	g1117780
BLAST score	224
E value	6.0e-19
Match length	53
% identity	83
NCBI Description	(D49367) 4-coumarate:CoA ligase [Lithospermum erythrorhizon]

Seq. No.	139780
Seq. ID	LIB24-063-Q1-E1-H8
Method	BLASTX
NCBI GI	g1174470
BLAST score	386
E value	1.0e-39
Match length	133
% identity	62
NCBI Description	OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) >gi_508543 (L34260) integral membrane protein 1 [Mus musculus] >gi_1588285_prf__2208301A integral membrane protein [Mus musculus]

Seq. No.	139781
Seq. ID	LIB24-064-Q1-E1-A10
Method	BLASTX
NCBI GI	g4468980
BLAST score	348
E value	4.0e-33
Match length	91
% identity	75
NCBI Description	(AL035605) formamidase-like protein [Arabidopsis thaliana]

Seq. No.	139782
Seq. ID	LIB24-064-Q1-E1-B5
Method	BLASTX

NCBI GI	g2129670
BLAST score	363
E value	1.0e-34
Match length	70
% identity	100
NCBI Description	phosphoinositide-specific phospholipase C - Arabidopsis thaliana >gi_857374_dbj_BAA09432_ (D50804) phosphoinositide specific phospholipase C [Arabidopsis thaliana]

Seq. No.	139783
Seq. ID	LIB24-064-Q1-E1-C11
Method	BLASTX
NCBI GI	g4567231
BLAST score	320
E value	1.0e-29
Match length	61
% identity	100
NCBI Description	(AC007119) putative glucose-1-phosphate adenylyltransferase [Arabidopsis thaliana]

Seq. No.	139784
Seq. ID	LIB24-064-Q1-E1-C4
Method	BLASTN
NCBI GI	g2351096
BLAST score	56
E value	3.0e-23
Match length	100
% identity	90
NCBI Description	Arabidopsis thaliana mRNA for ATMRK1, complete cds

Seq. No.	139785
Seq. ID	LIB24-064-Q1-E1-D12
Method	BLASTX
NCBI GI	g3983665
BLAST score	329
E value	1.0e-30
Match length	87
% identity	74
NCBI Description	(AB011271) importin-beta2 [Oryza sativa]

Seq. No.	139786
Seq. ID	LIB24-064-Q1-E1-D5
Method	BLASTX
NCBI GI	g3617741
BLAST score	249
E value	2.0e-21
Match length	51
% identity	100
NCBI Description	(AC005687) L3 cytoplasmic ribosomal protein [Arabidopsis thaliana]

Seq. No.	139787
Seq. ID	LIB24-064-Q1-E1-D7
Method	BLASTN
NCBI GI	g3985949
BLAST score	257
E value	1.0e-143

Match length	257
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOB24, complete sequence [Arabidopsis thaliana]

Seq. No.	139788
Seq. ID	LIB24-064-Q1-E1-E1
Method	BLASTN
NCBI GI	g4455262
BLAST score	106
E value	1.0e-52
Match length	282
% identity	90
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22 (ESSAII project)

Seq. No.	139789
Seq. ID	LIB24-064-Q1-E1-F1
Method	BLASTN
NCBI GI	g4249393
BLAST score	359
E value	0.0e+00
Match length	380
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T9J23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139790
Seq. ID	LIB24-064-Q1-E1-G12
Method	BLASTX
NCBI GI	g4467096
BLAST score	544
E value	6.0e-56
Match length	112
% identity	56
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]

Seq. No.	139791
Seq. ID	LIB24-064-Q1-E1-G3
Method	BLASTN
NCBI GI	g1877523
BLAST score	270
E value	1.0e-150
Match length	282
% identity	99
NCBI Description	Arabidopsis thaliana BAC T7I23, complete sequence [Arabidopsis thaliana]

Seq. No.	139792
Seq. ID	LIB24-064-Q1-E1-G9
Method	BLASTN
NCBI GI	g2760172
BLAST score	197
E value	1.0e-107
Match length	273
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUB3, complete sequence [Arabidopsis thaliana]

Seq. No.	139793
Seq. ID	LIB24-064-Q1-E1-H4
Method	BLASTX
NCBI GI	g2209087
BLAST score	292
E value	2.0e-26
Match length	108
% identity	53
NCBI Description	(AF000309) putative serine/threonine kinase [Colletotrichum lindemuthianum]

Seq. No.	139794
Seq. ID	LIB24-065-Q1-E1-C8
Method	BLASTX
NCBI GI	g1170606
BLAST score	193
E value	7.0e-15
Match length	53
% identity	70
NCBI Description	ADENYLATE KINASE, CHLOROPLAST (ATP-AMP TRANSPHOSPHORYLASE) >gi_629863_pir__S45634 adenylate kinase (EC 2.7.4.3), chloroplast - maize >gi_3114421_pdb_1ZAK_A Chain A, Adenylate Kinase From Maize In Complex With The Inhibitor P1,P5-Bis(Adenosine-5'-)pentaphosphate (Ap5a) >gi_3114422_pdb_1ZAK_B Chain B, Adenylate Kinase From Maize In Complex With The Inhibitor P1,P5-Bis(Adenosine-5'-)pentaphosphate (Ap5a)

Seq. No.	139795
Seq. ID	LIB24-065-Q1-E1-C9
Method	BLASTN
NCBI GI	g3033373
BLAST score	259
E value	1.0e-144
Match length	263
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F19I3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139796
Seq. ID	LIB24-065-Q1-E1-E6
Method	BLASTN
NCBI GI	g3080406
BLAST score	76
E value	8.0e-35
Match length	247
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F23E12 (ESSA project)

Seq. No.	139797
Seq. ID	LIB24-065-Q1-E1-G4
Method	BLASTN
NCBI GI	g4490324
BLAST score	226

E value	1.0e-124
Match length	280
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14 (ESSA project)

Seq. No.	139798
Seq. ID	LIB24-066-Q1-E1-C5
Method	BLASTX
NCBI GI	g2119848
BLAST score	422
E value	1.0e-41
Match length	80
% identity	100
NCBI Description	chlorophyll a/b-binding protein type I precursor Lhb1B1 - Arabidopsis thaliana >gi_16366_emb_CAA45789_ (X64459) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi_3128229 (AC004077) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337372 (AC004481) putative photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	139799
Seq. ID	LIB24-066-Q1-E1-C9
Method	BLASTN
NCBI GI	g4220643
BLAST score	114
E value	3.0e-57
Match length	391
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD22, complete sequence [Arabidopsis thaliana]

Seq. No.	139800
Seq. ID	LIB24-066-Q1-E1-F2
Method	BLASTX
NCBI GI	g1169201
BLAST score	439
E value	1.0e-43
Match length	112
% identity	81
NCBI Description	DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR >gi_421830_pir__S33707 DRT112 protein - Arabidopsis thaliana >gi_166696 (M98456) DRT112 [Arabidopsis thaliana]

Seq. No.	139801
Seq. ID	LIB24-066-Q1-E1-F5
Method	BLASTX
NCBI GI	g3204134
BLAST score	380
E value	4.0e-51
Match length	119
% identity	76
NCBI Description	(AJ006771) beta-galactosidase [Cicer arietinum]

Seq. No.	139802

Seq. ID	LIB24-066-Q1-E1-F7
Method	BLASTN
NCBI GI	g3985934
BLAST score	87
E value	1.0e-41
Match length	127
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJE7, complete sequence [Arabidopsis thaliana]

Seq. No.	139803
Seq. ID	LIB24-066-Q1-E1-H5
Method	BLASTN
NCBI GI	g4432829
BLAST score	100
E value	3.0e-49
Match length	217
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T1B3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139804
Seq. ID	LIB24-067-Q1-E1-C10
Method	BLASTN
NCBI GI	g2358139
BLAST score	167
E value	5.0e-89
Match length	304
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 YAC yUP8H12 complete sequence [Arabidopsis thaliana]

Seq. No.	139805
Seq. ID	LIB24-067-Q1-E1-C2
Method	BLASTN
NCBI GI	g3046854
BLAST score	19
E value	4.7e-01
Match length	124
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRG7, complete sequence [Arabidopsis thaliana]

Seq. No.	139806
Seq. ID	LIB24-067-Q1-E1-D11
Method	BLASTX
NCBI GI	g3522956
BLAST score	424
E value	4.0e-42
Match length	89
% identity	96
NCBI Description	(AC004411) putative pectinacetylesterase precursor [Arabidopsis thaliana]

Seq. No.	139807
Seq. ID	LIB24-067-Q1-E1-E11
Method	BLASTX

NCBI GI	g4580393
BLAST score	301
E value	2.0e-27
Match length	104
% identity	58
NCBI Description	(AC007171) hypothetical protein [Arabidopsis thaliana]

Seq. No.	139808
Seq. ID	LIB24-067-Q1-E1-E5
Method	BLASTX
NCBI GI	g3766248
BLAST score	440
E value	1.0e-43
Match length	102
% identity	81
NCBI Description	(Y18227) blue copper binding-like protein [Arabidopsis thaliana]

Seq. No.	139809
Seq. ID	LIB24-067-Q1-E1-F1
Method	BLASTX
NCBI GI	g2253583
BLAST score	184
E value	1.0e-13
Match length	63
% identity	62
NCBI Description	(U78721) hypothetical protein [Arabidopsis thaliana]

Seq. No.	139810
Seq. ID	LIB24-067-Q1-E1-F9
Method	BLASTN
NCBI GI	g2618601
BLAST score	170
E value	6.0e-91
Match length	218
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	139811
Seq. ID	LIB24-067-Q1-E1-G12
Method	BLASTX
NCBI GI	g4586106
BLAST score	653
E value	9.0e-69
Match length	120
% identity	100
NCBI Description	(AL049638) putative disease resistance protein (TMV N-like) [Arabidopsis thaliana]

Seq. No.	139812
Seq. ID	LIB24-067-Q1-E1-G2
Method	BLASTN
NCBI GI	g4467131
BLAST score	358
E value	0.0e+00
Match length	382

% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20M13 (ESSA project)

Seq. No.	139813
Seq. ID	LIB24-067-Q1-E1-G6
Method	BLASTN
NCBI GI	g3510347
BLAST score	121
E value	2.0e-61
Match length	334
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]

Seq. No.	139814
Seq. ID	LIB24-067-Q1-E1-H1
Method	BLASTX
NCBI GI	g166708
BLAST score	639
E value	5.0e-67
Match length	130
% identity	98
NCBI Description	(M64118) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No.	139815
Seq. ID	LIB24-069-Q1-E1-B12
Method	BLASTX
NCBI GI	g3281866
BLAST score	536
E value	5.0e-55
Match length	100
% identity	100
NCBI Description	(AL031004) putative protein [Arabidopsis thaliana]

Seq. No.	139816
Seq. ID	LIB24-069-Q1-E1-C6
Method	BLASTX
NCBI GI	g4006887
BLAST score	388
E value	6.0e-38
Match length	80
% identity	93
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	139817
Seq. ID	LIB24-069-Q1-E1-D7
Method	BLASTN
NCBI GI	g2264312
BLAST score	93
E value	3.0e-45
Match length	137
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK16, complete sequence [Arabidopsis thaliana]

Seq. No.	139818
Seq. ID	LIB24-069-Q1-E1-E12
Method	BLASTX
NCBI GI	g4586433
BLAST score	193
E value	8.0e-15
Match length	51
% identity	67
NCBI Description	(AB016798) ribosomal protein L29/cell surface heparin binding protein HIP [Sus scrofa] >gi_4586439_dbj_BAA76404.1_ (AB017196) ribosomal protein L29/heparin/heparan sulfate interacting protein [Sus scrofa]

Seq. No.	139819
Seq. ID	LIB24-069-Q1-E1-F11
Method	BLASTX
NCBI GI	g2632103
BLAST score	655
E value	7.0e-69
Match length	126
% identity	100
NCBI Description	(Z98759) arginyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.	139820
Seq. ID	LIB24-069-Q1-E1-F4
Method	BLASTX
NCBI GI	g2335108
BLAST score	548
E value	2.0e-56
Match length	127
% identity	82
NCBI Description	(AC002339) putative isulinase [Arabidopsis thaliana]

Seq. No.	139821
Seq. ID	LIB24-069-Q1-E1-G1
Method	BLASTN
NCBI GI	g4803835
BLAST score	90
E value	1.0e-43
Match length	90
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for a dynamin-like protein ADL3, complete cds

Seq. No.	139822
Seq. ID	LIB24-069-Q1-E1-G12
Method	BLASTX
NCBI GI	g417383
BLAST score	619
E value	1.0e-64
Match length	125
% identity	98
NCBI Description	NITRILASE 2 >gi_322548_pir__S31969 nitrilase (EC 3.5.5.1) - Arabidopsis thaliana >gi_22656_emb_CAA48377_ (X68305) nitrilase II [Arabidopsis thaliana] >gi_508733 (U09958) nitrilase [Arabidopsis thaliana]

Seq. No.	139823
Seq. ID	LIB24-069-Q1-E1-H2
Method	BLASTN
NCBI GI	g3510341
BLAST score	72
E value	1.0e-32
Match length	140
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFC16, complete sequence [Arabidopsis thaliana]

Seq. No.	139824
Seq. ID	LIB24-070-Q1-E1-A3
Method	BLASTX
NCBI GI	g3915023
BLAST score	546
E value	3.0e-56
Match length	121
% identity	84
NCBI Description	SUCROSE-PHOSPHATE SYNTHASE 1 (UDP-GLUCOSE-FRUCTOSE-PHOSPHATE GLUCOSYLTRANSFERASE 1) >gi_2588888_dbj_BAA23213_ (AB005023) sucrose-phosphate synthase [Citrus unshiu]

Seq. No.	139825
Seq. ID	LIB24-070-Q1-E1-A5
Method	BLASTX
NCBI GI	g1480078
BLAST score	479
E value	3.0e-48
Match length	96
% identity	99
NCBI Description	(X99696) shaggy-like protein kinase iota [Arabidopsis thaliana] >gi_2444277_gb_AAB71545.1_ (AF019927) GSK3/shaggy-like protein kinase [Arabidopsis thaliana]

Seq. No.	139826
Seq. ID	LIB24-070-Q1-E1-A7
Method	BLASTX
NCBI GI	g4510356
BLAST score	433
E value	6.0e-43
Match length	84
% identity	100
NCBI Description	(AC006921) putative kinesin-related protein TKRP125 [Arabidopsis thaliana]

Seq. No.	139827
Seq. ID	LIB24-070-Q1-E1-C9
Method	BLASTN
NCBI GI	g4454447
BLAST score	262
E value	1.0e-145
Match length	413
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F5H14 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139828
Seq. ID	LIB24-070-Q1-E1-G10
Method	BLASTN
NCBI GI	g3513725
BLAST score	388
E value	0.0e+00
Match length	412
% identity	98
NCBI Description	Arabidopsis thaliana BAC F8M12

Seq. No.	139829
Seq. ID	LIB24-070-Q1-E1-H2
Method	BLASTX
NCBI GI	g2501056
BLAST score	492
E value	7.0e-50
Match length	99
% identity	100
NCBI Description	SERYL-TRNA SYNTHETASE (SERINE--TRNA LIGASE) (SERRS) >gi_2129737_pir__S71293 seryl-tRNA synthetase - Arabidopsis thaliana >gi_1359497_emb_CAA94388_ (Z70313) seryl-tRNA Synthetase [Arabidopsis thaliana]

Seq. No.	139830
Seq. ID	LIB24-071-Q1-E1-A1
Method	BLASTX
NCBI GI	g2244859
BLAST score	305
E value	3.0e-28
Match length	84
% identity	68
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	139831
Seq. ID	LIB24-071-Q1-E1-C5
Method	BLASTN
NCBI GI	g3702736
BLAST score	42
E value	3.0e-14
Match length	66
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRI1, complete sequence [Arabidopsis thaliana]

Seq. No.	139832
Seq. ID	LIB24-071-Q1-E1-C8
Method	BLASTX
NCBI GI	g1352663
BLAST score	607
E value	3.0e-63
Match length	116
% identity	100
NCBI Description	SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-3 CATALYTIC SUBUNIT >gi_1076388_pir__S52659 phosphoprotein phosphatase (EC 3.1.3.16) 2A isoform 3 - Arabidopsis thaliana

>gi_466441 (M96841) Ser/Thr protein phosphatase [Arabidopsis thaliana]
>gi_4559341_gb_AAD23003.1_AC007087_22 (AC007087) serine/threonine protein phosphatase PP2A-3 catalytic subunit [Arabidopsis thaliana]
>gi_4567320_gb_AAD23731.1_AC005956_20 (AC005956) serine/threonine protein phosphatase [Arabidopsis thaliana]

Seq. No.	139833
Seq. ID	LIB24-071-Q1-E1-E7
Method	BLASTN
NCBI GI	g4079614
BLAST score	138
E value	1.0e-71
Match length	372
% identity	96
NCBI Description	Arabidopsis thaliana chromosome I BAC F21M11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139834
Seq. ID	LIB24-071-Q1-E1-G11
Method	BLASTX
NCBI GI	g4586254
BLAST score	207
E value	2.0e-16
Match length	73
% identity	60
NCBI Description	(AL049640) auxilin-like protein [Arabidopsis thaliana]

Seq. No.	139835
Seq. ID	LIB24-071-Q1-E1-G12
Method	BLASTN
NCBI GI	g3299824
BLAST score	98
E value	3.0e-48
Match length	134
% identity	93
NCBI Description	Arabidopsis thaliana BAC F4C21 from chromosome IV, top arm, near 17 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	139836
Seq. ID	LIB24-071-Q1-E1-H7
Method	BLASTN
NCBI GI	g3080406
BLAST score	86
E value	3.0e-41
Match length	86
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F23E12 (ESSA project)

Seq. No.	139837
Seq. ID	LIB24-071-Q1-E1-H9
Method	BLASTX
NCBI GI	g2832619
BLAST score	559
E value	1.0e-57

Match length	118
% identity	62
NCBI Description	(AL021711) major intrinsic protein (MIP)- like [Arabidopsis thaliana]

Seq. No.	139838
Seq. ID	LIB24-072-Q1-E1-A12
Method	BLASTN
NCBI GI	g3608126
BLAST score	114
E value	1.0e-57
Match length	158
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC T32F12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139839
Seq. ID	LIB24-072-Q1-E1-B3
Method	BLASTX
NCBI GI	g4191789
BLAST score	415
E value	5.0e-41
Match length	93
% identity	88
NCBI Description	(AC005917) putative transmembrane transport protein [Arabidopsis thaliana]

Seq. No.	139840
Seq. ID	LIB24-072-Q1-E1-B9
Method	BLASTX
NCBI GI	g681904
BLAST score	464
E value	2.0e-46
Match length	108
% identity	86
NCBI Description	(D31711) cp29 [Arabidopsis thaliana]

Seq. No.	139841
Seq. ID	LIB24-072-Q1-E1-C12
Method	BLASTX
NCBI GI	g2827700
BLAST score	657
E value	4.0e-69
Match length	132
% identity	100
NCBI Description	(AL021684) DEAD box ATP dependent helicase protein [Arabidopsis thaliana]

Seq. No.	139842
Seq. ID	LIB24-072-Q1-E1-E3
Method	BLASTX
NCBI GI	g2911057
BLAST score	152
E value	1.0e-32
Match length	76
% identity	99
NCBI Description	(AL021961) caffeoyl-CoA O-methyltransferase - like protein

[Arabidopsis thaliana]

Seq. No.	139843
Seq. ID	LIB24-072-Q1-E1-F10
Method	BLASTX
NCBI GI	g3482918
BLAST score	446
E value	2.0e-44
Match length	91
% identity	100
NCBI Description	(AC003970) Similar to ATP-citrate-lyase [Arabidopsis thaliana]

Seq. No.	139844
Seq. ID	LIB24-072-Q1-E1-F9
Method	BLASTX
NCBI GI	g115783
BLAST score	595
E value	7.0e-62
Match length	113
% identity	99
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	139845
Seq. ID	LIB24-072-Q1-E1-G1
Method	BLASTX
NCBI GI	g1946367
BLAST score	356
E value	7.0e-34
Match length	128
% identity	54
NCBI Description	(U93215) unknown protein [Arabidopsis thaliana]

Seq. No.	139846
Seq. ID	LIB24-072-Q1-E1-G5
Method	BLASTN
NCBI GI	g2618604
BLAST score	348
E value	0.0e+00
Match length	394
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTG13, complete sequence [Arabidopsis thaliana]

Seq. No.	139847
Seq. ID	LIB24-072-Q1-E1-G9
Method	BLASTX
NCBI GI	g2623307
BLAST score	760
E value	3.0e-81
Match length	141
% identity	99
NCBI Description	(AC002409) putative ubiquitin protease [Arabidopsis thaliana]

Seq. No.	139848
Seq. ID	LIB24-072-Q1-E1-H4
Method	BLASTN
NCBI GI	g2342673
BLAST score	202
E value	1.0e-110
Match length	313
% identity	100
NCBI Description	Sequence of BAC F7G19 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	139849
Seq. ID	LIB24-073-Q1-E1-A12
Method	BLASTN
NCBI GI	g3201608
BLAST score	251
E value	1.0e-139
Match length	263
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F7F1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139850
Seq. ID	LIB24-073-Q1-E1-C9
Method	BLASTX
NCBI GI	g3719211
BLAST score	448
E value	1.0e-44
Match length	110
% identity	81
NCBI Description	(U97021) UIP2 [Arabidopsis thaliana]

Seq. No.	139851
Seq. ID	LIB24-073-Q1-E1-D1
Method	BLASTN
NCBI GI	g3763915
BLAST score	105
E value	4.0e-52
Match length	269
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F14B2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139852
Seq. ID	LIB24-074-Q1-E1-C10
Method	BLASTX
NCBI GI	g2623296
BLAST score	360
E value	3.0e-34
Match length	105
% identity	71
NCBI Description	(AC002409) hypothetical protein [Arabidopsis thaliana]

Seq. No.	139853
Seq. ID	LIB24-074-Q1-E1-C11
Method	BLASTX

NCBI GI	g3876247
BLAST score	366
E value	5.0e-35
Match length	133
% identity	54
NCBI Description	(Z71262) similar to serine/threonine kinase; cDNA EST EMBL:D27596 comes from this gene; cDNA EST EMBL:D75765 comes from this gene; cDNA EST EMBL:D34336 comes from this gene; cDNA EST EMBL:D34931 comes from this gene; cDNA EST E

Seq. No.	139854
Seq. ID	LIB24-074-Q1-E1-C12
Method	BLASTX
NCBI GI	g4585974
BLAST score	592
E value	2.0e-61
Match length	129
% identity	88
NCBI Description	(AC005287) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	139855
Seq. ID	LIB24-074-Q1-E1-D4
Method	BLASTX
NCBI GI	g3668173
BLAST score	670
E value	1.0e-70
Match length	139
% identity	94
NCBI Description	(AB006777) vegetative storage protein [Arabidopsis thaliana]

Seq. No.	139856
Seq. ID	LIB24-074-Q1-E1-D9
Method	BLASTN
NCBI GI	g2281081
BLAST score	95
E value	6.0e-46
Match length	338
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F18O19 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139857
Seq. ID	LIB24-074-Q1-E1-E5
Method	BLASTN
NCBI GI	g3212846
BLAST score	115
E value	5.0e-58
Match length	115
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139858
Seq. ID	LIB24-074-Q1-E1-F8
Method	BLASTX
NCBI GI	g4558591

BLAST score	516
E value	1.0e-52
Match length	105
% identity	98
NCBI Description	(AC006555) putative beta-1,3-glucanase [Arabidopsis thaliana] >gi_4662638_gb_AAD26909.1_AC007233_1 (AC007233) putative beta-1,3-glucanase [Arabidopsis thaliana]

Seq. No.	139859
Seq. ID	LIB24-074-Q1-E1-G1
Method	BLASTN
NCBI GI	g3449317
BLAST score	228
E value	1.0e-125
Match length	390
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKM21, complete sequence [Arabidopsis thaliana]

Seq. No.	139860
Seq. ID	LIB24-074-Q1-E1-G11
Method	BLASTX
NCBI GI	g2499611
BLAST score	384
E value	4.0e-37
Match length	72
% identity	100
NCBI Description	MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 7 (MAP KINASE 7) (ATMPK7) >gi_629548_pir__S40473 mitogen-activated protein kinase 7 (EC 2.7.1.-) - Arabidopsis thaliana >gi_457406_dbj_BAA04870_ (D21843) MAP kinase [Arabidopsis thaliana]

Seq. No.	139861
Seq. ID	LIB24-075-Q1-E1-A3
Method	BLASTX
NCBI GI	g4557060
BLAST score	623
E value	4.0e-65
Match length	123
% identity	100
NCBI Description	(AC007154) putative chromosome-associated polypeptide, 5' partial [Arabidopsis thaliana]

Seq. No.	139862
Seq. ID	LIB24-075-Q1-E1-A7
Method	BLASTN
NCBI GI	g3869069
BLAST score	269
E value	1.0e-150
Match length	390
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence [Arabidopsis thaliana]

Seq. No.	139863
Seq. ID	LIB24-075-Q1-E1-B10

Method	BLASTX
NCBI GI	g3790567
BLAST score	347
E value	3.0e-33
Match length	69
% identity	97
NCBI Description	(AF078821) RING-H2 finger protein RHA1b [Arabidopsis thaliana]

Seq. No.	139864
Seq. ID	LIB24-075-Q1-E1-D7
Method	BLASTN
NCBI GI	g3212846
BLAST score	149
E value	4.0e-78
Match length	390
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139865
Seq. ID	LIB24-075-Q1-E1-E3
Method	BLASTX
NCBI GI	g586080
BLAST score	498
E value	1.0e-50
Match length	98
% identity	100
NCBI Description	TUBULIN GAMMA-2 CHAIN >gi_460131 (U03990) g2-tubulin [Arabidopsis thaliana]

Seq. No.	139866
Seq. ID	LIB24-075-Q1-E1-E8
Method	BLASTX
NCBI GI	g4262149
BLAST score	633
E value	3.0e-66
Match length	122
% identity	99
NCBI Description	(AC005275) putative xyloglucan endotransglycosylase [Arabidopsis thaliana]

Seq. No.	139867
Seq. ID	LIB24-075-Q1-E1-F9
Method	BLASTX
NCBI GI	g3157947
BLAST score	460
E value	5.0e-46
Match length	89
% identity	53
NCBI Description	(AC002131) Similar to protein gb_Z74962 from Brassica oleracea which is similar to bacterial YRN1 and HEAHIO proteins. ESTs gb_T21954, gb_T04283, gb_Z37609, gb_N37366, gb_R90704, gb_F15500 and gb_F14353 come from this gene. [Arabidopsis tha

Seq. No.	139868

Seq. ID	LIB24-075-Q1-E1-G10
Method	BLASTX
NCBI GI	g115783
BLAST score	557
E value	2.0e-57
Match length	105
% identity	99
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	139869
Seq. ID	LIB24-075-Q1-E1-G3
Method	BLASTX
NCBI GI	g3868857
BLAST score	530
E value	3.0e-54
Match length	101
% identity	100
NCBI Description	(AB013886) RAV1 [Arabidopsis thaliana]

Seq. No.	139870
Seq. ID	LIB24-076-Q1-E1-B11
Method	BLASTX
NCBI GI	g1001603
BLAST score	160
E value	6.0e-11
Match length	101
% identity	37
NCBI Description	(D64000) hypothetical protein [Synechocystis sp.]

Seq. No.	139871
Seq. ID	LIB24-076-Q1-E1-B9
Method	BLASTN
NCBI GI	g4538895
BLAST score	103
E value	6.0e-51
Match length	228
% identity	88
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17A8 (ESSA project)

Seq. No.	139872
Seq. ID	LIB24-076-Q1-E1-D10
Method	BLASTX
NCBI GI	g1709970
BLAST score	180
E value	8.0e-14
Match length	42
% identity	86
NCBI Description	60S RIBOSOMAL PROTEIN L10A

Seq. No.	139873
Seq. ID	LIB24-076-Q1-E1-D5
Method	BLASTN
NCBI GI	g3063438

BLAST score 285
E value 1.0e-159
Match length 359
% identity 97
NCBI Description Complete sequence of Arabidopsis F22013, complete sequence [Arabidopsis thaliana]

Seq. No. 139874
Seq. ID LIB24-076-Q1-E1-D8
Method BLASTX
NCBI GI g4006941
BLAST score 259
E value 1.0e-22
Match length 52
% identity 100
NCBI Description (AJ131391) voltage-dependent anion-selective channel protein [Arabidopsis thaliana]

Seq. No. 139875
Seq. ID LIB24-076-Q1-E1-F1
Method BLASTX
NCBI GI g543841
BLAST score 580
E value 4.0e-60
Match length 113
% identity 99
NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi_322518_pir__S28875 ADP-ribosylation factor 1 - Arabidopsis thaliana >gi_166586 (M95166) ADP-ribosylation factor [Arabidopsis thaliana] >gi_2275195 (AC002337) ADP-ribosylation factor [Arabidopsis thaliana] >gi_4630747_gb_AAD26597.1_AC007236_2 (AC007236) ADP-ribosylation factor [Arabidopsis thaliana]

Seq. No. 139876
Seq. ID LIB24-076-Q1-E1-F7
Method BLASTN
NCBI GI g4519191
BLAST score 333
E value 0.0e+00
Match length 414
% identity 100
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9P8, complete sequence

Seq. No. 139877
Seq. ID LIB24-076-Q1-E1-G7
Method BLASTN
NCBI GI g2264310
BLAST score 177
E value 7.0e-95
Match length 366
% identity 96
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKP11, complete sequence [Arabidopsis thaliana]

Seq. No. 139878
Seq. ID LIB24-077-Q1-E1-A12

Method	BLASTN
NCBI GI	g2191126
BLAST score	257
E value	1.0e-142
Match length	432
% identity	100
NCBI Description	Arabidopsis thaliana BAC IG002N01

Seq. No.	139879
Seq. ID	LIB24-077-Q1-E1-D12
Method	BLASTX
NCBI GI	g3522950
BLAST score	600
E value	2.0e-62
Match length	131
% identity	88
NCBI Description	(AC004411) hypothetical protein [Arabidopsis thaliana]

Seq. No.	139880
Seq. ID	LIB24-077-Q1-E1-D9
Method	BLASTX
NCBI GI	g2851577
BLAST score	143
E value	8.0e-09
Match length	55
% identity	51
NCBI Description	SERINE CARBOXYPEPTIDASE III PRECURSOR (CP-MIII) >gi_1877219_emb_CAA70817_ (Y09604) serine carboxypeptidase III, CP-MIII [Hordeum vulgare]

Seq. No.	139881
Seq. ID	LIB24-077-Q1-E1-H5
Method	BLASTN
NCBI GI	g2275194
BLAST score	200
E value	1.0e-108
Match length	387
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T08I13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139882
Seq. ID	LIB24-078-Q1-E1-C7
Method	BLASTN
NCBI GI	g4589436
BLAST score	434
E value	0.0e+00
Match length	434
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPA22, complete sequence

Seq. No.	139883
Seq. ID	LIB24-078-Q1-E1-E9
Method	BLASTX
NCBI GI	g2244985
BLAST score	394

E value	2.0e-38
Match length	73
% identity	100
NCBI Description	(Z97340) similarity to peroxidase [Arabidopsis thaliana]

Seq. No.	139884
Seq. ID	LIB24-078-Q1-E1-F11
Method	BLASTX
NCBI GI	g2961389
BLAST score	491
E value	1.0e-49
Match length	135
% identity	64
NCBI Description	(AL022141) purple acid phosphatase like protein [Arabidopsis thaliana] >gi_4006925_emb_CAB16853.1_ (Z99708) purple acid phosphatase like protein [Arabidopsis thaliana]

Seq. No.	139885
Seq. ID	LIB24-078-Q1-E1-F6
Method	BLASTN
NCBI GI	g2749918
BLAST score	108
E value	3.0e-54
Match length	140
% identity	94
NCBI Description	Arabidopsis thaliana chromosome I BAC F3I6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139886
Seq. ID	LIB24-078-Q1-E1-H5
Method	BLASTX
NCBI GI	g1653767
BLAST score	508
E value	1.0e-51
Match length	149
% identity	62
NCBI Description	(D90916) oligopeptidase A [Synechocystis sp.]

Seq. No.	139887
Seq. ID	LIB24-078-Q1-E1-H8
Method	BLASTX
NCBI GI	g3236261
BLAST score	420
E value	3.0e-41
Match length	146
% identity	49
NCBI Description	(AC004684) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	139888
Seq. ID	LIB24-079-Q1-E1-B11
Method	BLASTX
NCBI GI	g4455185
BLAST score	204
E value	2.0e-16
Match length	76
% identity	58

NCBI Description	(AL035521) putative protein [Arabidopsis thaliana]
Seq. No.	139889
Seq. ID	LIB24-079-Q1-E1-C6
Method	BLASTN
NCBI GI	g4756963
BLAST score	134
E value	2.0e-69
Match length	205
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23 (ESSA project)
Seq. No.	139890
Seq. ID	LIB24-079-Q1-E1-D3
Method	BLASTX
NCBI GI	g1769568
BLAST score	519
E value	6.0e-53
Match length	103
% identity	95
NCBI Description	(U82202) fumarase; fumarate hydratase [Arabidopsis thaliana]
Seq. No.	139891
Seq. ID	LIB24-079-Q1-E1-E11
Method	BLASTN
NCBI GI	g4757397
BLAST score	372
E value	0.0e+00
Match length	372
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MBG14, complete sequence
Seq. No.	139892
Seq. ID	LIB24-079-Q1-E1-E9
Method	BLASTX
NCBI GI	g3688182
BLAST score	643
E value	1.0e-67
Match length	123
% identity	100
NCBI Description	(AL031804) P-Protein - like protein [Arabidopsis thaliana]
Seq. No.	139893
Seq. ID	LIB24-079-Q1-E1-G5
Method	BLASTX
NCBI GI	g4512698
BLAST score	414
E value	4.0e-41
Match length	81
% identity	94
NCBI Description	(AC006569) hypothetical protein [Arabidopsis thaliana]
Seq. No.	139894
Seq. ID	LIB24-079-Q1-E1-G6

09604015.100100

Method	BLASTX
NCBI GI	g2660677
BLAST score	752
E value	3.0e-80
Match length	142
% identity	100
NCBI Description	(AC002342) unknown protein [Arabidopsis thaliana]

Seq. No.	139895
Seq. ID	LIB24-080-Q1-E1-C9
Method	BLASTX
NCBI GI	g4539944
BLAST score	201
E value	1.0e-15
Match length	61
% identity	64
NCBI Description	(AF133841) aldose reductase ALDRXV4 [Xerophyta viscosa]

Seq. No.	139896
Seq. ID	LIB24-080-Q1-E1-D11
Method	BLASTX
NCBI GI	g3335347
BLAST score	335
E value	1.0e-31
Match length	88
% identity	62
NCBI Description	(AC004512) Contains similarity to ARI, RING finger protein gb_X98309 from Drosophila melanogaster. ESTs gb_T44383, gb_W43120, gb_N65868, gb_H36013, gb_AA042241, gb_T76869 and gb_AA042359 come from this gene. [Arabidopsis thaliana]

Seq. No.	139897
Seq. ID	LIB24-081-Q1-E1-A10
Method	BLASTX
NCBI GI	g1399380
BLAST score	421
E value	1.0e-41
Match length	94
% identity	83
NCBI Description	(U43683) S-adenosyl-L-methionine:delta24-sterol-C-methyltransferase [Glycine max]

Seq. No.	139898
Seq. ID	LIB24-081-Q1-E1-A6
Method	BLASTX
NCBI GI	g4835245
BLAST score	151
E value	4.0e-10
Match length	84
% identity	33
NCBI Description	(AL049862) putative mitochondrial protein [Arabidopsis thaliana]

Seq. No.	139899
Seq. ID	LIB24-081-Q1-E1-C9
Method	BLASTX
NCBI GI	g119194

BLAST score	445
E value	3.0e-44
Match length	96
% identity	88
NCBI Description	ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU) >gi_81607_pir__S09152 translation elongation factor Tu precursor, chloroplast - Arabidopsis thaliana >gi_22565_emb_CAA36498_ (X52256) elongation factor Tu precursor [Arabidopsis thaliana] >gi_226817_prf__1607332A elongation factor Tu [Arabidopsis thaliana]

Seq. No.	139900
Seq. ID	LIB24-081-Q1-E1-D10
Method	BLASTN
NCBI GI	g3928542
BLAST score	85
E value	4.0e-40
Match length	249
% identity	84
NCBI Description	Arabidopsis thaliana mRNA for UDP-glucose glucosyltransferase, complete cds

Seq. No.	139901
Seq. ID	LIB24-081-Q1-E1-F5
Method	BLASTN
NCBI GI	g3402671
BLAST score	133
E value	1.0e-68
Match length	392
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T16B24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139902
Seq. ID	LIB24-081-Q1-E1-F7
Method	BLASTX
NCBI GI	g3335371
BLAST score	657
E value	4.0e-69
Match length	142
% identity	91
NCBI Description	(AC003028) putative ethylene-inducible protein [Arabidopsis thaliana]

Seq. No.	139903
Seq. ID	LIB24-081-Q1-E1-G2
Method	BLASTX
NCBI GI	g2632254
BLAST score	283
E value	9.0e-26
Match length	72
% identity	76
NCBI Description	(Y12465) serine/threonine kinase [Sorghum bicolor]

Seq. No.	139904
Seq. ID	LIB24-081-Q1-E1-G3
Method	BLASTX

NCBI GI	g2832679
BLAST score	427
E value	4.0e-42
Match length	83
% identity	100
NCBI Description	(AL021712) putative protein [Arabidopsis thaliana]

Seq. No.	139905
Seq. ID	LIB24-081-Q1-E1-G9
Method	BLASTX
NCBI GI	g1931642
BLAST score	756
E value	1.0e-80
Match length	144
% identity	100
NCBI Description	(U95973) Ser/Thr protein kinase isolog [Arabidopsis thaliana]

Seq. No.	139906
Seq. ID	LIB24-082-Q1-E1-B9
Method	BLASTX
NCBI GI	g4263795
BLAST score	166
E value	1.0e-11
Match length	48
% identity	60
NCBI Description	(AC006068) putative glucosyltransferase [Arabidopsis thaliana]

Seq. No.	139907
Seq. ID	LIB24-082-Q1-E1-C11
Method	BLASTN
NCBI GI	g2062691
BLAST score	33
E value	7.0e-09
Match length	58
% identity	48
NCBI Description	Human sodium phosphate transporter (NPT4) mRNA, complete cds

Seq. No.	139908
Seq. ID	LIB24-082-Q1-E1-C2
Method	BLASTN
NCBI GI	g2244991
BLAST score	96
E value	4.0e-47
Match length	124
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	139909
Seq. ID	LIB24-082-Q1-E1-D3
Method	BLASTN
NCBI GI	g4584841
BLAST score	92
E value	2.0e-44

Match length	203
% identity	92
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T23E23, complete sequence

Seq. No.	139910
Seq. ID	LIB24-082-Q1-E1-D7
Method	BLASTX
NCBI GI	g4204274
BLAST score	211
E value	5.0e-17
Match length	39
% identity	100
NCBI Description	(AC004146) ribulose bisphosphate carboxylase, small subunit [Arabidopsis thaliana]

Seq. No.	139911
Seq. ID	LIB24-082-Q1-E1-E4
Method	BLASTN
NCBI GI	g4220640
BLAST score	199
E value	1.0e-108
Match length	299
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPE11, complete sequence [Arabidopsis thaliana]

Seq. No.	139912
Seq. ID	LIB24-082-Q1-E1-G1
Method	BLASTX
NCBI GI	g135406
BLAST score	525
E value	1.0e-53
Match length	98
% identity	100
NCBI Description	TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi_99768_pir__A32712 tubulin alpha-5 chain - Arabidopsis thaliana >gi_166912 (M17189) alpha-tubulin [Arabidopsis thaliana] >gi_166918 (M84698) alpha-5 tubulin [Arabidopsis thaliana]

Seq. No.	139913
Seq. ID	LIB24-082-Q1-E1-G10
Method	BLASTN
NCBI GI	g2098816
BLAST score	373
E value	0.0e+00
Match length	377
% identity	100
NCBI Description	Arabidopsis thaliana BAC F19G10, complete sequence

Seq. No.	139914
Seq. ID	LIB24-082-Q1-E1-G9
Method	BLASTN
NCBI GI	g3236234
BLAST score	272
E value	1.0e-151
Match length	383

% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F13M22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139915
Seq. ID	LIB24-082-Q1-E1-H10
Method	BLASTX
NCBI GI	g4741942
BLAST score	400
E value	4.0e-39
Match length	103
% identity	81
NCBI Description	(AF134121) Lhca5 protein [Arabidopsis thaliana]

Seq. No.	139916
Seq. ID	LIB24-083-Q1-E1-C4
Method	BLASTX
NCBI GI	g600855
BLAST score	327
E value	7.0e-31
Match length	76
% identity	84
NCBI Description	(U17887) bZIP protein [Arabidopsis thaliana]

Seq. No.	139917
Seq. ID	LIB24-083-Q1-E1-D6
Method	BLASTX
NCBI GI	g4455332
BLAST score	217
E value	4.0e-18
Match length	72
% identity	56
NCBI Description	(AL035525) putative protein [Arabidopsis thaliana]

Seq. No.	139918
Seq. ID	LIB24-083-Q1-E1-E1
Method	BLASTN
NCBI GI	g3292807
BLAST score	270
E value	1.0e-150
Match length	274
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F7H19 (ESSAII project)

Seq. No.	139919
Seq. ID	LIB24-083-Q1-E1-E5
Method	BLASTX
NCBI GI	g4006867
BLAST score	320
E value	3.0e-30
Match length	64
% identity	95
NCBI Description	(Z99707) putative protein [Arabidopsis thaliana]

Seq. No.	139920
Seq. ID	LIB24-083-Q1-E1-G8

Method	BLASTN
NCBI GI	g4220640
BLAST score	177
E value	4.0e-95
Match length	213
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPE11, complete sequence [Arabidopsis thaliana]

Seq. No.	139921
Seq. ID	LIB24-084-Q1-E1-C10
Method	BLASTN
NCBI GI	g4589426
BLAST score	175
E value	1.0e-93
Match length	403
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDE13, complete sequence

Seq. No.	139922
Seq. ID	LIB24-084-Q1-E1-D11
Method	BLASTN
NCBI GI	g4263753
BLAST score	81
E value	7.0e-38
Match length	220
% identity	98
NCBI Description	Arabidopsis thaliana chromosome V map near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	139923
Seq. ID	LIB24-084-Q1-E1-D6
Method	BLASTN
NCBI GI	g4519194
BLAST score	187
E value	1.0e-101
Match length	325
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHM17, complete sequence

Seq. No.	139924
Seq. ID	LIB24-084-Q1-E1-D8
Method	BLASTN
NCBI GI	g2264318
BLAST score	214
E value	1.0e-117
Match length	316
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUP24, complete sequence [Arabidopsis thaliana]

Seq. No.	139925
Seq. ID	LIB24-084-Q1-E1-F11
Method	BLASTN
NCBI GI	g1931636

BLAST score	115
E value	4.0e-58
Match length	155
% identity	94
NCBI Description	Arabidopsis thaliana BAC T19D16 genomic sequence

Seq. No.	139926
Seq. ID	LIB24-085-Q1-E1-A4
Method	BLASTX
NCBI GI	g3549672
BLAST score	700
E value	4.0e-74
Match length	138
% identity	100
NCBI Description	(AL031394) putative protein [Arabidopsis thaliana]

Seq. No.	139927
Seq. ID	LIB24-085-Q1-E1-B11
Method	BLASTX
NCBI GI	g136636
BLAST score	399
E value	7.0e-39
Match length	73
% identity	100
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1) >gi_1076424_pir__S43781 ubiquitin-conjugating enzyme UBC1 - Arabidopsis thaliana >gi_442594_pdb_1AAK_ Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) >gi_2981894_pdb_2AAK_ Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana >gi_166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi_431260 (L19351) ubiquitin conjugating enzyme [Arabidopsis thaliana]

Seq. No.	139928
Seq. ID	LIB24-085-Q1-E1-C10
Method	BLASTN
NCBI GI	g4063735
BLAST score	318
E value	1.0e-179
Match length	431
% identity	68
NCBI Description	Arabidopsis thaliana BAC F18G18 from chromosome V near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	139929
Seq. ID	LIB24-085-Q1-E1-C8
Method	BLASTX
NCBI GI	g1906830
BLAST score	744
E value	3.0e-79
Match length	147
% identity	98
NCBI Description	(Y11829) heat shock protein [Arabidopsis thaliana]

Seq. No.	139930
Seq. ID	LIB24-085-Q1-E1-D11

Method	BLASTN
NCBI GI	g3128136
BLAST score	282
E value	1.0e-157
Match length	417
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1F13, complete sequence [Arabidopsis thaliana]

Seq. No.	139931
Seq. ID	LIB24-085-Q1-E1-D12
Method	BLASTX
NCBI GI	g4507067
BLAST score	332
E value	3.0e-42
Match length	140
% identity	62
NCBI Description	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 >gi_134584_sp_P28370_SN21_HUMAN POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L1 >gi_479804_pir__S35457 SNF2 protein homolog - human >gi_292496 (M88163) transcription activator [Homo sapiens]

Seq. No.	139932
Seq. ID	LIB24-085-Q1-E1-D2
Method	BLASTX
NCBI GI	g4512122
BLAST score	671
E value	1.0e-70
Match length	146
% identity	90
NCBI Description	(AF131219) chorismate mutase 3 [Arabidopsis thaliana]

Seq. No.	139933
Seq. ID	LIB24-085-Q1-E1-D8
Method	BLASTN
NCBI GI	g2980787
BLAST score	301
E value	1.0e-169
Match length	441
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, P1 clone M7J2 (ESSAII project)

Seq. No.	139934
Seq. ID	LIB24-085-Q1-E1-E5
Method	BLASTX
NCBI GI	g115783
BLAST score	595
E value	7.0e-62
Match length	113
% identity	99
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	139935
Seq. ID	LIB24-085-Q1-E1-E9
Method	BLASTN
NCBI GI	g1297184
BLAST score	50
E value	4.0e-19
Match length	392
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I cosmid g8261 DNA (cytosine-5-) methyltransferase, zinc finger protein 1, nucleoporin 98, poly A+ RNA export protein, plasma membrane ATPase 2, and serine/threonine protein kinase genes, co

Seq. No.	139936
Seq. ID	LIB24-085-Q1-E1-F2
Method	BLASTN
NCBI GI	g2894557
BLAST score	310
E value	1.0e-174
Match length	355
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T8O5 (ESSAII project)

Seq. No.	139937
Seq. ID	LIB24-086-Q1-E1-B12
Method	BLASTN
NCBI GI	g4589440
BLAST score	138
E value	1.0e-71
Match length	138
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSD21, complete sequence

Seq. No.	139938
Seq. ID	LIB24-086-Q1-E1-D1
Method	BLASTN
NCBI GI	g2351066
BLAST score	303
E value	1.0e-170
Match length	411
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOP9, complete sequence [Arabidopsis thaliana]

Seq. No.	139939
Seq. ID	LIB24-086-Q1-E1-D12
Method	BLASTN
NCBI GI	g4455168
BLAST score	323
E value	0.0e+00
Match length	323
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)

Seq. No.	139940
Seq. ID	LIB24-086-Q1-E1-D8
Method	BLASTX
NCBI GI	g3281850
BLAST score	783
E value	8.0e-84
Match length	150
% identity	99
NCBI Description	(AL031004) monogalactosyldiacylglycerol synthase - like protein [Arabidopsis thaliana]

Seq. No.	139941
Seq. ID	LIB24-086-Q1-E1-E11
Method	BLASTX
NCBI GI	g3688195
BLAST score	367
E value	2.0e-35
Match length	98
% identity	42
NCBI Description	(AJ010092) MAP3K beta 3 protein kinase [Arabidopsis thaliana]

Seq. No.	139942
Seq. ID	LIB24-086-Q1-E1-F5
Method	BLASTN
NCBI GI	g4467094
BLAST score	422
E value	0.0e+00
Match length	422
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10 (ESSA project)

Seq. No.	139943
Seq. ID	LIB24-086-Q1-E1-H8
Method	BLASTN
NCBI GI	g4220635
BLAST score	45
E value	3.0e-16
Match length	215
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDB19, complete sequence [Arabidopsis thaliana]

Seq. No.	139944
Seq. ID	LIB24-087-Q1-E1-E1
Method	BLASTX
NCBI GI	g3292821
BLAST score	172
E value	2.0e-12
Match length	76
% identity	53
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	139945
Seq. ID	LIB24-087-Q1-E1-F3

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Method	BLASTN
NCBI GI	g4678258
BLAST score	193
E value	1.0e-105
Match length	193
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I7 (ESSA project)

Seq. No.	139946
Seq. ID	LIB24-088-Q1-E1-B2
Method	BLASTN
NCBI GI	g4371278
BLAST score	63
E value	7.0e-27
Match length	139
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC T2N18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139947
Seq. ID	LIB24-088-Q1-E1-D1
Method	BLASTN
NCBI GI	g4159712
BLAST score	199
E value	1.0e-108
Match length	367
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWI23, complete sequence

Seq. No.	139948
Seq. ID	LIB24-088-Q1-E1-G6
Method	BLASTN
NCBI GI	g4757388
BLAST score	122
E value	3.0e-62
Match length	142
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F15L12, complete sequence

Seq. No.	139949
Seq. ID	LIB24-089-Q1-E1-A1
Method	BLASTN
NCBI GI	g3763944
BLAST score	345
E value	0.0e+00
Match length	345
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28A23 (ESSAII project)

Seq. No.	139950
Seq. ID	LIB24-089-Q1-E1-C1
Method	BLASTX
NCBI GI	g3281866

BLAST score	635
E value	1.0e-66
Match length	126
% identity	100
NCBI Description	(AL031004) putative protein [Arabidopsis thaliana]

Seq. No.	139951
Seq. ID	LIB24-089-Q1-E1-C3
Method	BLASTN
NCBI GI	g4510360
BLAST score	33
E value	7.0e-09
Match length	65
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC F11F19 genomic sequence, complete sequence

Seq. No.	139952
Seq. ID	LIB24-089-Q1-E1-E2
Method	BLASTX
NCBI GI	g2832683
BLAST score	349
E value	6.0e-33
Match length	68
% identity	100
NCBI Description	(AL021712) putative protein [Arabidopsis thaliana]

Seq. No.	139953
Seq. ID	LIB24-089-Q1-E1-F2
Method	BLASTN
NCBI GI	g3928074
BLAST score	365
E value	0.0e+00
Match length	386
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T7F6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139954
Seq. ID	LIB24-089-Q1-E1-G9
Method	BLASTN
NCBI GI	g4544381
BLAST score	67
E value	1.0e-29
Match length	153
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F16F14 genomic sequence, complete sequence

Seq. No.	139955
Seq. ID	LIB24-090-Q1-E1-A3
Method	BLASTN
NCBI GI	g3128134
BLAST score	335
E value	0.0e+00
Match length	339
% identity	100

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18G13, complete sequence [Arabidopsis thaliana]
Seq. No.	139956
Seq. ID	LIB24-090-Q1-E1-C2
Method	BLASTX
NCBI GI	g2462929
BLAST score	709
E value	3.0e-75
Match length	137
% identity	100
NCBI Description	(Y12295) glutathione transferase [Arabidopsis thaliana]
Seq. No.	139957
Seq. ID	LIB24-090-Q1-E1-E3
Method	BLASTX
NCBI GI	g132074
BLAST score	349
E value	1.0e-33
Match length	70
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain A1 precursor - Arabidopsis thaliana
Seq. No.	139958
Seq. ID	LIB24-090-Q1-E1-F11
Method	BLASTX
NCBI GI	g4567271
BLAST score	290
E value	4.0e-26
Match length	101
% identity	63
NCBI Description	(AC006841) putative kinesin protein [Arabidopsis thaliana]
Seq. No.	139959
Seq. ID	LIB24-090-Q1-E1-F12
Method	BLASTN
NCBI GI	g2341023
BLAST score	275
E value	1.0e-153
Match length	275
% identity	100
NCBI Description	Sequence of BAC F19P19 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]
Seq. No.	139960
Seq. ID	LIB24-090-Q1-E1-F2
Method	BLASTX
NCBI GI	g3152603
BLAST score	317
E value	2.0e-29
Match length	71
% identity	82
NCBI Description	(AC004482) unknown protein [Arabidopsis thaliana]

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Seq. No.	139961
Seq. ID	LIB24-090-Q1-E1-F4
Method	BLASTN
NCBI GI	g3449321
BLAST score	61
E value	5.0e-26
Match length	161
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTG10, complete sequence [Arabidopsis thaliana]

Seq. No.	139962
Seq. ID	LIB24-090-Q1-E1-G6
Method	BLASTX
NCBI GI	g3915639
BLAST score	510
E value	7.0e-52
Match length	117
% identity	87
NCBI Description	ALTERNATIVE OXIDASE 1A PRECURSOR >gi_2506083_dbj_BAA22625_ (D89875) alternative oxidase [Arabidopsis thaliana]

Seq. No.	139963
Seq. ID	LIB24-090-Q1-E1-H5
Method	BLASTN
NCBI GI	g4204173
BLAST score	95
E value	1.0e-46
Match length	95
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T2K10 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139964
Seq. ID	LIB24-091-Q1-E1-B10
Method	BLASTN
NCBI GI	g4538990
BLAST score	294
E value	1.0e-165
Match length	313
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T5L19 (ESSA project)

Seq. No.	139965
Seq. ID	LIB24-091-Q1-E1-C12
Method	BLASTX
NCBI GI	g2827712
BLAST score	645
E value	1.0e-67
Match length	122
% identity	100
NCBI Description	(AL021684) endoxyloglucan tranferase-like protein [Arabidopsis thaliana]

Seq. No.	139966
Seq. ID	LIB24-091-Q1-E1-D8

Method	BLASTX
NCBI GI	g115767
BLAST score	443
E value	4.0e-44
Match length	84
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	139967
Seq. ID	LIB24-091-Q1-E1-E11
Method	BLASTX
NCBI GI	g1563719
BLAST score	352
E value	2.0e-33
Match length	104
% identity	66
NCBI Description	(Y08320) cyclophylin [Digitalis lanata]

Seq. No.	139968
Seq. ID	LIB24-091-Q1-E1-F12
Method	BLASTN
NCBI GI	g1877523
BLAST score	329
E value	0.0e+00
Match length	337
% identity	99
NCBI Description	Arabidopsis thaliana BAC T7I23, complete sequence [Arabidopsis thaliana]

Seq. No.	139969
Seq. ID	LIB24-091-Q1-E1-F2
Method	BLASTN
NCBI GI	g3241927
BLAST score	314
E value	1.0e-176
Match length	385
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTE17, complete sequence [Arabidopsis thaliana]

Seq. No.	139970
Seq. ID	LIB24-091-Q1-E1-F4
Method	BLASTN
NCBI GI	g3128142
BLAST score	181
E value	3.0e-97
Match length	376
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQN23, complete sequence [Arabidopsis thaliana]

Seq. No.	139971
Seq. ID	LIB24-091-Q1-E1-G9
Method	BLASTX
NCBI GI	g136636
BLAST score	475
E value	8.0e-48
Match length	87
% identity	100
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1) >gi_1076424_pir__S43781 ubiquitin-conjugating enzyme UBC1 - Arabidopsis thaliana >gi_442594_pdb_1AAK_ Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) >gi_2981894_pdb_2AAK_ Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana >gi_166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi_431260 (L19351) ubiquitin conjugating enzyme [Arabidopsis thaliana]

Seq. No.	139972
Seq. ID	LIB24-091-Q1-E1-H8
Method	BLASTN
NCBI GI	g4567300
BLAST score	124
E value	9.0e-64
Match length	124
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II P1 MHK10 genomic sequence, complete sequence

Seq. No.	139973
Seq. ID	LIB24-092-Q1-E1-C11
Method	BLASTX
NCBI GI	g4206206
BLAST score	342
E value	3.0e-32
Match length	91
% identity	79
NCBI Description	(AF071527) putative M-type thioredoxin [Arabidopsis thaliana] >gi_4263039_gb_AAD15308_ (AC005142) putative M-type thioredoxin [Arabidopsis thaliana]

Seq. No.	139974
Seq. ID	LIB24-092-Q1-E1-C8
Method	BLASTN
NCBI GI	g3548797
BLAST score	39
E value	1.0e-13
Match length	39
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T18E12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139975
Seq. ID	LIB24-092-Q1-E1-D4
Method	BLASTX
NCBI GI	g1491712
BLAST score	254

E value	7.0e-22
Match length	109
% identity	47
NCBI Description	(X99961) unknown [Homo sapiens]

Seq. No.	139976
Seq. ID	LIB24-092-Q1-E1-D8
Method	BLASTX
NCBI GI	g1906830
BLAST score	718
E value	3.0e-76
Match length	141
% identity	99
NCBI Description	(Y11829) heat shock protein [Arabidopsis thaliana]

Seq. No.	139977
Seq. ID	LIB24-092-Q1-E1-F6
Method	BLASTN
NCBI GI	g3869074
BLAST score	169
E value	3.0e-90
Match length	271
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMI9, complete sequence [Arabidopsis thaliana]

Seq. No.	139978
Seq. ID	LIB24-092-Q1-E1-G1
Method	BLASTX
NCBI GI	g4406384
BLAST score	369
E value	3.0e-35
Match length	70
% identity	100
NCBI Description	(AF112303) serine acetyltransferase [Arabidopsis thaliana]

Seq. No.	139979
Seq. ID	LIB24-092-Q1-E1-H2
Method	BLASTX
NCBI GI	g3687249
BLAST score	467
E value	5.0e-47
Match length	98
% identity	96
NCBI Description	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]

Seq. No.	139980
Seq. ID	LIB24-092-Q1-E1-H5
Method	BLASTX
NCBI GI	g3258570
BLAST score	58
E value	4.0e-62
Match length	135
% identity	94
NCBI Description	(U89959) Unknown protein [Arabidopsis thaliana]

Seq. No.	139981
Seq. ID	LIB24-092-Q1-E1-H6
Method	BLASTN
NCBI GI	g2244829
BLAST score	197
E value	1.0e-107
Match length	281
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	139982
Seq. ID	LIB24-093-Q1-E1-A9
Method	BLASTX
NCBI GI	g3688799
BLAST score	160
E value	2.0e-11
Match length	32
% identity	100
NCBI Description	(AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis thaliana]

Seq. No.	139983
Seq. ID	LIB24-093-Q1-E1-B8
Method	BLASTX
NCBI GI	g4539423
BLAST score	460
E value	4.0e-46
Match length	109
% identity	85
NCBI Description	(AL049171) pyrophosphate-dependent phosphofructo-1-kinase [Arabidopsis thaliana]

Seq. No.	139984
Seq. ID	LIB24-093-Q1-E1-B9
Method	BLASTN
NCBI GI	g4432811
BLAST score	405
E value	0.0e+00
Match length	405
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F16D14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139985
Seq. ID	LIB24-093-Q1-E1-C11
Method	BLASTX
NCBI GI	g4406765
BLAST score	544
E value	7.0e-56
Match length	120
% identity	92
NCBI Description	(AC006836) putative cold-regulated protein cor15 [Arabidopsis thaliana]

Seq. No.	139986
Seq. ID	LIB24-093-Q1-E1-C7

Method	BLASTN
NCBI GI	g4490291
BLAST score	283
E value	1.0e-158
Match length	366
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17M5 (ESSA project)

Seq. No.	139987
Seq. ID	LIB24-093-Q1-E1-D12
Method	BLASTX
NCBI GI	g4506387
BLAST score	150
E value	1.0e-09
Match length	73
% identity	41
NCBI Description	RAD23 (S. cerevisiae) homolog B >gi_1709985_sp_P54727_R23B_HUMAN UV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMOLOG B (HHR23B) (XP-C REPAIR COMPLEMENTING COMPLEX 58 KD PROTEIN) (P58) >gi_1082758_pir__S44346 RAD23 protein homolog - human >gi_498148_dbj_BAA04652_ (D21090) XP-C repair complementing protein (p58/HHR23B) [Homo sapiens]

Seq. No.	139988
Seq. ID	LIB24-093-Q1-E1-F11
Method	BLASTN
NCBI GI	g2245073
BLAST score	84
E value	2.0e-39
Match length	100
% identity	49
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	139989
Seq. ID	LIB24-093-Q1-E1-H4
Method	BLASTX
NCBI GI	g4056433
BLAST score	178
E value	4.0e-13
Match length	54
% identity	54
NCBI Description	(AC005990) Similar to anter-specific proline-rich protein (CEX) gb_X60376 from Brassica napus. [Arabidopsis thaliana]

Seq. No.	139990
Seq. ID	LIB24-093-Q1-E1-H8
Method	BLASTX
NCBI GI	g3860247
BLAST score	49
E value	4.0e-26
Match length	87
% identity	70
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]

Seq. No.	139991
Seq. ID	LIB24-094-Q1-E1-A1
Method	BLASTN
NCBI GI	g4406805
BLAST score	247
E value	1.0e-136
Match length	377
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T27K22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	139992
Seq. ID	LIB24-094-Q1-E1-B11
Method	BLASTN
NCBI GI	g4581161
BLAST score	202
E value	1.0e-110
Match length	387
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T20G20 genomic sequence, complete sequence

Seq. No.	139993
Seq. ID	LIB24-094-Q1-E1-D3
Method	BLASTX
NCBI GI	g1621539
BLAST score	657
E value	4.0e-69
Match length	129
% identity	42
NCBI Description	(U28415) annexin-like protein [Arabidopsis thaliana]

Seq. No.	139994
Seq. ID	LIB24-094-Q1-E1-E11
Method	BLASTX
NCBI GI	g2497753
BLAST score	263
E value	6.0e-23
Match length	95
% identity	49
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3) >gi_1321915_emb_CAA65477_ (X96716) lipid transfer protein [Prunus dulcis]

Seq. No.	139995
Seq. ID	LIB24-094-Q1-E1-G3
Method	BLASTX
NCBI GI	g3258569
BLAST score	569
E value	7.0e-59
Match length	119
% identity	100
NCBI Description	(U89959) Similar to yeast general negative regulator of transcription subunit 1 [Arabidopsis thaliana]

Seq. No.	139996
Seq. ID	LIB24-094-Q1-E1-H7

Method	BLASTX
NCBI GI	g2129550
BLAST score	436
E value	3.0e-43
Match length	113
% identity	76
NCBI Description	calcium-dependent protein kinase (EC 2.7.1.-) CDPK6 - Arabidopsis thaliana >gi_2129554_pir__S71901 calcium-dependent protein kinase 6 - Arabidopsis thaliana >gi_836940 (U20623) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_836944 (U20625) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_4454034_emb_CAA23031.1_ (AL035394) calcium-dependent protein kinase (CDPK6) [Arabidopsis thaliana]

Seq. No.	139997
Seq. ID	LIB24-095-Q1-E1-C1
Method	BLASTN
NCBI GI	g2351066
BLAST score	331
E value	0.0e+00
Match length	339
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOP9, complete sequence [Arabidopsis thaliana]

Seq. No.	139998
Seq. ID	LIB24-095-Q1-E1-D10
Method	BLASTX
NCBI GI	g3643611
BLAST score	647
E value	5.0e-68
Match length	123
% identity	98
NCBI Description	(AC005395) putative casein kinase [Arabidopsis thaliana]

Seq. No.	139999
Seq. ID	LIB24-095-Q1-E1-E12
Method	BLASTN
NCBI GI	g4371278
BLAST score	99
E value	2.0e-48
Match length	347
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T2N18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	140000
Seq. ID	LIB24-095-Q1-E1-E7
Method	BLASTN
NCBI GI	g4581084
BLAST score	71
E value	9.0e-32
Match length	227
% identity	90
NCBI Description	Arabidopsis thaliana chromosome I BAC T30F21 genomic sequence, complete sequence

Seq. No.	140001
Seq. ID	LIB24-095-Q1-E1-F3
Method	BLASTX
NCBI GI	g1053047
BLAST score	267
E value	5.0e-24
Match length	54
% identity	98
NCBI Description	(U38425) histone H3 [Glycine max] >gi_1053049 (U38426) histone H3 [Glycine max] >gi_1053051 (U38427) histone H3 [Glycine max]

Seq. No.	140002
Seq. ID	LIB24-095-Q1-E1-F4
Method	BLASTN
NCBI GI	g4589438
BLAST score	92
E value	7.0e-45
Match length	92
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQJ2, complete sequence

Seq. No.	140003
Seq. ID	LIB24-095-Q1-E1-G10
Method	BLASTX
NCBI GI	g479413
BLAST score	654
E value	9.0e-69
Match length	131
% identity	100
NCBI Description	myosin-like protein - Arabidopsis thaliana

Seq. No.	140004
Seq. ID	LIB24-095-Q1-E1-H12
Method	BLASTN
NCBI GI	g3212846
BLAST score	68
E value	7.0e-30
Match length	132
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	140005
Seq. ID	LIB24-095-Q1-E1-H7
Method	BLASTN
NCBI GI	g4263753
BLAST score	118
E value	6.0e-60
Match length	207
% identity	100
NCBI Description	Arabidopsis thaliana chromosome V map near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	140006

Seq. ID	LIB24-096-Q1-E1-A11
Method	BLASTX
NCBI GI	g1171978
BLAST score	440
E value	9.0e-44
Match length	106
% identity	35
NCBI Description	POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2) (PABP 2) >gi_304109 (L19418) poly(A)-binding protein [Arabidopsis thaliana] >gi_2911051_emb_CAA17561_ (AL021961) poly(A)-binding protein [Arabidopsis thaliana]

Seq. No.	140007
Seq. ID	LIB24-096-Q1-E1-A6
Method	BLASTN
NCBI GI	g2673901
BLAST score	378
E value	0.0e+00
Match length	403
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T24P15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	140008
Seq. ID	LIB24-096-Q1-E1-C9
Method	BLASTX
NCBI GI	g3062791
BLAST score	325
E value	3.0e-30
Match length	84
% identity	73
NCBI Description	(AB010433) Lipid transfer protein [Brassica rapa]

Seq. No.	140009
Seq. ID	LIB24-096-Q1-E1-E5
Method	BLASTN
NCBI GI	g4589433
BLAST score	55
E value	2.0e-22
Match length	120
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNI5, complete sequence

Seq. No.	140010
Seq. ID	LIB24-096-Q1-E1-E6
Method	BLASTX
NCBI GI	g585536
BLAST score	615
E value	3.0e-64
Match length	111
% identity	100
NCBI Description	MYROSINASE PRECURSOR (SINIGRINASE) (THIOGLUCOSIDASE) >gi_1362006_pir__S56653 thioglucosidase (EC 3.2.3.1) - Arabidopsis thaliana >gi_304115 (L11454) thioglucosidase [Arabidopsis thaliana] >gi_871990_emb_CAA55786_ (X79194) thioglucosidase [Arabidopsis thaliana]

Seq. No.	140011
Seq. ID	LIB24-096-Q1-E1-G12
Method	BLASTX
NCBI GI	g115783
BLAST score	479
E value	2.0e-48
Match length	90
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No.	140012
Seq. ID	LIB24-096-Q1-E1-G6
Method	BLASTX
NCBI GI	g2213594
BLAST score	697
E value	8.0e-74
Match length	132
% identity	100
NCBI Description	(AC000348) T7N9.14 [Arabidopsis thaliana]

Seq. No.	140013
Seq. ID	LIB24-097-Q1-E1-A2
Method	BLASTX
NCBI GI	g2826900
BLAST score	487
E value	4.0e-49
Match length	146
% identity	68
NCBI Description	(AB004461) DNA polymerase alpha catalytic subunit [Oryza sativa]

Seq. No.	140014
Seq. ID	LIB24-097-Q1-E1-A4
Method	BLASTN
NCBI GI	g3241927
BLAST score	423
E value	0.0e+00
Match length	423
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTE17, complete sequence [Arabidopsis thaliana]

Seq. No.	140015
Seq. ID	LIB24-097-Q1-E1-B2
Method	BLASTX
NCBI GI	g3927837
BLAST score	423
E value	9.0e-42
Match length	81
% identity	100
NCBI Description	(AC005727) putative core protein [Arabidopsis thaliana]

Seq. No.	140016

Seq. ID	LIB24-097-Q1-E1-B4
Method	BLASTX
NCBI GI	g99741
BLAST score	491
E value	1.0e-49
Match length	103
% identity	95
NCBI Description	P-glycoprotein pgp1 - Arabidopsis thaliana

Seq. No.	140017
Seq. ID	LIB24-097-Q1-E1-B8
Method	BLASTX
NCBI GI	g4262228
BLAST score	319
E value	2.0e-29
Match length	124
% identity	52
NCBI Description	(AC006200) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	140018
Seq. ID	LIB24-097-Q1-E1-C2
Method	BLASTN
NCBI GI	g4063737
BLAST score	116
E value	5.0e-59
Match length	116
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F24D13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	140019
Seq. ID	LIB24-097-Q1-E1-C6
Method	BLASTN
NCBI GI	g4741184
BLAST score	420
E value	0.0e+00
Match length	420
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone T23J7 (ESSA project)

Seq. No.	140020
Seq. ID	LIB24-097-Q1-E1-C7
Method	BLASTN
NCBI GI	g2760169
BLAST score	341
E value	0.0e+00
Match length	408
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFB13, complete sequence [Arabidopsis thaliana]

Seq. No.	140021
Seq. ID	LIB24-097-Q1-E1-E5
Method	BLASTX
NCBI GI	g1362003

BLAST score	735
E value	3.0e-78
Match length	143
% identity	99
NCBI Description	protein phosphatase 2A B regulatory chain 55K - Arabidopsis thaliana >gi_710330 (U18129) 55 kDa B regulatory subunit of phosphatase 2A [Arabidopsis thaliana]

Seq. No.	140022
Seq. ID	LIB24-097-Q1-E1-F1
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	140023
Seq. ID	LIB24-097-Q1-E1-F5
Method	BLASTN
NCBI GI	g4249393
BLAST score	292
E value	1.0e-163
Match length	394
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T9J23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	140024
Seq. ID	LIB24-097-Q1-E1-F7
Method	BLASTX
NCBI GI	g3367534
BLAST score	629
E value	8.0e-66
Match length	143
% identity	90
NCBI Description	(AC004392) Strong similarity to coatamer alpha subunit (HEPCOP) homolog gb_U24105 from Homo sapiens. [Arabidopsis thaliana]

Seq. No.	140025
Seq. ID	LIB24-097-Q1-E1-H6
Method	BLASTX
NCBI GI	g1350680
BLAST score	731
E value	9.0e-78
Match length	142
% identity	99
NCBI Description	60S RIBOSOMAL PROTEIN L1

Seq. No.	140026
Seq. ID	LIB24-097-Q1-E1-H8
Method	BLASTX
NCBI GI	g4585981
BLAST score	292
E value	2.0e-26

Match length	68
% identity	88
NCBI Description	(AC005287) similar to Na+/H+-exchanging proteins [Arabidopsis thaliana]

Seq. No.	140027
Seq. ID	LIB24-099-Q1-E1-A1
Method	BLASTX
NCBI GI	g3885340
BLAST score	562
E value	3.0e-58
Match length	101
% identity	99
NCBI Description	(AC005623) unknown protein [Arabidopsis thaliana]

Seq. No.	140028
Seq. ID	LIB24-099-Q1-E1-A4
Method	BLASTN
NCBI GI	g4371278
BLAST score	149
E value	2.0e-78
Match length	197
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T2N18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	140029
Seq. ID	LIB24-099-Q1-E1-C6
Method	BLASTN
NCBI GI	g3241917
BLAST score	153
E value	7.0e-81
Match length	193
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19B1, complete sequence [Arabidopsis thaliana]

Seq. No.	140030
Seq. ID	LIB24-099-Q1-E1-F10
Method	BLASTN
NCBI GI	g4455339
BLAST score	46
E value	3.0e-17
Match length	85
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T12J5 (ESSAII project)

Seq. No.	140031
Seq. ID	LIB24-099-Q1-E1-F3
Method	BLASTN
NCBI GI	g2924732
BLAST score	273
E value	1.0e-152
Match length	281
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUA2, complete sequence [Arabidopsis thaliana]

Seq. No.	140032
Seq. ID	LIB24-099-Q1-E1-F5
Method	BLASTX
NCBI GI	g4567286
BLAST score	74
E value	2.0e-15
Match length	57
% identity	84
NCBI Description	(AC006841) putative coatomer alpha subunit [Arabidopsis thaliana]

Seq. No.	140033
Seq. ID	LIB24-099-Q1-E1-G8
Method	BLASTX
NCBI GI	g464524
BLAST score	139
E value	8.0e-09
Match length	31
% identity	87
NCBI Description	RAS-RELATED PROTEIN RAB-1A >gi_345404_pir__S32206 RAB1 protein - great pond snail >gi_481217_pir__S38339 rab1 protein - great pond snail >gi_288934_emb_CAA51233_ (X72688) RAB1 [Lymnaea stagnalis]

Seq. No.	140034
Seq. ID	LIB24-099-Q1-E1-H1
Method	BLASTX
NCBI GI	g132939
BLAST score	461
E value	2.0e-46
Match length	91
% identity	96
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi_81657_pir__JQ0771 ribosomal protein L3 (ARP1) - Arabidopsis thaliana >gi_166858 (M32654) ribosomal protein [Arabidopsis thaliana]

Seq. No.	140035
Seq. ID	LIB24-099-Q1-E1-H12
Method	BLASTX
NCBI GI	g3702314
BLAST score	606
E value	3.0e-63
Match length	116
% identity	100
NCBI Description	(AC002535) similar to SWI/SNF complex subunit BAF170 [Arabidopsis thaliana]

Seq. No.	140036
Seq. ID	LIB24-100-Q1-E1-A11
Method	BLASTX
NCBI GI	g1345594
BLAST score	546
E value	4.0e-56
Match length	123
% identity	93

NCBI Description	14-3-3-LIKE PROTEIN GF14 KAPPA >gi_1022780 (U36447) GF14 Kappa isoform [Arabidopsis thaliana]
Seq. No.	140037
Seq. ID	LIB24-100-Q1-E1-A6
Method	BLASTX
NCBI GI	g1903347
BLAST score	308
E value	2.0e-28
Match length	93
% identity	73
NCBI Description	(AC000104) EST gb_ATTS5672 comes from this gene. [Arabidopsis thaliana]
Seq. No.	140038
Seq. ID	LIB24-100-Q1-E1-B8
Method	BLASTN
NCBI GI	g2760168
BLAST score	337
E value	0.0e+00
Match length	412
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MEE6, complete sequence [Arabidopsis thaliana]
Seq. No.	140039
Seq. ID	LIB24-100-Q1-E1-D12
Method	BLASTN
NCBI GI	g4757662
BLAST score	277
E value	1.0e-154
Match length	301
% identity	98
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome I, complete sequence
Seq. No.	140040
Seq. ID	LIB24-100-Q1-E1-D6
Method	BLASTN
NCBI GI	g4757417
BLAST score	207
E value	1.0e-113
Match length	271
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: T30G6, complete sequence
Seq. No.	140041
Seq. ID	LIB24-100-Q1-E1-F9
Method	BLASTN
NCBI GI	g3599967
BLAST score	254
E value	1.0e-141
Match length	254
% identity	100
NCBI Description	Arabidopsis thaliana clp protease (CLP) mRNA, partial cds

Seq. No.	140042
Seq. ID	LIB24-100-Q1-E1-G10
Method	BLASTN
NCBI GI	g2264316
BLAST score	65
E value	2.0e-28
Match length	77
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRO11, complete sequence [Arabidopsis thaliana]

Seq. No.	140043
Seq. ID	LIB24-100-Q1-E1-G12
Method	BLASTX
NCBI GI	g2688544
BLAST score	201
E value	1.0e-15
Match length	101
% identity	39
NCBI Description	(AE001163) 4-methyl-5(b-hydroxyethyl)-thiazole monophosphate biosynthesis protein (thiJ) [Borrelia burgdorferi]

Seq. No.	140044
Seq. ID	LIB24-101-Q1-E1-F2
Method	BLASTX
NCBI GI	g2507587
BLAST score	284
E value	2.0e-25
Match length	57
% identity	88
NCBI Description	METALLOTHIONEIN-LIKE PROTEIN 2A (MT-2A) (MT-K) (MT-1G) >gi_1361998_pir__S57861 metallothionein 2a - Arabidopsis thaliana >gi_555976 (U15108) metallothionein-like protein [Arabidopsis thaliana] >gi_1580892_prf__2116236A metallothionein 1 [Arabidopsis thaliana]

Seq. No.	140045
Seq. ID	LIB24-101-Q1-E1-G5
Method	BLASTX
NCBI GI	g3298327
BLAST score	345
E value	7.0e-33
Match length	71
% identity	100
NCBI Description	(AB010416) delta-VM23 [Raphanus sativus]

Seq. No.	140046
Seq. ID	LIB24-102-Q1-E1-A10
Method	BLASTN
NCBI GI	g2832639
BLAST score	71
E value	3.0e-32
Match length	114
% identity	91
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28J12 (ESSAII project)

Seq. No.	140047
Seq. ID	LIB24-102-Q1-E1-B11
Method	BLASTX
NCBI GI	g3292821
BLAST score	272
E value	5.0e-24
Match length	105
% identity	54
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	140048
Seq. ID	LIB24-102-Q1-E1-D4
Method	BLASTN
NCBI GI	g3540210
BLAST score	124
E value	1.0e-63
Match length	172
% identity	93
NCBI Description	Arabidopsis thaliana chromosome I BAC F5A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	140049
Seq. ID	LIB24-102-Q1-E1-E8
Method	BLASTX
NCBI GI	g4249382
BLAST score	209
E value	9.0e-17
Match length	55
% identity	80
NCBI Description	(AC005966) Strong similarity to gi_3337350 F13P17.3 putative permease from Arabidopsis thaliana BAC gb_AC004481. [Arabidopsis thaliana]

Seq. No.	140050
Seq. ID	LIB24-102-Q1-E1-F4
Method	BLASTX
NCBI GI	g1710549
BLAST score	277
E value	1.0e-24
Match length	51
% identity	98
NCBI Description	60S RIBOSOMAL PROTEIN L39

Seq. No.	140051
Seq. ID	LIB24-102-Q1-E1-G10
Method	BLASTN
NCBI GI	g4455229
BLAST score	261
E value	1.0e-145
Match length	294
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F13M23 (ESSAII project)

Seq. No.	140052
Seq. ID	LIB24-102-Q1-E1-H12

Method	BLASTX
NCBI GI	g486784
BLAST score	581
E value	3.0e-60
Match length	130
% identity	27
NCBI Description	Golgi-associated particle 102K chain - human

Seq. No.	140053
Seq. ID	LIB24-102-Q1-E1-H8
Method	BLASTN
NCBI GI	g4263753
BLAST score	117
E value	4.0e-59
Match length	327
% identity	61
NCBI Description	Arabidopsis thaliana chromosome V map near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	140054
Seq. ID	LIB24-103-Q1-E1-A1
Method	BLASTX
NCBI GI	g3850587
BLAST score	343
E value	6.0e-33
Match length	68
% identity	97
NCBI Description	(AC005278) Strong similarity to gi_2244780 hypothetical protein from Arabidopsis thaliana chromosome 4 contig gb_Z97335. [Arabidopsis thaliana]

Seq. No.	140055
Seq. ID	LIB24-103-Q1-E1-A5
Method	BLASTX
NCBI GI	g585421
BLAST score	524
E value	1.0e-53
Match length	97
% identity	100
NCBI Description	LIPOXYGENASE, CHLOROPLAST PRECURSOR >gi_541879_pir__JQ2391 lipoxygenase (EC 1.13.11.12) AtLox2 - Arabidopsis thaliana >gi_431258 (L23968) lipoxygenase [Arabidopsis thaliana]

Seq. No.	140056
Seq. ID	LIB24-103-Q1-E1-B8
Method	BLASTX
NCBI GI	g1669389
BLAST score	545
E value	6.0e-56
Match length	100
% identity	100
NCBI Description	(U42007) actin 8 [Arabidopsis thaliana]

Seq. No.	140057
Seq. ID	LIB24-103-Q1-E1-G5
Method	BLASTX
NCBI GI	g1169599

BLAST score	364
E value	8.0e-35
Match length	87
% identity	80
NCBI Description	OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR >gi_541883_pir__JQ2336 omega-3 fatty acid desaturase (EC 1.14.99.-) CFD - Arabidopsis thaliana >gi_408481 (L22961) omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_468434_dbj_BAA05040_ (D26019) plastid fatty acid desaturase [Arabidopsis thaliana] >gi_541653_dbj_BAA03106_ (D14007) omega-3-desaturase [Arabidopsis thaliana]

Seq. No.	140058
Seq. ID	LIB24-103-Q1-E1-G8
Method	BLASTX
NCBI GI	g2443755
BLAST score	573
E value	3.0e-59
Match length	125
% identity	83
NCBI Description	(AF020433) cyclophilin [Arabidopsis thaliana]

Seq. No.	140059
Seq. ID	LIB24-104-Q1-E2-A11
Method	BLASTX
NCBI GI	g267073
BLAST score	144
E value	1.0e-09
Match length	29
% identity	86
NCBI Description	TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin beta chain - Arabidopsis thaliana >gi_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701) beta-3 tubulin [Arabidopsis thaliana]

Seq. No.	140060
Seq. ID	LIB24-104-Q1-E2-C7
Method	BLASTX
NCBI GI	g3337366
BLAST score	469
E value	4.0e-47
Match length	121
% identity	42
NCBI Description	(AC004481) unknown protein [Arabidopsis thaliana]

Seq. No.	140061
Seq. ID	LIB24-104-Q1-E2-D5
Method	BLASTN
NCBI GI	g1905875
BLAST score	96
E value	4.0e-47
Match length	96
% identity	100
NCBI Description	Arabidopsis thaliana biotin carboxylase subunit (CAC2) mRNA, complete cds

Seq. No.	140062

Seq. ID	LIB24-104-Q1-E2-F10
Method	BLASTX
NCBI GI	g4510346
BLAST score	400
E value	5.0e-39
Match length	124
% identity	62
NCBI Description	(AC006921) hypothetical protein [Arabidopsis thaliana]

Seq. No.	140063
Seq. ID	LIB24-106-Q1-E1-B12
Method	BLASTN
NCBI GI	g3176694
BLAST score	225
E value	1.0e-123
Match length	368
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC T14N5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	140064
Seq. ID	LIB24-106-Q1-E1-C10
Method	BLASTX
NCBI GI	g4589965
BLAST score	503
E value	5.0e-51
Match length	100
% identity	100
NCBI Description	(AC007169) putative glyoxalase II [Arabidopsis thaliana]

Seq. No.	140065
Seq. ID	LIB24-106-Q1-E1-D12
Method	BLASTX
NCBI GI	g2244904
BLAST score	166
E value	1.0e-11
Match length	139
% identity	9
NCBI Description	(Z97339) similar to hypothetical protein C02F5.7 - Caenorha [Arabidopsis thaliana]

Seq. No.	140066
Seq. ID	LIB24-106-Q1-E1-E1
Method	BLASTN
NCBI GI	g2264318
BLAST score	387
E value	0.0e+00
Match length	387
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUP24, complete sequence [Arabidopsis thaliana]

Seq. No.	140067
Seq. ID	LIB24-106-Q1-E1-E5
Method	BLASTN
NCBI GI	g4159706
BLAST score	114

E value	1.0e-57
Match length	184
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGL6, complete sequence

Seq. No.	140068
Seq. ID	LIB24-106-Q1-E1-F1
Method	BLASTX
NCBI GI	g3395588
BLAST score	149
E value	5.0e-10
Match length	58
% identity	45
NCBI Description	(AL031179) serine-threonine protein phosphatase [Schizosaccharomyces pombe]

Seq. No.	140069
Seq. ID	LIB24-106-Q1-E1-F4
Method	BLASTN
NCBI GI	g3236479
BLAST score	245
E value	1.0e-135
Match length	302
% identity	95
NCBI Description	Arabidopsis thaliana BAC F9H3, from chromosome IV near 18.8 cM, complete sequence

Seq. No.	140070
Seq. ID	LIB24-106-Q1-E1-G8
Method	BLASTX
NCBI GI	g4510424
BLAST score	512
E value	4.0e-52
Match length	99
% identity	100
NCBI Description	(AC006929) putative carboxypeptidase [Arabidopsis thaliana]

Seq. No.	140071
Seq. ID	LIB24-107-Q1-E1-A10
Method	BLASTX
NCBI GI	g4539383
BLAST score	474
E value	7.0e-48
Match length	93
% identity	97
NCBI Description	(AL035526) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	140072
Seq. ID	LIB24-107-Q1-E1-B12
Method	BLASTN
NCBI GI	g2245073
BLAST score	173
E value	1.0e-92
Match length	258
% identity	100

NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No
Seq. No.	140073
Seq. ID	LIB24-107-Q1-E1-C9
Method	BLASTX
NCBI GI	g4539314
BLAST score	251
E value	1.0e-21
Match length	114
% identity	43
NCBI Description	(AL035679) kinesin like protein [Arabidopsis thaliana]
Seq. No.	140074
Seq. ID	LIB24-107-Q1-E1-D7
Method	BLASTX
NCBI GI	g2443890
BLAST score	354
E value	1.0e-33
Match length	125
% identity	58
NCBI Description	(AC002294) similar to NAM (gp_X92205_1321924) and CUC2 (gp_AB002560_1944132) proteins [Arabidopsis thaliana]
Seq. No.	140075
Seq. ID	LIB24-107-Q1-E1-E8
Method	BLASTX
NCBI GI	g4049351
BLAST score	515
E value	1.0e-52
Match length	96
% identity	99
NCBI Description	(AL034567) nodulin-like protein [Arabidopsis thaliana]
Seq. No.	140076
Seq. ID	LIB24-107-Q1-E1-F12
Method	BLASTN
NCBI GI	g4263586
BLAST score	269
E value	1.0e-150
Match length	342
% identity	91
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F28K20 sequence, complete sequence
Seq. No.	140077
Seq. ID	LIB24-107-Q1-E1-G11
Method	BLASTN
NCBI GI	g2570223
BLAST score	160
E value	9.0e-85
Match length	368
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F20D22 sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	140078

Seq. ID	LIB24-107-Q1-E1-G6
Method	BLASTN
NCBI GI	g3738275
BLAST score	188
E value	1.0e-101
Match length	352
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F17A22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	140079
Seq. ID	LIB24-107-Q1-E1-H12
Method	BLASTX
NCBI GI	g3149952
BLAST score	491
E value	1.0e-49
Match length	126
% identity	77
NCBI Description	(AB010259) DRH1 [Arabidopsis thaliana]

Seq. No.	140080
Seq. ID	LIB24-108-Q1-E1-A5
Method	BLASTN
NCBI GI	g4159705
BLAST score	300
E value	1.0e-168
Match length	382
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGD8, complete sequence

Seq. No.	140081
Seq. ID	LIB24-108-Q1-E1-D11
Method	BLASTN
NCBI GI	g4580454
BLAST score	308
E value	1.0e-173
Match length	312
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T2G17 genomic sequence, complete sequence

Seq. No.	140082
Seq. ID	LIB24-108-Q1-E1-F12
Method	BLASTN
NCBI GI	g2564051
BLAST score	98
E value	2.0e-48
Match length	98
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD9, complete sequence [Arabidopsis thaliana]

Seq. No.	140083
Seq. ID	LIB24-108-Q1-E1-H1
Method	BLASTX
NCBI GI	g4587549

BLAST score	363
E value	1.0e-34
Match length	75
% identity	84
NCBI Description	(AC006577) Similar to gb_U55861 RNA binding protein nucleolysin (TIAR) from Mus musculus and contains several PF_00076 RNA recognition motif domains. ESTs gb_T21032 and gb_T44127 come from this gene. [Arabidopsis t

Seq. No.	140084
Seq. ID	LIB24-109-Q1-E1-B10
Method	BLASTN
NCBI GI	g3335356
BLAST score	366
E value	0.0e+00
Match length	404
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F16M14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	140085
Seq. ID	LIB24-109-Q1-E1-B3
Method	BLASTX
NCBI GI	g4006880
BLAST score	435
E value	3.0e-43
Match length	100
% identity	87
NCBI Description	(Z99707) putative protein [Arabidopsis thaliana]

Seq. No.	140086
Seq. ID	LIB24-109-Q1-E1-C1
Method	BLASTN
NCBI GI	g4519194
BLAST score	145
E value	4.0e-76
Match length	193
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHM17, complete sequence

Seq. No.	140087
Seq. ID	LIB24-109-Q1-E1-E10
Method	BLASTX
NCBI GI	g3522948
BLAST score	682
E value	5.0e-72
Match length	137
% identity	92
NCBI Description	(AC004411) hypothetical protein [Arabidopsis thaliana]

Seq. No.	140088
Seq. ID	LIB24-109-Q1-E1-E12
Method	BLASTX
NCBI GI	g115783
BLAST score	598
E value	3.0e-62

Match length	113
% identity	99
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]
Seq. No.	140089
Seq. ID	LIB24-109-Q1-E1-E9
Method	BLASTX
NCBI GI	g818849
BLAST score	230
E value	2.0e-19
Match length	77
% identity	52
NCBI Description	(U25430) nucleotide pyrophosphatase precursor [Oryza sativa]
Seq. No.	140090
Seq. ID	LIB24-109-Q1-E1-F1
Method	BLASTN
NCBI GI	g4519197
BLAST score	219
E value	1.0e-120
Match length	235
% identity	51
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MTC11, complete sequence
Seq. No.	140091
Seq. ID	LIB24-109-Q1-E1-F10
Method	BLASTN
NCBI GI	g4454004
BLAST score	124
E value	2.0e-63
Match length	128
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F24A6 (ESSAII project)
Seq. No.	140092
Seq. ID	LIB24-109-Q1-E1-F12
Method	BLASTN
NCBI GI	g3831448
BLAST score	414
E value	0.0e+00
Match length	414
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T32F6 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	140093
Seq. ID	LIB24-109-Q1-E1-F6
Method	BLASTX
NCBI GI	g4539383
BLAST score	191
E value	2.0e-14

09604705.960804

Match length	137
% identity	29
NCBI Description	(AL035526) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	140094
Seq. ID	LIB24-109-Q1-E1-F9
Method	BLASTX
NCBI GI	g4678280
BLAST score	263
E value	7.0e-23
Match length	140
% identity	41
NCBI Description	(AL049660) zinc finger-like protein [Arabidopsis thaliana]

Seq. No.	140095
Seq. ID	LIB24-109-Q1-E1-G5
Method	BLASTN
NCBI GI	g3212846
BLAST score	294
E value	1.0e-164
Match length	437
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	140096
Seq. ID	LIB24-109-Q1-E1-H5
Method	BLASTX
NCBI GI	g2494125
BLAST score	702
E value	2.0e-74
Match length	139
% identity	100
NCBI Description	(AC002376) Strong similarity to Cucumis acetyl-CoA acyltransferase (gb_D70895). [Arabidopsis thaliana]

Seq. No.	140097
Seq. ID	LIB24-110-Q1-E1-A7
Method	BLASTN
NCBI GI	g4519193
BLAST score	212
E value	1.0e-116
Match length	415
% identity	51
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC11, complete sequence

Seq. No.	140098
Seq. ID	LIB24-110-Q1-E1-A9
Method	BLASTX
NCBI GI	g1076442
BLAST score	271
E value	5.0e-24
Match length	68
% identity	71
NCBI Description	beta-glucosidase (EC 3.2.1.21) - rape

>gi_757740_emb_CAA57913_ (X82577) beta-glucosidase [Brassica napus]

Seq. No.	140099
Seq. ID	LIB24-110-Q1-E1-B7
Method	BLASTX
NCBI GI	g3395426
BLAST score	459
E value	6.0e-46
Match length	102
% identity	86
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	140100
Seq. ID	LIB24-110-Q1-E1-D4
Method	BLASTN
NCBI GI	g4581103
BLAST score	67
E value	3.0e-29
Match length	67
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T24I21 genomic sequence, complete sequence

Seq. No.	140101
Seq. ID	LIB24-110-Q1-E1-F10
Method	BLASTN
NCBI GI	g2264313
BLAST score	34
E value	2.0e-09
Match length	110
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOP10, complete sequence [Arabidopsis thaliana]

Seq. No.	140102
Seq. ID	LIB24-110-Q1-E1-F8
Method	BLASTX
NCBI GI	g4204257
BLAST score	438
E value	2.0e-43
Match length	97
% identity	82
NCBI Description	(AC005223) 5493 [Arabidopsis thaliana]

Seq. No.	140103
Seq. ID	LIB24-110-Q1-E1-H11
Method	BLASTN
NCBI GI	g3241922
BLAST score	120
E value	7.0e-61
Match length	374
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLM24, complete sequence [Arabidopsis thaliana]

Seq. No.	140104

Seq. ID	LIB24-110-Q1-E1-H12
Method	BLASTX
NCBI GI	g4006856
BLAST score	565
E value	3.0e-58
Match length	146
% identity	77
NCBI Description	(Z99707) receptor kinase-like protein [Arabidopsis thaliana]

Seq. No.	140105
Seq. ID	LIB24-111-Q1-E1-B7
Method	BLASTX
NCBI GI	g4415914
BLAST score	79
E value	6.0e-18
Match length	139
% identity	45
NCBI Description	(AC006282) unknown protein [Arabidopsis thaliana]

Seq. No.	140106
Seq. ID	LIB24-111-Q1-E1-B8
Method	BLASTX
NCBI GI	g3914658
BLAST score	595
E value	8.0e-62
Match length	143
% identity	83
NCBI Description	50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR >gi_1694974_emb_CAA70851_ (Y09635) plastid ribosomal protein [Arabidopsis thaliana]

Seq. No.	140107
Seq. ID	LIB24-111-Q1-E1-B9
Method	BLASTN
NCBI GI	g4589439
BLAST score	309
E value	1.0e-173
Match length	454
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQM1, complete sequence

Seq. No.	140108
Seq. ID	LIB24-111-Q1-E1-C6
Method	BLASTN
NCBI GI	g3980374
BLAST score	155
E value	1.0e-81
Match length	414
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F16P2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	140109
Seq. ID	LIB24-111-Q1-E1-C7
Method	BLASTX

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NCBI GI	g4406819
BLAST score	321
E value	1.0e-29
Match length	144
% identity	49
NCBI Description	(AC006201) unknown protein [Arabidopsis thaliana]

Seq. No.	140110
Seq. ID	LIB24-111-Q1-E1-C8
Method	BLASTN
NCBI GI	g2459406
BLAST score	136
E value	9.0e-71
Match length	176
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F4P9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	140111
Seq. ID	LIB24-111-Q1-E1-D11
Method	BLASTN
NCBI GI	g2760173
BLAST score	293
E value	1.0e-164
Match length	409
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH19, complete sequence [Arabidopsis thaliana]

Seq. No.	140112
Seq. ID	LIB24-111-Q1-E1-F11
Method	BLASTN
NCBI GI	g4028969
BLAST score	250
E value	1.0e-138
Match length	420
% identity	99
NCBI Description	Arabidopsis thaliana pollenless3 (178) gene, complete cds; beta-9 tubulin (TUB9) gene, partial cds; and unknown gene

Seq. No.	140113
Seq. ID	LIB24-111-Q1-E1-F12
Method	BLASTX
NCBI GI	g3395443
BLAST score	357
E value	6.0e-34
Match length	87
% identity	84
NCBI Description	(AC004683) putative ammonium transporter, 3' partial [Arabidopsis thaliana]

Seq. No.	140114
Seq. ID	LIB24-111-Q1-E1-F2
Method	BLASTX
NCBI GI	g2827621
BLAST score	536
E value	5.0e-55

Match length	124
% identity	90
NCBI Description	(AL021636) putative protein [Arabidopsis thaliana]

Seq. No.	140115
Seq. ID	LIB24-111-Q1-E1-F6
Method	BLASTN
NCBI GI	g4325336
BLAST score	389
E value	0.0e+00
Match length	442
% identity	99
NCBI Description	Arabidopsis thaliana BAC F15P23

Seq. No.	140116
Seq. ID	LIB24-111-Q1-E1-G10
Method	BLASTX
NCBI GI	g3881133
BLAST score	178
E value	6.0e-13
Match length	123
% identity	28
NCBI Description	(Z99278) similar to WD domain, G-beta repeats (4 domains) [Caenorhabditis elegans]

Seq. No.	140117
Seq. ID	LIB24-111-Q1-E1-H3
Method	BLASTX
NCBI GI	g1345595
BLAST score	598
E value	3.0e-62
Match length	122
% identity	100
NCBI Description	14-3-3-LIKE PROTEIN GF14 LAMBDA (14-3-3-LIKE PROTEIN AFT1) >gi_1084332_pir__S53727 14-3-3-like protein (ATF1) - Arabidopsis thaliana >gi_953221 (U02565) 14-3-3-like protein 1 [Arabidopsis thaliana] >gi_1549404 (U68545) GF14 lambda [Arabidopsis thaliana]

Seq. No.	140118
Seq. ID	LIB24-112-Q1-E1-B5
Method	BLASTX
NCBI GI	g1170503
BLAST score	568
E value	1.0e-58
Match length	109
% identity	100
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1) >gi_322503_pir__JC1452 translation initiation factor eIF-4A1 - Arabidopsis thaliana >gi_16554_emb_CAA46188_ (X65052) eukaryotic translation initiation factor 4A-1 [Arabidopsis thaliana]

Seq. No.	140119
Seq. ID	LIB24-112-Q1-E1-B7
Method	BLASTN
NCBI GI	g16353

BLAST score	253
E value	1.0e-140
Match length	253
% identity	100
NCBI Description	A.thaliana kin2 gene

Seq. No.	140120
Seq. ID	LIB24-112-Q1-E1-C4
Method	BLASTX
NCBI GI	g2635703
BLAST score	290
E value	4.0e-26
Match length	135
% identity	50
NCBI Description	(Z99120) similar to hypothetical proteins [Bacillus subtilis]

Seq. No.	140121
Seq. ID	LIB24-112-Q1-E1-D1
Method	BLASTN
NCBI GI	g3510347
BLAST score	387
E value	0.0e+00
Match length	387
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]

Seq. No.	140122
Seq. ID	LIB24-112-Q1-E1-D11
Method	BLASTN
NCBI GI	g2564050
BLAST score	140
E value	8.0e-73
Match length	312
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUA22, complete sequence [Arabidopsis thaliana]

Seq. No.	140123
Seq. ID	LIB24-112-Q1-E1-E12
Method	BLASTN
NCBI GI	g3152947
BLAST score	115
E value	3.0e-58
Match length	139
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for polygalacturonase

Seq. No.	140124
Seq. ID	LIB24-112-Q1-E1-E3
Method	BLASTN
NCBI GI	g2924651
BLAST score	334
E value	0.0e+00
Match length	398
% identity	100

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana]
Seq. No.	140125
Seq. ID	LIB24-112-Q1-E1-E4
Method	BLASTN
NCBI GI	g710625
BLAST score	380
E value	0.0e+00
Match length	401
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for ERD15 protein, complete cds
Seq. No.	140126
Seq. ID	LIB24-112-Q1-E1-F5
Method	BLASTN
NCBI GI	g2264321
BLAST score	398
E value	0.0e+00
Match length	398
% identity	33
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXM12, complete sequence [Arabidopsis thaliana]
Seq. No.	140127
Seq. ID	LIB24-113-Q1-E1-C6
Method	BLASTX
NCBI GI	g280386
BLAST score	479
E value	3.0e-48
Match length	98
% identity	98
NCBI Description	ubiquitin / ribosomal protein CEP52 - Arabidopsis thaliana >gi_166930 (J05507) ubiquitin extension protein (UBQ1) [Arabidopsis thaliana] >gi_166932 (J05508) ubiquitin extension protein (UBQ2) [Arabidopsis thaliana] >gi_4678227_gb_AAD26972.1_AC007135_8 (AC007135) ubiquitin/ribosomal protein CEP52 [Arabidopsis thaliana]
Seq. No.	140128
Seq. ID	LIB24-113-Q1-E1-D9
Method	BLASTN
NCBI GI	g4584841
BLAST score	246
E value	1.0e-136
Match length	246
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T23E23, complete sequence
Seq. No.	140129
Seq. ID	LIB24-113-Q1-E1-F7
Method	BLASTX
NCBI GI	g3549654
BLAST score	263
E value	6.0e-23
Match length	141

% identity	41
NCBI Description	(AL031394) metal-transporting P-type ATPase (fragment) [Arabidopsis thaliana]

Seq. No.	140130
Seq. ID	LIB24-113-Q1-E1-F8
Method	BLASTX
NCBI GI	g2832629
BLAST score	295
E value	8.0e-27
Match length	111
% identity	45
NCBI Description	(AL021711) 4-coumarate-CoA ligase - like [Arabidopsis thaliana]

Seq. No.	140131
Seq. ID	LIB24-113-Q1-E1-H1
Method	BLASTN
NCBI GI	g3449333
BLAST score	223
E value	1.0e-122
Match length	227
% identity	52
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXF12, complete sequence [Arabidopsis thaliana]

Seq. No.	140132
Seq. ID	LIB24-113-Q1-E1-H3
Method	BLASTX
NCBI GI	g4309728
BLAST score	379
E value	2.0e-36
Match length	109
% identity	72
NCBI Description	(AC006439) putative ADP-ribosylation factor [Arabidopsis thaliana]

Seq. No.	140133
Seq. ID	LIB24-114-Q1-E1-A4
Method	BLASTN
NCBI GI	g2505873
BLAST score	71
E value	1.0e-31
Match length	96
% identity	100
NCBI Description	Arabidopsis thaliana DNA, 40 kb surrounding ACS1 locus

Seq. No.	140134
Seq. ID	LIB24-114-Q1-E1-A6
Method	BLASTN
NCBI GI	g972918
BLAST score	211
E value	1.0e-115
Match length	231
% identity	98
NCBI Description	Arabidopsis thaliana IAA8 (IAA8) gene complete cds

Seq. No.	140135
Seq. ID	LIB24-114-Q1-E1-B12
Method	BLASTX
NCBI GI	g4249386
BLAST score	193
E value	5.0e-15
Match length	37
% identity	100
NCBI Description	(AC005966) Strong similarity to gb_AF061286 gamma-adaptin 1 from Arabidopsis thaliana. EST gb_H37393 comes from this gene. [Arabidopsis thaliana]

Seq. No.	140136
Seq. ID	LIB24-114-Q1-E1-E1
Method	BLASTX
NCBI GI	g3851584
BLAST score	260
E value	1.0e-22
Match length	61
% identity	84
NCBI Description	(AF092563) chromosome-associated protein-E [Homo sapiens]

Seq. No.	140137
Seq. ID	LIB24-114-Q1-E1-H11
Method	BLASTX
NCBI GI	g464621
BLAST score	408
E value	4.0e-40
Match length	97
% identity	79
NCBI Description	60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__S28586 ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16 [Mesembryanthemum crystallinum]

Seq. No.	140138
Seq. ID	LIB24-115-Q1-E1-A11
Method	BLASTX
NCBI GI	g2880048
BLAST score	644
E value	1.0e-67
Match length	122
% identity	98
NCBI Description	(AC002340) unknown protein [Arabidopsis thaliana]

Seq. No.	140139
Seq. ID	LIB24-115-Q1-E1-A5
Method	BLASTX
NCBI GI	g99688
BLAST score	690
E value	5.0e-73
Match length	133
% identity	100
NCBI Description	translation elongation factor eEF-1 alpha chain (gene A4) - Arabidopsis thaliana >gi_295789_emb_CAA34456_ (X16432) elongation factor 1-alpha [Arabidopsis thaliana]

Seq. No.	140140
Seq. ID	LIB24-115-Q1-E1-A7
Method	BLASTX
NCBI GI	g4406756
BLAST score	657
E value	4.0e-69
Match length	129
% identity	100
NCBI Description	(AC006836) putative integral membrane protein A3 [Arabidopsis thaliana]

Seq. No.	140141
Seq. ID	LIB24-115-Q1-E1-A8
Method	BLASTN
NCBI GI	g3789706
BLAST score	333
E value	0.0e+00
Match length	341
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F15K9 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	140142
Seq. ID	LIB24-115-Q1-E1-A9
Method	BLASTN
NCBI GI	g166589
BLAST score	287
E value	1.0e-160
Match length	303
% identity	99
NCBI Description	Arabidopsis thaliana transcription factor (AGL2) mRNA, complete cds

Seq. No.	140143
Seq. ID	LIB24-115-Q1-E1-C1
Method	BLASTN
NCBI GI	g3292807
BLAST score	211
E value	1.0e-115
Match length	369
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F7H19 (ESSAII project)

Seq. No.	140144
Seq. ID	LIB24-115-Q1-E1-D12
Method	BLASTN
NCBI GI	g4662609
BLAST score	153
E value	2.0e-80
Match length	427
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10A5, complete sequence

Seq. No.	140145
Seq. ID	LIB24-115-Q1-E1-D8

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Method	BLASTX
NCBI GI	g115767
BLAST score	317
E value	1.0e-29
Match length	65
% identity	94
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana]

Seq. No.	140146
Seq. ID	LIB24-115-Q1-E1-F4
Method	BLASTN
NCBI GI	g2435510
BLAST score	186
E value	1.0e-100
Match length	194
% identity	99
NCBI Description	Arabidopsis thaliana BAC TM017A05

Seq. No.	140147
Seq. ID	LIB24-115-Q1-E1-F5
Method	BLASTN
NCBI GI	g2864607
BLAST score	260
E value	1.0e-144
Match length	356
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6 (ESSAII project)

Seq. No.	140148
Seq. ID	LIB24-115-Q1-E1-F9
Method	BLASTN
NCBI GI	g3985958
BLAST score	290
E value	1.0e-162
Match length	358
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZN1, complete sequence [Arabidopsis thaliana]

Seq. No.	140149
Seq. ID	LIB24-115-Q1-E1-G10
Method	BLASTX
NCBI GI	g1762935
BLAST score	199
E value	5.0e-16
Match length	45
% identity	91
NCBI Description	(U66264) ubiquitin [Nicotiana tabacum]

Seq. No.	140150

Seq. ID	LIB24-115-Q1-E1-G5
Method	BLASTN
NCBI GI	g3869074
BLAST score	129
E value	2.0e-66
Match length	249
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMI9, complete sequence [Arabidopsis thaliana]

Seq. No.	140151
Seq. ID	LIB24-116-Q1-E1-A2
Method	BLASTX
NCBI GI	g4538963
BLAST score	271
E value	3.0e-24
Match length	53
% identity	100
NCBI Description	(AL049488) chlorophyll a/b-binding protein-like [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1 (AF134129) Lhcb5 protein [Arabidopsis thaliana]

Seq. No.	140152
Seq. ID	LIB24-116-Q1-E1-A8
Method	BLASTN
NCBI GI	g2244747
BLAST score	205
E value	1.0e-111
Match length	396
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	140153
Seq. ID	LIB24-116-Q1-E1-C2
Method	BLASTX
NCBI GI	g1402904
BLAST score	657
E value	4.0e-69
Match length	126
% identity	100
NCBI Description	(X98313) peroxidase [Arabidopsis thaliana]

Seq. No.	140154
Seq. ID	LIB24-116-Q1-E1-C4
Method	BLASTN
NCBI GI	g4757392
BLAST score	84
E value	8.0e-40
Match length	148
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K14A17, complete sequence

Seq. No.	140155
Seq. ID	LIB24-116-Q1-E1-D7
Method	BLASTN

NCBI GI	g4581084
BLAST score	373
E value	0.0e+00
Match length	377
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC T30F21 genomic sequence, complete sequence

Seq. No.	140156
Seq. ID	LIB24-116-Q1-E1-D8
Method	BLASTX
NCBI GI	g2618725
BLAST score	637
E value	9.0e-67
Match length	144
% identity	89
NCBI Description	(U49074) IAA18 [Arabidopsis thaliana]

Seq. No.	140157
Seq. ID	LIB24-116-Q1-E1-D9
Method	BLASTN
NCBI GI	g4159712
BLAST score	119
E value	1.0e-60
Match length	214
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWI23, complete sequence

Seq. No.	140158
Seq. ID	LIB24-116-Q1-E1-E10
Method	BLASTX
NCBI GI	g464707
BLAST score	582
E value	2.0e-60
Match length	115
% identity	100
NCBI Description	40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal protein S18.A - Arabidopsis thaliana >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]

Seq. No.	140159
Seq. ID	LIB24-116-Q1-E1-E4
Method	BLASTX
NCBI GI	g2623990